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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: July 16, 2003, 19:41:51 ; Search time 937.041 Seconds

(without alignments)

3404.880 Million cell updates/sec

Title: US-09-917-265-50

Perfect score: 994

Sequence: 1 RSLPTASRSPGIFQCLNHSO.....HAFRIRAVTIDRMSYLNSS 197

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame.p2n.model -DEV=xlh
-O=/cgn2_1/USPTO/spool/US09917265/runat_15072003_092107_1610/app.query.fasta_1_3114
-DB=EST -QFMT=fastlap -SUFIX=p2n.rst -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biom62 -TRANS=human40.cdi -LIST=45
-LOCALIGN=200 -THR.SCORE=PCT -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=Pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09917265.ecgn_1_1_6304.qrunat_15072003_092107_1610 -NCPU=6 -ICPU=3
-NO_MMAPP -LARGEOUERY -NEG.SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOC
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST :
1: em_estba : *
2: em_esthum : *
3: em_estlin : *
4: em_estlmu : *
5: em_estrov : *
6: em_estrpl : *
7: em_estro : *
8: em_hlc : *
9: gb_est1 : *
10: gb_est2 : *
11: gb_hlc : *
12: gb_est3 : *
13: gb_est4 : *
14: gb_est5 : *
15: em_estlun : *
16: em_estom : *
17: gb_gss : *
18: em_gss_hum : *
19: em_gss_inv : *
20: em_gss_pln : *
21: em_gss_vrt : *
22: em_gss_fun : *
23: em_gss_mam : *
24: em_gss_mus : *
25: em_gss_other : *
26: em_gss_pro : *
27: em_gss_pod : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 394.5 | 39.7 | 812 | 12 | BG702253 |
| 2 | 391 | 39.3 | 589 | 9 | AI050362 |
| 3 | 384 | 38.6 | 1099 | 13 | B1523344 |
| 4 | 335 | 33.7 | 373 | 12 | BF552757 |
| 5 | 305 | 30.7 | 832 | 13 | B1523569 |
| 6 | 176.5 | 17.8 | 342 | 13 | BM257856 |
| 7 | 131 | 13.2 | 447 | 13 | B1824638 |
| 8 | 104 | 10.5 | 528 | 9 | AI332701 |
| 9 | 98 | 9.9 | 982 | 17 | CNS06H7X |
| 10 | 94 | 9.5 | 880 | 14 | BQ420717 |
| 11 | 93.5 | 9.4 | 1007 | 14 | BM904933 |
| 12 | 93 | 9.4 | 928 | 17 | A2541842 |
| 13 | 92 | 9.3 | 786 | 17 | BH249132 |
| 14 | 91 | 9.2 | 994 | 14 | BQ222548 |
| 15 | 90.5 | 9.1 | 811 | 9 | AL557307 |
| 16 | 90.5 | 9.1 | 932 | 9 | AL548620 |
| 17 | 90.5 | 9.1 | 1017 | 13 | BM552614 |
| 18 | 90.5 | 9.1 | 1171 | 13 | BM467146 |
| 19 | 90.5 | 9.1 | 1398 | 11 | BC004543 |
| 20 | 90.5 | 9.1 | 1398 | 11 | BC014060 |
| 21 | 90 | 9.1 | 563 | 10 | AW657864 |
| 22 | 89 | 9.0 | 504 | 10 | BE336896 |
| 23 | 89 | 9.0 | 939 | 14 | BQ072253 |
| 24 | 89 | 9.0 | 1127 | 13 | BM554145 |
| 25 | 88 | 8.9 | 852 | 17 | BH157950 |
| 26 | 88 | 8.9 | 944 | 17 | BH133696 |
| 27 | 88 | 8.9 | 1071 | 17 | CNS07688 |
| 28 | 87.5 | 8.8 | 403 | 14 | BQ201205 |
| 29 | 87.5 | 8.8 | 684 | 12 | BF047027 |
| 30 | 87.5 | 8.8 | 755 | 12 | BE86561 |
| 31 | 87.5 | 8.8 | 871 | 13 | B1217873 |
| 32 | 87 | 8.8 | 1004 | 11 | AK013272 |
| 33 | 87 | 8.8 | 1060 | 14 | BQ068020 |
| 34 | 86 | 8.7 | 637 | 13 | BJ419292 |
| 35 | 86 | 8.7 | 653 | 9 | AF179467 |
| 36 | 86 | 8.7 | 897 | 17 | A2675904 |
| 37 | 85.5 | 8.6 | 730 | 12 | BF384131 |
| 38 | 85.5 | 8.6 | 1003 | 13 | BM459145 |
| 39 | 85 | 8.6 | 358 | 9 | AA282459 |
| 40 | 85 | 8.6 | 568 | 10 | BB610019 |
| 41 | 85 | 8.6 | 714 | 13 | B1149083 |
| 42 | 85 | 8.6 | 771 | 12 | BG620068 |
| 43 | 85 | 8.6 | 771 | 13 | BG21069 |
| 44 | 85 | 8.6 | 812 | 13 | B1158376 |
| 45 | 85 | 8.6 | 957 | 12 | BF385608 |

ALIGNMENTS

| RESULT 1 | 812 bp | mrna | linear | EST 07-MAY-2001 |
|------------|--------|------|--------|-----------------|
| BG702253 | | | | |
| LOCUS | | | | |
| DEFINITION | | | | |
| ACCESSION | | | | |
| VERSION | | | | |
| KEYWORDS | | | | |
| SOURCE | | | | |
| ORGANISM | | | | |
| REFERENCE | | | | |
| AUTHORS | | | | |
| TITLE | | | | |

| | | | |
|------------------------|---|--|------------------------------|
| Oy | 92 | GLYLYSALASerPheMetThrValLeuYsLeuSerTlETyGluAspLeuYsMet | 111 |
| Db | 288 | CAGAAAGACGCTTTTGATATATACACCTGTGGCTTGATACATCTATAGAGACTTGAAAGATG | 347 |
| Oy | 112 | TyGlnMetGluPheYsAlaMetAsnAlaYsLeuMetAspProLYsArgGlnLe | 131 |
| Db | 348 | TACACAGACAGCTTCACGCCATCACACACAGACTTCAGAAATCACACCATCAGCAGATC | 407 |
| Oy | 132 | PheLeuAspGlnAsnMetLeuThrAlaAlleAspGluLeuGlnAlaLeuAsnPheAsn | 151 |
| Db | 408 | ATTCTAGACAAAGGACATCTGGTGCCATGCATGACGTGATGACACTCTCAATCATTAAT | 467 |
| Oy | 152 | serVa1ThrValProGlnIys | 158 |
| Db | 468 | GCCGAGACTCTGCCCGACGAA | 488 |
| RESULT 3 | | | |
| B1523344/c | | | |
| LOCUS | B1523344 | 1099 bp | mRNA |
| DEFINITION | 603175938r1 NIH_MGC_121 | Homo sapiens | CDNA clone IMAGE:5240216 3', |
| ACCESSION | B1523344 | | |
| VERSION | B1523344.1 | GI:15348136 | |
| KEYWORDS | EST. | | |
| SOURCE | human. | | |
| ORGANISM | Homo sapiens | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| AUTHORS | Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. | | |
| TITLE | 1 (bases 1 to 1099) | | |
| JOURNAL | NIH-MGC http://mgc.ncl.nih.gov/ . | | |
| COMMENT | Unpublished (1999) | | |
| | Contact: Robert Strausberg, Ph.D. | | |
| | Email: cgabers-remail.nih.gov | | |
| | Tissue Procurement: Life Technologies, Inc. | | |
| | CDNA Library Preparation: Life Technologies, Inc. | | |
| | CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) | | |
| | DNA Sequencing by: Incyte Genomics, Inc. | | |
| | clone distribution: MGC clone distribution information can be | | |
| | found through the I.M.A.G.E. Consortium/LLNL at: | | |
| | http://image.llnl.gov | | |
| | Plate: LLAM1605 row: 1 column: 09 | | |
| | High quality sequence start: 40 | | |
| | High quality sequence stop: 727. | | |
| FEATURES | | | |
| source | 1..1099 | | |
| | /organism="Homo sapiens" | | |
| | /db_xref="taxon:9606" | | |
| | /clone="IMAGE:5240216" | | |
| | /clone_1fb="NIH_MGC_121" | | |
| | /lab_host="DH10B" | | |
| | /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; | | |
| | Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 | | |
| | fetal brains, female age 20 weeks, female age 24 weeks, | | |
| | and male age 26 weeks. Library is oligo-dT primed and | | |
| | directionally cloned (EcoRV site 1.7 kb, insert size range | | |
| | 0.7-3.5 kb. Library is normalized and enriched for | | |
| | full-length clones and was constructed by C. Gruber | | |
| | (Invitrogen). Research Genetics tracking code 017. Note: | | |
| | this is a NIH_MGC Library." | | |
| BASE COUNT | 359 a | 244 c | 218 g |
| ORIGIN | | 276 t | 2 others |
| Alignment Scores: | | | |
| Pred. NO.: | 6,04e-38 | Length: | 1099 |
| Score: | 384.00 | Matches: | 86 |
| Percent Similarity: | 90.10% | Conservative: | 5 |
| Best Local Similarity: | 85.15% | Mismatches: | 7 |
| Query Match: | 38.63% | Indels: | 4 |
| DB: | 13 | Gaps: | 0 |

| FEATURES | Source |
|-----------|--|
| REFERENCE | 1 (bases 1 to 373) |
| AUTHORS | Bonaldo, M.F., Lennon, G. and Soares, M.B. |
| TITLE | Normalization and subtraction: two approaches to facilitate gene discovery |
| JOURNAL | Genome Res. 6 (9), 791-806 (1996) |
| MEDLINE | 97044477 |
| COMMENT | Contact: Soares, MB Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565 Email: msoares@blue.weeg.uiowa.edu cDNA Library Preparation: M.B. Soares Lab Clone distribution: Clones will be available through Research Genetics (www.resgen.com) This clone is also available through the I.M.A.G.E. Consortium at LMU. (info@image.llnl.gov). IMAGE ID= 1782759 Seq primer: M13 Forward. |
| FEATURES | Location/Qualifiers |
| Source | 1..373 |
| | /organism="Rattus norvegicus" |
| | /strain="Sprague-Dawley" |
| | /db_xref="taxon:10116" |
| | /clone="UI-R-C0-12-d-02-0-UI" |
| | /clone_lib="UI-R-C0" |
| | /dev_stage="adult" |
| | /note="DH10B (Life Technologies)" |
| | /map="vector: pRT3D-Pac (Pharmacia) with a modified |
| | polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C0 |
| | library is a subtracted library derived from the UI-R-A1 |
| | and UI-R-E1 libraries. The UI-R-A1 library consisted of a |
| | mixture of individually tagged normalized libraries |
| | constructed from rat placenta, adult lung, brain, liver, |
| | kidney, heart, spleen, ovary, and muscle. The UI-R-E1 |
| | library consisted of a mixture of individually tagged |
| | normalized libraries constructed from 8, 12 and 18-day |
| | embryo. The tag is a string of 3-5 nucleotides present |
| | between the Not I site and the oligo-dT track which |

```
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLML1605 row: 1 column: 09  
High quality sequence start: 23  
High quality sequence stop: 821  
Location/Qualifiers  
1..832  
/organism="Homo sapiens"  
/db_xref="GeneBank:"
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FEATURES
Source

Location/Qualifiers
1. .832

High quality sequence start: 23
High quality sequence stop: 821.

image: /usr/share/fonts/truetype/freefont/FreeMono-9.ttf
LAME11605 row: 1 column: 05
utf sequence start: 33

through the I.M.A.G.E. Consortium
made.11n1.gov

sequencing by: Incyte Genomics, Inc.
distribution: MGC clone distribution information can be

Library Preparation: Life Technologies, Inc.
Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Procurement: Life Technologies, Inc.
Library Preparation: Life Technologies, Inc.

page

TITLE
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle

JOURNAL
Genome Res. 11 (4), 626-630 (2001)

MEDLINE
21180013

COMMENT
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt-trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACACCTATGACCAT
BACKWARD: GTTTTCGAGTCAGCAGC
Plate: 125 row: E column: 18
Seq primer: ATTACGTGACACTATAG.
Location/Qualifiers
1..342
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 380V"
/issue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."

BASE COUNT
67 a 135 c 74 g 66 t

ORIGIN
Alignment Scores:
Pred. No.: 2,55e-12 Length: 342
Score: 176.50 Matches: 37
Percent Similarity: 86.96% Conservative: 3
Best Local Similarity: 80.43% Mismatches: 5
Query Match: 17.76% Indels: 1
DB: 13 Gaps: 1

US-09-917-265-50 (1-197) x BM257856 (1-342)

QY 1 ArgSerLeuProThrAlaSerProSerProGlyLlePhehdIncysLeuAsnHisserGln 20
|||||
Db 207 AGGAGCCTCCGCCACACACAGCAGACCCAGCA---AGCAGCTGCTCGACTCCCAA 263
QY 21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 40
|||||
Db 264 AACCTGCTGAGGCTGTGACGACAGCAGCCTACAGACAGCCAGACAACCTAGAAATTTTAC 323
QY 41 SerCysThrSerGluGlu 46
|||||
Db 324 TCCTCCACTTGTGAGAG 341

RESULT 7
BI824638 447 bp mRNA linear EST 04-OCT-2001
LOCUS
DEFINITION
603033580F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5175018 5',
mRNA sequence.
ACCESSION
BI824638
VERSION
BI824638.1 GI:15936188
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
NIH-MGC <http://mgc.ncl.nih.gov/>
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM1435 row: 0 column: 19
High quality sequence start: 3
High quality sequence stop: 445.
Location/Qualifiers
1..447
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:5175018"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector:
PCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH-MGC Library."

BASE COUNT
149 a 63 c 87 g 148 t

ORIGIN
Alignment Scores:
Pred. No.: 2,75e-06 Length: 447
Score: 131.00 Matches: 26
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 92.86% Mismatches: 0
Query Match: 13.18% Indels: 0
DB: 13 Gaps: 0

US-09-917-265-50 (1-197) x BI824638 (1-447)

QY 170 LysIleLysLeuGlySileLeuLeuHisAlaPheArgIleArgAlaValThrIleAspArg 189
|||||
Db 1 AAATCAAGCTGTGACTCTTTCATGCTTTCAGAAATTCGGCAGTATGTAGAGA 60
QY 190 MetMetSerTyrIleuAsnSerSer 197
:::
Db 61 GTGATGAGCTATCTGAATGCTTCC 84

RESULT 8
AI332701 528 bp mRNA linear EST 13-FEB-1999
LOCUS
DEFINITION
q919607.x1 Soares_NhMHPu_S1 Homo sapiens cDNA clone IMAGE:1932948
3', similar to gb:M65291 INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (HUMAN
);, mRNA sequence.
ACCESSION
AI332701
VERSION
AI332701.1 GI:4069260
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
COMMENT
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1469 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 451.


```

Db      380 GTGCTGGATCGGATTAATCTGTTCCACA-----ATGCTT 418
Qy      100 LeucylserSerIleTyrGluAspLeuMetyrGlnMetGluPhelysAlaMet 119
         |||||
Db      419 ACTAGTCTTTCTTCATATTTCTCA-----GCATTCAAGGTGAG 457
Qy      120 AsnAlaLysLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThr 139
         ||| |||||
Db      458 AATTGCCACTGTTGCACGCCGACTTCAAGTATTTCTTGAAATTCAGTACCCAAAT 517
Qy      140 AlaIleAspGluLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSer 159
         ||| |||||
Db      518 GCGTCGATCATATGATGATGCA-----AACTCGACTACTTTTCCCAAGATTCC 568
Qy      160 SerLeu 161
         |||||
Db      569 TCGTTG 574

RESULT 10
BQ420717      880 bp      mRNA      linear      EST 23-MAY-2002
LOCUS      BQ420717
DEFINITION      AGENCOURT_7771502 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:6019246
ACCESSION      BQ420717
VERSION      BQ420717.1 GI:21116032
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 880)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cga@bbs-femail.nih.gov
              Tissue Procurement: ATCC
              CDNA Library Preparation: Life Technologies, Inc.
              DNA Sequencing by: Agencourt Bioscience Corporation
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLAM13221 row: 9 column: 23
              High quality sequence stop: 649.
FEATURES
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        location/Qualifiers
            1..880
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:6019246"
                /clone_lib="NIH_MGC_70"
                /tissue_type="epithelial carcinoma"
                /lab_host="DH10B (phage-resistant)"
                /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: NotI;
                Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                Average insert size 1.1 kb. Library constructed by Life
                Technologies."
BASE COUNT      276 a      198 c      232 g      174 t
ORIGIN
Alignment Scores:
Pred. No.:      0.512      Length:      880
Score:          94.00      Matches:      44
Best Local Similarity: 44.00%      Conservative: 22
                    29.33%      Mismatches:      34
Query Match:    9.46%      Indels:      30
DB:             14      Gaps:      8

US-09-917-265-50 (1-197) x BQ420717 (1-880)
Qy      16 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeu---GlnLysAlaArg 34
         ||| ||||| |||||
Db      342 CTCGAAGACAGAACGACGCTGTAGAACCCCTCAACAGCAGTTGCACGACGAGTTGACT 401

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```

Qy      35 GlnThrLeuGluLeuTyrSerCysThrSerGluGlnIleAspHisGluAspIleThrLys 54
         ::|||
Db      402 GAAACT-----CAGGAGAGCTGAG 422
Qy      55 AspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCys 74
         ||| |||||
Db      423 GACCTGACCCCAAGAGGTAG-----CTGCTGGAAGAACTTCGGGACAACGT 470
Qy      75 LeuAla-----SerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
         ||||| |||||
Db      471 TTGGCAATTTTGGAGAGCAGGAGGCTTCATCCAGCTTAGCGGAGAGACCTGCGACATCA 530
Qy      92 GlyLysAlaSer-----PheMetThrValLeuCysLeuSerSerIleTyrGlu 107
         ::||| |||||
Db      531 CGACAGAAATCCACTACTGATGATCAGATGAGATGCTATGTTGCTTGAACACTTTGCAAGAG 590
Qy      108 AspLeuLysMetyr-----GlnMet---GluPheLysAlaMetAsn 120
         ::||| |||||
Db      591 GAGCTGAAGCTTTTAAACGAAACAGCCAAAGAGATGAGAGATTACAGGCTTAAAG 650
Qy      121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeu----- 138
         . ||||| |||
Db      651 GTAAAGCTGGAGATGAAGAGAAAGATCCGATTCCTAAGAACGAAACCTTATGTAAAC 710
Qy      139 ThrAlaIleAspGluLeuGlnAlaLeu 148
         ::||| |||||
Db      711 AATCAAGTAAATGATTAAACACAGCCCTTA 740

RESULT 11
BQ604933      1007 bp      mRNA      linear      EST 12-MAR-2002
LOCUS      BQ604933
DEFINITION      AGENCOURT_6699344 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5557760
ACCESSION      BQ604933
VERSION      BQ604933.1 GI:19355312
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 1007)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cga@bbs-femail.nih.gov
              Tissue Procurement: ATCC/DCTD/DTF
              CDNA Library Preparation: Life Technologies, Inc.
              DNA Sequencing by: Agencourt Bioscience Corporation
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLAM12279 row: k column: 09
              High quality sequence stop: 638.
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        location/Qualifiers
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                /db_xref="taxon:9606"
                /clone="IMAGE:5557760"
                /clone_lib="NIH_MGC_72"
                /tissue_type="melanotic melanoma"
                /lab_host="DH10B (phage-resistant)"
                /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                Average insert size 2 kb. Library constructed by Life
                Technologies."
BASE COUNT      312 a      231 c      256 g      208 t
ORIGIN
Alignment Scores:
Pred. No.:      0.758      Length:      1007

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|------------------------|--------|---------------|----|
| Score: | 93.50 | Matches: | 47 |
| Percent Similarity: | 41.76% | Conservative: | 24 |
| Best Local Similarity: | 27.65% | Mismatches: | 51 |
| Query Match: | 9.41% | Indels: | 48 |
| DB: | 14 | Gaps: | 8 |

US-09-917-265-50 (1-197) x BM904933 (1-1007)

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| OY | | 16 | LeuansnHisSerGlnAsnIleuLeuArgAlaValSerAsnThrLeu--- | GlnLysAlaArg | 34 |
| Db | | 349 | CTCAAGCAGAACAACACACTGTGTGAAGACCCTCAACAAGCACTTGCACACAAAGTTGACT | | 408 |
| OY | | 35 | GlnThrIeuGluLeuTYrSerCysThrSerglueGluIleaspHISgluaSplLeuThrllys | ---: | 54 |
| Db | | 409 | GAACCT----- | -----CAGGAGAGCTGAAG | 429 |
| OY | | 55 | AspYsrThrSerThrValGluAlaCysLeuProIeuGluLeuThrMetAsnGlusercys | 74 | |
| Db | | 430 | GACCTGACCCAGAAAGTAGAG----- | -TCGTGGAGAACATTGGGACAAACGT | 477 |
| OY | | 75 | LeuAlaI-----SerArgGluIleSerIeuiIleThrAsnGlySerCysLysalaser | 91 | |
| Db | | 478 | TTCGCAATTTTGAGAGCAAGGCCCTTATCCAGCTTTAAGCACAGACACCTCGCATCA | | 537 |
| OY | | 92 | GlyLysalaser----- | -PheMetThrValLeuCysLeuSerSerIetyrglu | 107 |
| Db | | 538 | CGACAAGATCCACTACTGATACATGAGCTCTATGCTGTGTGAATACTTTGCCAAGAG | 597 | |
| OY | | 108 | AspLeuIysMetTy----- | -Glnmet---GluPhelAlaMetasn | 120 |
| Db | | 598 | GAGCTGAAGCTTTTAAACGAACAACCCAAAAAGCAGATGAGAGATTACAGGCTTAAG | 657 | |
| OY | | 121 | AlaLysLeuLeuMetaspProLysArsglInIlePheLeuAspGln----- | 135 | |
| Db | | 658 | GTAAGAGCTGGAGATGAAGAGAAAGAGCTCGATTCTTGAAGAACACCAAACCTATGTATAC | 717 | |
| OY | | 136 | ----- | -AsmMetLeuThrAlaIleaspGluLeuGlnAlaIleuasnPheasn | 151 |
| Db | | 718 | AATCAAGTAAATGATTTAAACAACACCCTTAAGCAAAATGAGACAGCTATTAGAATGTGA | 777 | |
| OY | | 152 | SerValThrValProGlnLysSerSerIeu | 161 | |
| Db | | 778 | GAAGAAACAGTGGCCAGATGGCTCCTC | 807 | |
| RESULT 12 | | | | | |
| AZ541842/c | | | | | |
| LOCUS | | AZ541842 | 928 bp | DNA | linear GSS 14-NOV-2000 |
| DEFINITION | | ENFER19TR Entamoeba histolytica sheared DNA | | | Entamoeba histolytica genomic, DNA sequence. |
| ACCESSION | | AZ541842 | | | |
| VERSION | | AZ541842.1 | GI:11149954 | | GSS. |
| KEYWORDS | | | | | |
| SOURCE | | | | | |
| ORGANISM | | | | | Entamoeba histolytica. Entamoebidae: Entamoeba. Eukaryota; Eumetazoa; Loftus,B., Van Aken,S. and Fraser,C. Determination of clone end sequences from Entamoeba histolytica HMI:IMSS sheared DNA library Unpublished (2000) |
| JOURNAL COMMENT | | | | | Contact: Brendan J Loftus Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0208 Fax: 301 838 3543 Email: b1loftus@tigr.org Clones are derived from the Entamoeba histolytica HMI:IMSS sheared DNA library Seq primer: M13--Reverse Class: shotgun High quality sequence start: 16 High quality sequence stop: 808. |

FEATURES
Source

| FEATURES | SOURCE |
|---------------------|--|
| Location/Qualifiers | 1. .928 |
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| | /strain="HMI:IMSS" |
| | /db_xref="taxon:5759" |
| | /clone_lib="Entamoeba histolytica Sheared DNA" |
| | /note="Vector: pHOSt1 Site_1: Bst I; Constructed at The |
| | Institute for Genomic Research (TIGR), Rockville, MD. |
| | Genomic DNA isolated from broth cultures of E. histolytica |
| | using a method described by Clark and Diamond (Clark, |
| | C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a |
| | method for isolate identification. Exp. Parasitol. |
| | 77:450.). The DNA was mechanically sheared to give a |
| | light size distribution (~2 kb). The v + i method used for |
| | the library construction is described in detail in Smith, |
| | H.O. and Venter, J.C. (Making small insert libraries for |
| | Whole genome shotgun sequencing projects. In Genome |
| | Sequencing: A Practical Approach, eds. M. Vaund and B. |
| | Barrell, Oxford University Press, 1999)." |

| | | | | |
|------------|-------|-------|-------|-------|
| BASE COUNT | 320 a | 120 c | 151 g | 337 t |
| ORIGIN | | | | |

ORIGIN

Alignment Scores:

| | | | |
|------------------------|--------|---------------|----|
| Pred. No.: | 0.757 | length: | 92 |
| Score: | 93.00 | Matches: | 47 |
| Percent Similarity: | 43.53% | Conservative: | 27 |
| Best Local Similarity: | 27.65% | Mismatches: | 67 |
| Query Match: | 9.36% | Indels: | 29 |
| DB: | 17 | Gaps: | 9 |

US-09-917-265-50 (1-197) x AZ541842 (1-928)

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|----|-----|---|-----|
| QY | 1 | AspHisSerGlnAsnLeuLeuAlaArgAlaValSerSnrThrLeuGlnLysAlaArg----- | 34 |
| | | | |
| Db | 625 | AAACATCATTTACTATTATTTACCTTACAAAAGACATGTTTATATCAGAAAGATTATAC | 566 |
| QY | 35 | --GlnThrLeuGluLeuTySerCysThrSer-GluGluLe----- | 47 |
| | | | |
| Db | 565 | TGTAAACCTAGTGCCTTGGAGGTGCACACTATCAGACACATTTATATTAAGAAACC | 506 |
| QY | 48 | ----AspHisGluAspIleThrLysAspLysThrSerThrVal----- | 64 |
| | | | |
| Db | 505 | AAACGATCATCAATAATATCAAGAAGATTATTAATATGATTGTAAAGCTGAATATCAATC | 446 |
| QY | 64 | uProLeuGluLeuThrMetLeuAsnGlySerCysLeuAlaSerArgGluIleSerLeuIleTh | 84 |
| | | | |
| Db | 445 | TCCGGAATGATGATATTTATTTATGAAATCAACCATTTAGTGGAAAAAGATATCTGGGC | 386 |
| QY | 84 | rAsnGlySerCysLeu-----AlaSerGlyLysAlaSerPheMetThrValLeuCy | 101 |
| | | | |
| Db | 385 | ACTTGATGTTTATTTGTTGTGAGACTGCATATGGAAACACCATCTCTCGACACCTTTG | 326 |
| QY | 101 | sLeuSerSerIleTyrglu--AspLeuLysMetTyrglnMetGlnPheLysAlaMetAs | 120 |
| | | | |
| Db | 325 | CATTTCGATGATAAACAATTAGATTATTAAGTATTCAGTAAATGTCA--AAACGAATGAA | 269 |
| QY | 120 | nAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln-----As | 136 |
| | | | |
| Db | 268 | ATCTTACTT-----AAAGAAATCCTGTTTTCATCATCAAAATTAACGGCCTAA | 221 |
| QY | 136 | mMetLeuThrAlaIleaspGluLeuLeuGlnAlaLeuAsnDheAsnSerValIThrValPr | 156 |
| | | | |
| Db | 220 | TATATACATATCTAGAACATTTTATAGCAGAGTTGTGATTTAATAAC-----CC | 170 |
| QY | 156 | oGlnLysSerSerLeuGlnLysProasp | 165 |
| | | | |
| Db | 169 | ATATAATCATTTATGAAGAAACTGAT | 142 |

RESULT 13

LOCUS BH249132

DEFINITION BCGAT194Tfr BCGA Brassica oleracea genomic clone BCGAT194, DNA Sequence.

786 bp DNA linear GSS 26-NOV-2001


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QY      121 AlAlysLeuLeuMetaspProLysArgGlnIlePheLeuAspGlnAsnMetLeu----- 138
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Db      656 GTAAGCTGTGAGTAAAGAGCAAGAGCCGATTCCTAGACAGCAAACTTATGTAAAC 715
QY      139 ThrAlaIleAspGlnLeuGlnAlaLeu-----AspPhe 150
      :|||:||||| |||||
Db      716 AATCAAGTAATGATTTTAACACACAGCCCTTTAGGAATGAGACAGCTATTAGAAATGTA 775
QY      151 AsnSerValThrValProGlnLysSerSerLeu 161
      ||| ||| :|||:|||||
Db      776 AGAAGACAGCAAGTGGCCGAGATGGCTCCCTC 808

RESULT 15
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LOCUS      AL557307
DEFINITION      AL557307 LIT_FL012.TC1 Homo sapiens cDNA clone CS0DH004YG21 5 prime
              ' mRNA sequence.
ACCESSION      AL557307
VERSION      AL557307.1 GI:12900784
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE      Li,W.B., Gruber,C., Jesse,J., and Polayes,D.
JOURNAL      Full-length cDNA libraries and normalization
COMMENT      Unpublished (2001)
CONTACT      Genoscope
GENOSCOPE      Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segreff@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
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        1..811
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            /lab_host="DH108"
            /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
            with a NotI-oligo(dT) primer. Five prime end enriched,
            double-stranded cDNA was digested with Not I and cloned
            into the Not I and Eco RV sites of the pCMVSPORT 6 vector.
            Library was constructed by life technologies. Contact :
            Feng Liang Life Technologies, a division of Invitrogen
            9600 Medical Center Drive Rockville, Maryland 20850, USA
            Fax : (1) 301 610 8371 Email : fliang@lifestech.com URL :
            http://fulllength.invitrogen.com"
BASE COUNT      268 a 173 c 209 g 156 t 5 others
ORIGIN
Alignment Scores:
Pred. No.:      1..24      Length:      811
Score:          90.50      Matches:      45
Percent Similarity: 42.04%      Conservative: 21
Best Local Similarity: 28.66%      Mismatches: 50
Query Match:    9.10%      Indels:      41
DB:            9          Gaps:      8

US-09-917-265-50 (1-197) x AL557307 (1-811)
QY      16 LeuAsnHisSerGlnAsnLeuArgAlaValSerAsnThrLeu---GlnLysAlaArg 34
      ||||| ||||| |||||:|||||
Db      373 CTCAGGACACAGACCAAGCTGTAGAAAGCCGTACACAGAGCTTGACCAAGATTGACT 432
QY      35 GlnThrLeuGlnLeuTyrSerCysThrSerGlnGlnIleAspHisGlnLysPrlleThrLys 54
      :|||:||||| |||||
Db      433 GAAACT-----CAGGAGAGAGCTGAAG 453
QY      55 AspLysThrSerThrValGlnAlaCysLeuProLeuGlnLeuThrMetAsnGlnSerCys 74
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```

```

Db      454 GACCTGACCCGAGAGGTAGAG-----CTGCTGGAGAGATTTCGGGACCAACTGT 501
QY      75 LeuAla-----SerArgGlnIleSerLeuIleThrAsnLysSerCysLeuAlaSer 91
      ||||| ||||| :|||:|||||
Db      502 TTGGCAATTTTGGAGAGCAAGGCGCTTGATCCAGCTTTAGCGATGAGACCCCTGGCATCA 561
QY      92 GlyLysAlaSer-----PheMetThrValLeuCysLeuSerSerLleTyrGlu 107
      :||| ||| :|||:||||| |||||
Db      562 CGACAGAAATCCACTACTGATCAGATGACATGACTCTATGTTGCTGTAGAAACTTTGCAAGAG 621
QY      108 AspLeuLysMetLys-----GlnMet---GlnPheLysAlaMetAsn 120
      :|||:|||||:|||||
Db      622 GAGCTGAAGCTTTTAAACGAAGACCAAGAGAGGAGGATTACAGAGCTTTAAAG 661
QY      121 AlAlysLeuLeuMetaspProLysArgGlnIlePheLeuAspGlnAsnMetLeu----- 138
      ||||| ||| :||| |||||:|||||
Db      682 GTAAGCTGTGAGTAAAGAGCAAGAGCCGATTCCTAGACAGCAAACTTATGTAAAC 741
QY      139 -----ThrAlaIleAspGlnLeuGlnAlaLeu 148
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Db      742 AATCAAGTAATGATTTTAACACACAGCCCTTTAGGAATGAGACAGCTATTA 792

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Search completed: July 17, 2003, 09:27:01
 Job time : 940.041 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_p2n model

Run on: July 16, 2003, 19:43:49 ; Search time 27.7808 Seconds
(without alignments)
2174.711 Million cell updates/sec

Title: US-09-917-265-50

Perfect score: 994
Sequence: 1 RSLPTASPGIFGCLNHSQ.....HAFRIRAVTIDRMSTYLNSS 197

Scoring table:

BLOSUM62
Xgapop 10.0 , Ygapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame-p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US09917265/runat_15072003_092107_1619/app-query.fasta_1.3114
-DB=Issued_Patents_NA -QPM=fastat -SUFFIX=p2n.rn1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS-human40.cdl
-LIST=45 -DOCALIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=p2n -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09917265.@CGN_1.1.119.@runat_15072003_092107_1619 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NLS_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -DELOP=6 -DELEX=7

Database : Issued Patents_NA.*

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2: /cgn2_6/plodata/1/lna/5B.COMB.seq.*
3: /cgn2_6/plodata/1/lna/6A.COMB.seq.*
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5: /cgn2_6/plodata/1/lna/PCrus.COMB.seq.*
6: /cgn2_6/plodata/1/lna/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 994 | 100.0 | 669 | 4 | US-09-079-984A-12 |
| 2 | 989 | 99.5 | 669 | 4 | US-09-079-984A-2 |
| 3 | 875 | 88.0 | 660 | 1 | US-08-186-529-3 |
| 4 | 875 | 88.0 | 660 | 1 | US-08-640-386A-3 |
| 5 | 875 | 88.0 | 762 | 4 | US-08-848-760B-21 |
| 6 | 875 | 88.0 | 1316 | 2 | US-08-684-687-3 |
| 7 | 875 | 88.0 | 1316 | 4 | US-09-851-520-3 |
| 8 | 875 | 88.0 | 1364 | 1 | US-08-265-087-3 |
| 9 | 875 | 88.0 | 1364 | 1 | US-08-621-493-3 |
| 10 | 875 | 88.0 | 1364 | 2 | US-08-965-688-3 |
| 11 | 875 | 88.0 | 1364 | 4 | US-09-260-173-3 |
| 12 | 875 | 88.0 | 1645 | 4 | US-09-310-842-2 |

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| 13 | 869 | 87.4 | 721 | 2 | US-08-184-009-199 | Sequence 199, App |
| 14 | 869 | 87.4 | 721 | 2 | US-08-458-356-199 | Sequence 199, App |
| 15 | 869 | 87.4 | 721 | 4 | US-08-460-736-199 | Sequence 199, App |
| 16 | 869 | 87.4 | 1026 | 2 | US-08-751-767A-1 | Sequence 1, Appl1 |
| 17 | 868 | 87.3 | 1560 | 2 | US-08-751-767A-11 | Sequence 11, Appl1 |
| 18 | 868 | 87.3 | 1623 | 2 | US-08-751-767A-9 | Sequence 9, Appl1 |
| 19 | 868 | 87.3 | 6139 | 2 | US-08-751-767A-7 | Sequence 7, Appl1 |
| 20 | 553 | 55.6 | 713 | 2 | US-08-385-335A-10 | Sequence 10, Appl1 |
| 21 | 518 | 52.1 | 6295 | 2 | US-08-650-206A-4 | Sequence 4, Appl1 |
| 22 | 518 | 52.1 | 7287 | 4 | US-08-650-206A-1 | Sequence 1, Appl1 |
| 23 | 88.5 | 8.9 | 7577 | 4 | US-08-961-527-46 | Sequence 46, Appl1 |
| 24 | 86.5 | 8.7 | 1853 | 1 | US-07-849-438-2 | Sequence 2, Appl1 |
| 25 | 85.5 | 8.6 | 4868 | 1 | US-08-139-937-12 | Sequence 12, Appl1 |
| 26 | 85.5 | 8.6 | 4868 | 5 | PCT-US93-11310-12 | Sequence 12, Appl1 |
| 27 | 84.5 | 8.5 | 8789 | 1 | US-08-328-254-5 | Sequence 5, Appl1 |
| 28 | 83.5 | 8.4 | 10136 | 1 | US-08-353-700-2 | Sequence 2, Appl1 |
| 29 | 83.5 | 8.4 | 10136 | 5 | PCT-US95-16216-2 | Sequence 2, Appl1 |
| 30 | 80.5 | 8.1 | 675 | 4 | US-08-209-603E-12 | Sequence 12, Appl1 |
| 31 | 79.5 | 8.0 | 5599 | 2 | US-08-477-451-9 | Sequence 9, Appl1 |
| 32 | 79.5 | 8.0 | 5599 | 2 | US-08-477-451-13 | Sequence 13, Appl1 |
| 33 | 78.5 | 7.9 | 7308 | 4 | US-09-011-745-3 | Sequence 3, Appl1 |
| 34 | 78.5 | 7.9 | 7308 | 4 | US-09-011-745-4 | Sequence 4, Appl1 |
| 35 | 78.5 | 7.9 | 7616 | 4 | US-09-011-745-2 | Sequence 2, Appl1 |
| 36 | 78.5 | 7.9 | 19932 | 2 | US-08-477-451-25 | Sequence 25, Appl1 |
| 37 | 77 | 7.7 | 14231 | 4 | US-08-961-527-81 | Sequence 81, Appl1 |
| 38 | 75 | 7.5 | 1401 | 3 | US-08-331-625A-56 | Sequence 56, Appl1 |
| 39 | 75 | 7.5 | 1401 | 3 | US-09-494-151-56 | Sequence 56, Appl1 |
| 40 | 75 | 7.5 | 4359 | 4 | US-08-331-625A-1 | Sequence 1, Appl1 |
| 41 | 75 | 7.5 | 4359 | 4 | US-09-494-151-1 | Sequence 1, Appl1 |
| 42 | 75 | 7.5 | 4359 | 5 | PCT-US93-04384-17 | Sequence 17, Appl1 |
| 43 | 75 | 7.5 | 4359 | 5 | PCM-US93-04692-1 | Sequence 1, Appl1 |
| 44 | 74.5 | 7.5 | 8948 | 4 | US-09-643-5597-119 | Sequence 119, App |
| 45 | 74 | 7.4 | 2520 | 1 | US-08-405-254-9 | Sequence 9, Appl1 |

ALIGNMENTS

RESULT 1
US-09-079-984A-12
Sequence 12, Application US/09079984A
Patent No. 6231850
GENERAL INFORMATION:
Applicant: Okano, Fumiyoshi, Satoh, Masahiro,
Applicant: Yamada, Katsushige
TITLE OF INVENTION: Canine interleukin 12, a production method
TITLE OF INVENTION: thereof, an immune disease treatment method and preventive
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Miller & Christenbury Intellectual Property
ADDRESSEE: Department of Schnader, Harrison, Segal and Lewis, LLP
STREET: 1600 Market Street, 39th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,984A
FILING DATE: 15-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Austlin R. Miller
REGISTRATION NUMBER: 16,602
REFERENCE/DOCKET NUMBER: 1051-98
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-1810
TELEFAX: (215) 568-6946
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:

LENGTH: 669 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE: Canis familiaris
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: Canine IL12
LOCATION: 1 to 666
IDENTIFICATION METHOD: Similarity
US-09-079-984A-12

Alignment Scores:
Pred. No.: 3,17e-122 Length: 669
Score: 994.00 Matches: 197
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-917-265-50 (1-197) x US-09-079-984A-12 (1-669)

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QY 21 AsnLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 40
Db 136 AACCTGCTGAGAGCGGTCAGACACACCTTCAGAGAGCCAGACAACTCTAGAAATATAT 195
QY 41 SerCysThrSerGlnGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
Db 196 TCCTGCACCTCCGAGAGATTGATCATGAGATATACAAAGGATAAACACAGACAGCTG 255
QY 61 GluAlaCysLeuProLeuGlnLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
Db 256 GAGGCGCTGTACACACGGAATTAACCATGAGAGATTGCCGCTCCAGAGAGATC 315
QY 81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
Db 316 TCTTTGATTAATAAGGAGATTGCTGCTGGAAGAGCCCTTTTATGACGCTCTG 375
QY 101 CysLeuSerSerIleTyrGluAspLeuLysMetLysGlnMetGluPheLysAlaMetAsn 120
Db 376 TGCCTTAGCAGCATCTATGAGACTTGAGATGACAGATGGAATTCAGAGCCATGAC 435
QY 121 AlaLysLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
Db 436 GCAAAAGCTTTTAATGATCCCAAGAGGAGATCTTCTGATCAAAACATGCTGACAGCT 495
QY 141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
Db 496 ATGATGAGCTGTACAGGCGCTGGAATTCACAGATGATGCTGACCAAGAAATCTCTCC 555
QY 161 LeuGlnGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
Db 556 CTGGAAGAGCGGATTTTATAAACAATCAAGCTCTGCATCTTCTTCAATGCTTTC 615
QY 181 ArgIleArgAlaValThrIleAspArgMetSerLysLeuAsnSerSer 197
Db 616 AGAATTCGTGGGTGACCATGATGATGATGATGATGATGATGATGATGATGATGATG 666

RESULT 2
US-09-079-984A-2
: Sequence 2, Application US/09079984A
: Patent No. 6231850
: GENERAL INFORMATION:
: APPLICANT: Okano, Fumiyoshi, Satoh, Masahiro,
: APPLICANT: Yamada, Katsushige
: TITLE OF INVENTION: Canine interleukin 12, a production method
: TITLE OF INVENTION: thereof, an immune disease treatment method and preventive
: TITLE OF INVENTION: method using it

NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Miller & Christenbury Intellectual Property
ADDRESSEE: Department of Schnader, Harrison, Segal and Lewis, LLP
STREET: 1600 Market Street, 39th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,984A
FILING DATE: 15-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Austin R. Miller
REGISTRATION NUMBER: 16,602
REFERENCE/DOCKET NUMBER: 1051-98
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-1810
TELEFAX: (215) 568-6946
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 669 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: Canine IL12
LOCATION: 1 to 666
IDENTIFICATION METHOD: Similarity
US-09-079-984A-2

Alignment Scores:
Pred. No.: 1,45e-121 Length: 669
Score: 989.00 Matches: 196
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.49% Mismatches: 0
Query Match: 99.50% Indels: 0
Gaps: 0

US-09-917-265-50 (1-197) x US-09-079-984A-2 (1-669)

QY 1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
Db 76 AGAGAGCCTCCCAAGAGCCTCCAGAGCCAGGAATATTCAGTGCCTCAACCACTCCCAA 135
QY 21 AsnLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 40
Db 136 AACCTGCTGAGAGCGGTCAGACACACCTTCAGAGAGCCAGACAACTCTAGAAATATAT 195
QY 41 SerCysThrSerGlnGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
Db 196 TCCTGCACCTCCGAGAGATTGATCATGAGATATACAAAGGATAAACACAGACAGTG 255
QY 61 GluAlaCysLeuProLeuGlnLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
Db 256 GAGGCGCTGTACACACGGAATTAACCATGAGAGATTGCCGCTCCAGAGAGATC 315
QY 81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
Db 316 TCTTTGATTAATAAGGAGATTGCTGCTGGAAGAGCCCTTTTATGACGCTCTG 375
QY 101 CysLeuSerSerIleTyrGluAspLeuLysMetLysGlnMetGluPheLysAlaMetAsn 120
Db 376 TGCCTTAGCAGCATCTATGAGACTTGAGATGACAGATGGAATTCAGAGCCATGAC 435

QY 121 AlalysleuMetAspProlysaArglnilepheleuAspGlnAsnMetleuthrala 140
Db 436 GCAAGGCTTTTAATGATGCCAGAGCAGATCTTCTGATCAAAACATGCTGACGGCT 495
QY 141 ILeaspGluLeuGlnAlaLeuAsnPhaenSerValThrValProGlnlySerSer 160
Db 496 ATCATGTAGCTGTACAGCCCTGAAATTCACAGCTGACGTGCCAGAAATCCTCC 555
QY 161 LeuGluGluProAspPheTyrIleThrlyslleleuLeuGlyleleuLeuHisaIaphe 180
Db 556 CTTCAGAGCCGCGATTTTATATAAACTAAATCAAGCTCTGCATACCTTCTCATGCTTTC 615
QY 181 ArgIleArgAlaValThrIleAspArgMetSerTyrIleuAsnSerSer 197
Db 616 AGAATTCGTGCGTGACCATGCACAGAAATGATGACTATCTGATGTTTCC 666

RESULT 3
US-08-186-529-3
Sequence 3, Application US/08186529
Patent No. 5573764
GENERAL INFORMATION:
APPLICANT: Sykes, Megan
APPLICANT: Wolf, Stanley F.
TITLE OF INVENTION: USE OF INTERLEUKIN-12 TO PREVENT
TITLE OF INVENTION: GRAFT-VERSUS-HOST DISEASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc., Legal Affairs
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/186,529
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, Patricia A.
REGISTRATION NUMBER: 33,194
REFERENCE/DOCKET NUMBER: GI 5225
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-498-8401
TELEFAX: 617-876-5851
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 660 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: Lymphoblast
CELL LINE: RPMI 8866
FEATURE:
NAME/KEY: CDS
LOCATION: 1..660
US-08-186-529-3

Alignment Scores:
Pred. No.: 1.71e-106 Length: 660
Score: 875.00 Matches: 171
Percent Similarity: 90.86% Conservatave: 8
Best Local Similarity: 86.80% Mismatches: 18
Query Match: 88.03% Indels: 0
DB: 1 Gaps: 0

US-09-917-265-50 (1-197) x US-08-186-529-3 (1-660)
QY 1 ArgSerleuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
Db 67 AGAAACCTCCCGGCGGACCTCCAGACCCAGGAATGTTCCATGCGCTTGACACCTCCAA 126
QY 21 AsnleuLeuArgAlaValSerAsnThrleuGlnlyslAlaArgGlnThrleuGluLeuTyr 40
Db 127 AACCTGCGAGCGCCGCTGACACATGCTCCAGAAAGGCCAGCAAACTCTGAATTTTAC 186
QY 41 SerCysThrSerGluGluIleAspHiscluasplIethrlyAspLysThrSerThraVal 60
Db 187 CCTTCACCTTCTGAAGATGATCATCATGAATATCACAAAAGATAAAAACGACAGCTG 246
QY 61 GluAlaCysleuProleuGluLeuThrMetAsnGlySerCysleuAlaSerArgIuile 80
Db 247 GAGGCTGTTTACCTTGAATTAACCAAGATGAGATGCTGTAATTCAGAGAGAC 306
QY 81 SerleuIleThrAsnGlySerCysleuAlaSerGlylyslAlaSerPheMetThrValleu 100
Db 307 TCTTTCATACATAATGGAGATTGCTGCGCTCCAGAAAGACCTCTTTATATGATGCGCCTG 366
QY 101 CysleuSerSerIleTyrGluAspleuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
Db 367 TGCCCTTACTAGATTATTAAGACCTTGAAGATGTACCAGGTGAGTTCAGACCATGAAT 426
QY 121 AlalysleuMetAspProlysaArglnilepheleuAspGlnAsnMetleuthrala 140
Db 427 GCAAGCTTGTGATGATCTTAAGAGCGAGATCTTCTGATCAAAACATGCTGCGACTT 486
QY 141 ILeaspGluLeuGlnAlaLeuAsnPhaenSerValThrValProGlnlySerSer 160
Db 487 ATGTGATGAGCTGATGACAGCCCTGGAATTTCAACAGTGAAGCTGCCCAAAATCCTCC 546
QY 161 LeuGluGluProAspPheTyrIleThrlyslleleuLeuGlyleleuLeuHisaIaphe 180
Db 547 CTTCAGAGCCGCGATTTTATATAAACTAAATCAAGCTCTGCATACCTTCTCATGCTTTC 606
QY 181 ArgIleArgAlaValThrIleAspArgMetSerTyrIleuAsnSerSer 197
Db 607 AGAATTCGGGCGATGACTATTGATGAGTGAAGTGAATGCTTCC 657

RESULT 4
US-08-640-386A-3
Sequence 3, Application US/08640386A
Patent No. 5756085
GENERAL INFORMATION:
APPLICANT: Sykes, Megan
APPLICANT: Wolf, Stanley F.
TITLE OF INVENTION: USE OF INTERLEUKIN-12 TO PREVENT
TITLE OF INVENTION: GRAFT-VERSUS-HOST DISEASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc., Legal Affairs
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/640,386A
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: GI 5225A
TELECOMMUNICATION INFORMATION:

[illegible]

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1  APPLICANT : Chang, Lung-Ji
2  TITLE OF INVENTION : Animal Model For Evaluation Of Vaccines
3  NUMBER OF SEQUENCES : 33
4  CORRESPONDENCE ADDRESSES :
5  ADDRESSSEE : Saliwanchik, Lloyd & Saliwanchik
6  STREET : 2421 N.W. 41st Street, Suite A-1
7  CITY : Gainesville
8  STATE : Florida
9  COUNTRY : United States of America
10 ZIP : 32606
11
12 COMPUTER READABLE FORM :
13 MEDIUM TYPE : Floppy disk
14 COMPUTER : IBM PC compatible
15 OPERATING SYSTEM : PC-DOS/MS-DOS
16 SOFTWARE : PatentIn Release #1.0, Version #1.30
17
18 CURRENT APPLICATION DATA :
19 APPLICATION NUMBER : US/08/848,760B
20 FILING DATE : 25-Jan-2001
21 CLASSIFICATION : <unknown>
22 PRIOR APPLICATION DATA :
23 APPLICATION NUMBER : 08/838,702
24 FILING DATE : 09-Apr-1997
25
26 ATTORNEY/AGENT INFORMATION :
27 NAME : PACE, DORAN R.
28 REGISTRATION NUMBER : 38,261
29 REFERENCE/DOCKET NUMBER : CNG-100C1
30 TELECOMMUNICATION INFORMATION :
31 TELEPHONE : (352) 375-8100
32 TELEFAX : (352) 372-5800
33
34 INFORMATION FOR SEQ ID NO: 21 :
35
36 SEQUENCE CHARACTERISTICS :
37 LENGTH : 762 base pairs
38 TYPE : nucleic acid
39 STRANDEDNESS : double
40 TOPOLOGY : linear
41
42 MOLECULE TYPE : other nucleic acid
43 DESCRIPTION : /desc = "DNA
44 SEQUENCE DESCRIPTION : SEQ ID NO: 21 :
45
46 US-08-848-760B-21
47
48 Alignment Scores :
49 Pred. No.:
50
51 2,14e-106
52
53 Score: 875.00
54 Length: 762
55
56 Percent Similarity: 90.86%
57 Matches: 171
58
59 Best Local Similarity: 86.80%
60 Conservative: 8
61
62 Query Match: 88.03%
63 Mismatches: 18
64
65 DB: 4
66 Indels: 0
67 Gaps: 0
68
69 US-09-917-265-50 (1-197) x US-08-848-760B-21 (1-762)
70
71
72 Oy 1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
73 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
74 Db 169 AGAAGACCTCCCGCTGGCCACCTCCAGACCAGGAATGTTCCCATGCTTCACACACTCCCAA 228
75
76 Oy 21 AsnLeuLeuAlaGlnAlaValSerAsnThrLeuGlnGlnGlnGlnGlnGlnGlnGlnGln 40
77 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
78 Db 229 AACCTGCTGAGGCGCTCCAGCAACATGCTCCAGAAAGCCAGACAAACTTGAAATTTTAC 268
79
80 Oy 41 SerCysThrSerGlnGlnIleAspHisGlnAspIleThrTrpLysAspLysThrSerThrVal 60
81 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
82 Db 289 CTTTGACACTTCGAAAGACATGATGATCATGATGATGATGATGATGATGATGATGATGATG 348
83
84 Oy 61 GlnAlaCysLeuProLeuGlnLeuThrTrpMetAsnGlnSerCysLeuAlaSerArgGlnIle 80
85 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
86 Db 349 GAGGCGCTGTTACCATTTGAATTAACCAAGAAATGAGACTTCCTTAATTTCCAGAGAACCC 408
87
88 Oy 81 SerLeuIleThrAsnGlnSerCysLeuAlaSerGlnGlnGlnGlnGlnGlnGlnGlnGln 100
89 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
90 Db 409 TCTTTTATATAACTAAATGAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 468
91
92 Oy 101 CysLeuSerSerIleTryGlnAspLeuLysMetTryGlnMetGlnPheLysAlaMetAsn 120
93 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
94 Db 469 TGGCTTAGAGATGATTTATGAAGACTTGAAGATGTACCCAGGTGAGATTCAGACCATGAAT 528
95

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Oy 121 lalysleuleumleasprolysarvginilpeleuasglahsmelleurrla 140
Db 529 GCAAGCTTCTGATCGATCTTAGAGCGACGATCTTTCTAGATCAAAACATGCTGGCAGTT 588
Oy 141 lileaspluleuleuglnalaleuanspneasnservalthValproclnlysser 160
Db 589 ATTGATGAGCTGATCGACGCCCTCGAATTTCAACACAGTGAACACGTGGCACAAATCTCC 648
Oy 161 leuclugluProaspheryrlslyshrlsllelysleucysllleuleuhisalaphe 180
Db 649 CTTGACAGACCGGATTTTATMAACTMAATCAAGCTCTGCATCTTCATCGCTTTC 708
Oy 181 ArgilearGalavalThrIleasparmetmetserTyrleuanser 197
Db 709 AGAATTCGGCAGCTGACTATTGATATGAGTGAAGTGAAGTGAATCTTCC 759

RESULT 6
US-08-684-687-3
: Sequence 3, Application US/08684687
: Patent No. 5830451
: GENERAL INFORMATION:
: APPLICANT: KIEFF, ELLIOTT D.
: APPLICANT: DEVERGNE, ODILE
: TITLE OF INVENTION: A NOVEL HAEMATOPOIETIC CYTOKINE AND USES
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESS: WOLF, GREENFIELD & SACKS, P.C.
: STREET: 600 ATLANTIC AVENUE
: CITY: BOSTON
: STATE: MA
: COUNTRY: USA
: ZIP: 02210
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/684,687
: FILING DATE:
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/005,092
: FILING DATE: 11-OCT-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: GATES, EDWARD R.
: REGISTRATION NUMBER: 31,616
: REFERENCE/DOCKET NUMBER: B0801/7051
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-720-3500
: TELEFAX: 617-720-2441
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1316 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: HOMO SAPIENS
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 102..863
: US-08-684-687-3

Alignment Scores:
Score: No.: 5,02e-106 length: 1316
Score: 875.00 Matches: 171
Percent Similarity: 90.86% Conservative: 8

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| | | | |
|------------------------|--------|-------------|----|
| Best Local Similarity: | 86.80% | Mismatches: | 18 |
| Query Match: | 88.03% | Indels: | 0 |
| DB: | 2 | Gaps: | 0 |

US-09-917-265-50 (1-197) x US-08-684-687-3 (1-1316)

| | | | |
|----|-----|---|-----|
| QY | 1 | ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln | 20 |
| DB | 270 | AGAAACCTCCCGGCGCCACCTCCAGACCAGGAATGTTCCATGCTTCACCACTCCAA | 329 |
| QY | 21 | AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr | 40 |
| DB | 330 | AACTCGCTGAGGGCGCTCAGCACACTGCTCCGAAAGGCCAGACAAACTCTACATTTTAC | 389 |
| QY | 41 | SerCysThrSerGluGlnIleAspHisGluAspIleThrLysAspLysThrSerThrVal | 60 |
| DB | 390 | CCTTGCACTCTTGAAGAGATTGATCATGAAGTATACAAAAGATAAAACCGACAGTGG | 449 |
| QY | 61 | GluAlaCysLeuProLeuGlnLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle | 80 |
| DB | 450 | GAGGCTGTTTACCACTTGAATTAACCAAGATGAGAGTGGCTTAATTCCAGAGAGACC | 509 |
| QY | 81 | SerLeuLeuThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu | 100 |
| DB | 510 | TCTTTCAATACCAATAGGAGGAGTTGCTGGCTCCAGAAACCTCTTTTATGATGGCCG | 569 |
| QY | 101 | CysLeuSerSerIleTyrGlnAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn | 120 |
| DB | 570 | TGCCTTAGTATTATTATGAAGACTTGAAGATGTACCAAGGTGAGCTTCAAGACCATGAT | 629 |
| QY | 121 | AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAlaGlnAsnMetLeuThrAla | 140 |
| DB | 630 | GCAAAAGCTTGATGATGATCTTAAGAGCAGATCTTTAGATCAAAACATGCTGGCAGTT | 689 |
| QY | 141 | IleAspGlnLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer | 160 |
| DB | 690 | ATTGATGACGTGATGATCAGGCCCTGAATTTTCAACAGTGAAGACTGTGCCACAAAAATCTCC | 749 |
| QY | 161 | LeuGlnGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe | 180 |
| DB | 750 | CTTGAGAACCGGATTTTATATAAACTAAATCAAGCTCTGCATCTTCTCATGCTTTC | 809 |
| QY | 181 | ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer | 197 |
| DB | 810 | AGAATTCGGCAGTGACTATGTAGATGATGATGACACTATCTGAATGCTTCC | 860 |

RESULT 7

US-09-851-520-3

Sequence 3, Application US/09851520

Patent No. 6399379

GENERAL INFORMATION:

APPLICANT: Brenda F. Baker

APPLICANT: Susan M. Freier

TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION

FILE REFERENCE: R1S-0241

CURRENT APPLICATION NUMBER: US/09/851,520

CURRENT FILING DATE: 2001-05-07

NUMBER OF SEQ ID NOS: 88

SEQ ID NO 3

LENGTH: 1316

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (102)...(863)

US-09-851-520-3

Alignment Scores:

| | | | |
|------------------------|-----------|---------------|------|
| Pred. NO.: | 5.02e-106 | Length: | 1316 |
| Score: | 875.00 | Matches: | 171 |
| Percent Similarity: | 90.86% | Conservative: | 8 |
| Best Local Similarity: | 86.80% | Mismatches: | 18 |
| Query Match: | 88.03% | Indels: | 0 |

GENERAL INFORMATION:
APPLICANT: Scott, Phillip
APPLICANT: Trincheri, Giorgio
TITLE OF INVENTION: Compositions and Methods for Use of
TITLE OF INVENTION: IL-12 as an Adjuvant
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Center, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,493
FILING DATE: 25-MAR-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/265,087
FILING DATE: 17-JUN-1994
APPLICATION NUMBER: US 08/229,282
FILING DATE: 18-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST51AUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1364 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 101..859
US-08-621-493-3
US-08-621-493-3
Alignment Scores:
Pred. No.: 5.3e-106 Length: 1364
Score: 875.00 Matches: 171
Percent Similarity: 90.86% Conservative: 8
Best Local Similarity: 86.80% Mismatches: 18
Query Match: 88.03% Indels: 0
Gaps: 0
US-09-917-265-50 (1-197) x US-08-621-493-3 (1-1364)
QY 1 ArgSerLeuProThrAlaSerProSerProGlyLeuPheGlnCysLeuAsnHisSerGln 20
Db 269 AGAAACCTCCCGCTGGCCACTCCAGACCCAGAAATGTTCCCTTCACACCTCCCAA 328
QY 21 AsnLeuLeuAlaValaIserAsnThrLeuGlnIysAlaArgGlnThrLeuGluLeuTyr 40
Db 329 AACCTGCTGAGCGCCGTCAGCAACATGCTCCAGAAAGCCACACAACCTAGAAATTTAC 388
QY 41 SerCysThrSerGluGluIleAspHisGluAspIleThrIlyAspLysThrSerThrVal 60
Db 389 CTTGCCACTCTCTGAAGAGATTGATCATGATGATCAAAAGATTAAGCCACGACGAGTG 448
QY 61 GluAlaCysLeuProLeuGluLeuThrMetAsnGlnSerCysLeuAlaIserArgGluIle 80
Db 449 GAGGCGCTGTATTACATTGCAATTACCAAGATGAGAGTTGCCCTAAATTCCAGAGAGACC 508
QY 81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyAlaSerPheMetThrValLeu 100

Db 509 TCTTCATACATAAGGAGGTGGCTGGCCTCCAGAAAGACCTCTTATGATGGCCCTG 568
QY 101 CysLeuSerSerIleTyrGluAspLeuIysMetTyrGlnMetGluPheLysAlaMetAsn 120
Db 569 TGCCTTAGTATTATGAAAGACTTGAAGATGTACCAAGGTGGAGCTTCAGACCATGAAT 628
QY 121 AlalysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
Db 629 GCAAAGCTTGTGATGATCTTAAGAGCGAGATCTTTAGATCAAAACATGCTGGCAGTT 688
QY 141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
Db 689 ATGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 748
QY 161 LeuGluGluProAspPheTyrIlyThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
Db 749 CTTGAAGAACCGGATTTTATTAACCTAAAGCTCTGCATACCTTCATGATGCTTTC 808
QY 181 ArgIleArgAlaValThrIleAspArgMetLysTyrIleuAsnSerSer 197
Db 809 AGAATTCGGCAGTCACTATTGATGATGATGATGATGATGATGATGATGATGATGATG 859
RESULT 10
US-08-965-688-3
Sequence 3, Application US/08965688
Patent No. 5976539
GENERAL INFORMATION:
APPLICANT: Scott, Phillip
APPLICANT: Trincheri, Giorgio
TITLE OF INVENTION: Compositions and Methods for Use of
TITLE OF INVENTION: IL-12 as an Adjuvant
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Center, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,688
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/621,493
FILING DATE: 25-MAR-1996
APPLICATION NUMBER: 08/265,087
FILING DATE: 17-JUN-1994
APPLICATION NUMBER: US 08/229,282
FILING DATE: 18-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST51AUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1364 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 101..859

Pred. No.: 1.22e-105 Length: 721
 Score: 869.00 Matches: 170
 Percent Similarity: 90.36% Conservative: 8
 Best Local Similarity: 86.29% Mismatches: 19
 Query Match: 87.42% Indels: 0
 DB: 2 Gaps: 0

US-09-917-265-50 (1-197) x US-08-184-009-199 (1-721)

QY 1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
 DB 128 AGAAGCTCCCGGCGGCACATCCAGACCCAGAGATGTTCCATGCTTCCACCATCTCCAA 187
 QY 21 AsnLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuYr 40
 DB 188 AACCTGCTGAGGCGCGTCAGACATGCTCCAGAAAGCCACAAACTGTAATTTTAC 247
 QY 41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
 DB 248 CTTTGCACTTCTGAAGATTTGATGATGATGATGATGATGATGATGATGATGATGATG 307
 QY 61 GluAlaCysLeuProLeuGluLeuThrMetAsnGlnSerCysLeuAlaSerArgGluLe 80
 DB 308 GAGGCTGTTTACCATTTGGAATTAACCAAGATGAGACTTCCCTAATTCAGAGAGACC 367
 QY 81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
 DB 368 TCTTTCATTAACATAATGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 427
 QY 101 CysLeuSerSerIleThrGluAspLeuLysMetGlyGlnMetGluPheLysAlaMetAsn 120
 DB 428 TGCCTTAGTATTATTATGAGACTTGAAGATGATGATGATGATGATGATGATGATGAT 487
 QY 121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
 DB 488 GCAAGCTTCTGATGATGATCTTAAGAGCAGATCTTCTAGATCAAAACATCTGCGACTT 547
 QY 141 IleAspGluLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
 DB 548 ATTGATGAGTGAATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 607
 QY 161 LeuGlnGluProAspPheThrLysThrLysIleLysLeuGlyIleLeuLeuHisAlaPhe 180
 DB 608 CTTGAGAACCGGATTTTATTAATAAATCAAGCTTCTGATGATGATGATGATGATGATG 667
 QY 181 ArgIleArgAlaValThrIleAspArgMetMetSerThrLeuAsnSerSer 197
 DB 668 AGAATTCGGGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGCTTC 718

RESULT 14

US-08-458-356-199
 : Sequence 199, Application US/08458356
 : Patent No. 5942235
 : GENERAL INFORMATION:
 : APPLICANT: Paoletti, Enzo
 : APPLICANT: Tartaglia, James
 : APPLICANT: Cox, William I.
 : TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
 : NUMBER OF SEQUENCES: 217
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Curtis, Morris & Safford
 : STREET: 530 Fifth Avenue
 : CITY: New York
 : STATE: NY
 : COUNTRY: USA
 : ZIP: 10036
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/458,356

FILING DATE: 02-JUN-1995
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/184,009
 FILING DATE: 19-JAN-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Frommer, William S.
 REGISTRATION NUMBER: 25,506
 REFERENCE/DOCKET NUMBER: 454310-2530
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 840-3333
 TELEFAX: (212) 840-0712
 TELEX: 425066CURTMS
 : INFORMATION FOR SEQ ID NO: 199:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 721 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: cDNA
 : US-08-458-356-199

Alignment Scores:

Pred. No.: 1.22e-105 Length: 721
 Score: 869.00 Matches: 170
 Percent Similarity: 90.36% Conservative: 8
 Best Local Similarity: 86.29% Mismatches: 19
 Query Match: 87.42% Indels: 0
 DB: 2 Gaps: 0

US-09-917-265-50 (1-197) x US-08-458-356-199 (1-721)

QY 1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
 DB 128 AGAAGCTCCCGGCGGCACATCCAGACCCAGAGATGTTCCATGCTTCCACCATCTCCAA 187
 QY 21 AsnLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuYr 40
 DB 188 AACCTGCTGAGGCGCGTCAGACATGCTCCAGAAAGCCACAAACTGTAATTTTAC 247
 QY 41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
 DB 428 TGCCTTAGTATTATTATGAGACTTGAAGATGATGATGATGATGATGATGATGATGAT 487
 QY 121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
 DB 488 GCAAGCTTCTGATGATGATCTTAAGAGCAGATCTTCTAGATCAAAACATCTGCGACTT 547
 QY 141 IleAspGluLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
 DB 548 ATTGATGAGTGAATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 607
 QY 161 LeuGlnGluProAspPheThrLysThrLysIleLysLeuGlyIleLeuLeuHisAlaPhe 180
 DB 608 CTTGAGAACCGGATTTTATTAATAAATCAAGCTTCTGATGATGATGATGATGATGATG 667
 QY 181 ArgIleArgAlaValThrIleAspArgMetMetSerThrLeuAsnSerSer 197
 DB 668 AGAATTCGGGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGCTTC 718

RESULT 15

US-08-460-736-199
: Sequence 199, Application US/08460736
: Patent No. 6265189
: GENERAL INFORMATION:
: APPLICANT: Paolietti, Enzo
: APPLICANT: Tartaglia, James
: APPLICANT: Cox, William I.
: TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
: NUMBER OF SEQUENCES: 217
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Curtiss, Morris & Safford
: STREET: 530 Fifth Avenue
: CITY: New York
: STATE: NY
: COUNTRY: USA
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/460,736
: FILING DATE: 02-JUN-1995
: CLASSIFICATION: 514
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 08/184,009
: FILING DATE: 19-JAN-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Frommer, William S.
: REGISTRATION NUMBER: 25,506
: REFERENCE/DOCKET NUMBER: 454310-2530
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 840-3333
: TELEFAX: (212) 840-0712
: TELEX: 425066CURTMS
: INFORMATION FOR SEQ ID NO: 199:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 721 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: US-08-460-736-199

Alignment Scores:
Pred. No.: 1.22e-105 Length: 721
Score: 869.00 Matches: 170
Percent Similarity: 90.36% Conservative: 8
Best Local Similarity: 86.29% Mismatches: 19
Query Match: 87.42% Indels: 0
DB: 4 Gaps: 0

US-09-917-265-50 (1-197) x US-08-460-736-199 (1-721)
QY 1 ArgserLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
Db 128 AGAAACCTCCCGTGGCCAGACCTCCAGCAAGATGTTCCATGCCCTTCACCACTCCCAA 187
QY 21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgLInThrLeuGlnLeuTyr 40
Db 188 AACCTGCTGAGGCGCGCTCAGCAACATGCTCCAGAAAGCCAGCAAAAGCTTACAAATTTTAC 247
QY 41 SerCysThrSerGlnGluIleAspHisGlnAspIleThrLysAspLysThrSerThrVal 60
Db 248 CCTTCACCTTCTGAAGAGATTGATCATGATGATCACAAGAAAGATAAACCCAGCACACTG 307
QY 61 GluAlaCysLeuProLeuGlnLeuThrMetAsnGlnSerCysLeuAlaSerArgGluIle 80
Db 308 GAGGCGCTGTTACCATTTGCAATTACCAAGAAATGAGAGTGGCTTAATTCAGAGAGACC 367
QY 81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100

Db 368 TCTTTCATACTAATGGAGATTGCCCTGCCCTCCAGAAAGACCTCTTTATGATGGCCCTG 427
QY 101 CysLeuSerSerIleTyrGlnAspLeuLysMetTyrGlnMetGlnPheLysAlaMetAsn 120
Db 428 TCCCTTAGTAGTATTATGAGAGCTTGAAGATGTACAGGTGAGATTCAAGACCATGAAT 487
QY 121 AlaLysLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
Db 488 GCAAGCTTCTGATGATGATCTCTAAGAGCGAGATCTTTCTGATGATCAAAACATGCTGCGAGTT 547
QY 141 IleAspGlnLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
Db 548 ATTGATGAGCTGATGAGCGCCCTGAAATTTCAACAGTGAGAGACTGTCCACAAAATCCTCC 607
QY 161 LeuGlnGlnProAspPheTyrTrpLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
Db 608 CTTGAAGAACCGGATTTTATFAAACTAAATCAACCTCTGCATCTCTTCATGCTTC 667
QY 181 ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 197
Db 668 AGAATTCGGGCGAGTGACTATTGACAGAGTGACGAGCTATCTGATGCTTC 718

Search completed: July 17, 2003, 09:32:04
Job time : 29.7808 secs

| Result No. | Score | Query Match | length | DB | ID | Description |
|------------|-------|-------------|--------|----|------------------|-------------------|
| 1 | 994 | 100.0 | 591 | 10 | US-09-917-265-49 | Sequence 49, App1 |

| | | | | | | | |
|---|----|-----|-------|------|----|-------------------|--------------------|
| C | 2 | 994 | 100.0 | 591 | 10 | US-09-917-265-51 | Sequence 45, Appl |
| C | 3 | 994 | 100.0 | 666 | 10 | US-09-917-265-46 | Sequence 46, Appl |
| C | 4 | 994 | 100.0 | 666 | 10 | US-09-917-265-44 | Sequence 48, Appl |
| C | 5 | 994 | 100.0 | 1455 | 10 | US-09-917-265-104 | Sequence 104, Appl |
| C | 6 | 994 | 100.0 | 1455 | 10 | US-09-917-265-106 | Sequence 106, Appl |
| C | 7 | 969 | 97.5 | 1533 | 10 | US-09-917-265-66 | Sequence 66, Appl |
| C | 8 | 969 | 97.5 | 1533 | 10 | US-09-917-265-68 | Sequence 68, Appl |
| C | 9 | 969 | 97.5 | 1599 | 10 | US-09-917-265-61 | Sequence 61, Appl |
| C | 10 | 969 | 97.5 | 1599 | 10 | US-09-917-265-63 | Sequence 63, Appl |
| C | 11 | 932 | 93.8 | 591 | 15 | US-10-079-616-9 | Sequence 9, Appl |
| C | 12 | 932 | 93.8 | 689 | 15 | US-10-079-616-26 | Sequence 26, Appl |
| C | 13 | 932 | 93.8 | 1441 | 15 | US-10-079-616-8 | Sequence 26, Appl1 |
| C | 14 | 929 | 93.5 | 591 | 10 | US-09-917-265-35 | Sequence 35, Appl1 |
| C | 15 | 929 | 93.5 | 591 | 10 | US-09-917-265-37 | Sequence 37, Appl |
| C | 16 | 929 | 93.5 | 666 | 10 | US-09-917-265-32 | Sequence 32, Appl2 |
| C | 17 | 929 | 93.5 | 666 | 10 | US-09-917-265-34 | Sequence 34, Appl |
| C | 18 | 929 | 93.5 | 1533 | 10 | US-09-917-265-43 | Sequence 43, Appl |
| C | 19 | 929 | 93.5 | 1533 | 10 | US-09-917-265-45 | Sequence 45, Appl |
| C | 20 | 929 | 93.5 | 1599 | 10 | US-09-917-265-38 | Sequence 38, Appl |
| C | 21 | 929 | 93.5 | 1599 | 10 | US-09-917-265-38 | Sequence 40, Appl |
| C | 22 | 889 | 89.4 | 561 | 10 | US-09-917-265-101 | Sequence 101, Appl |
| C | 23 | 889 | 89.4 | 561 | 10 | US-09-917-265-103 | Sequence 103, Appl |
| C | 24 | 875 | 88.0 | 762 | 11 | US-09-826-825-21 | Sequence 21, Appl |
| C | 25 | 875 | 88.0 | 1395 | 11 | US-09-924-703-5 | Sequence 5, Appl1 |
| C | 26 | 875 | 88.0 | 1645 | 15 | US-10-028-811-2 | Sequence 2, Appl1 |
| C | 27 | 875 | 88.0 | 8578 | 10 | US-09-828-825-1 | Sequence 1, Appl1 |
| C | 28 | 875 | 88.0 | 8578 | 10 | US-09-828-825-3 | Sequence 3, Appl1 |
| C | 29 | 875 | 88.0 | 8608 | 10 | US-09-828-825-7 | Sequence 7, Appl1 |
| C | 30 | 875 | 88.0 | 8623 | 10 | US-09-828-825-5 | Sequence 5, Appl1 |
| C | 31 | 875 | 88.0 | 8623 | 10 | US-09-828-825-15 | Sequence 15, Appl1 |
| C | 32 | 875 | 88.0 | 8638 | 10 | US-09-828-825-9 | Sequence 9, Appl1 |
| C | 33 | 875 | 88.0 | 8644 | 10 | US-09-828-825-13 | Sequence 13, Appl1 |
| C | 34 | 875 | 88.0 | 8659 | 10 | US-09-828-825-11 | Sequence 11, Appl |
| C | 35 | 869 | 87.4 | 660 | 11 | US-09-754-014-6 | Sequence 6, Appl1 |
| C | 36 | 869 | 87.4 | 660 | 11 | US-09-836-066-4 | Sequence 6, Appl1 |
| C | 37 | 869 | 87.4 | 1026 | 11 | US-10-172-399-5 | Sequence 4, Appl1 |
| C | 38 | 847 | 85.2 | 660 | 11 | US-09-754-014-7 | Sequence 7, Appl1 |
| C | 39 | 844 | 84.9 | 660 | 11 | US-09-754-014-8 | Sequence 8, Appl1 |
| C | 40 | 553 | 55.6 | 1265 | 15 | US-10-172-399-1 | Sequence 1, Appl1 |
| C | 41 | 134 | 13.5 | 79 | 15 | US-10-079-616-24 | Sequence 24, Appl |
| C | 42 | 89 | 9.0 | 1971 | 14 | US-10-137-866-13 | Sequence 139, Appl |
| C | 43 | 89 | 9.0 | 1971 | 14 | US-10-146-726-139 | Sequence 139, Appl |
| C | 44 | 89 | 9.0 | 1971 | 14 | US-10-146-727-139 | Sequence 139, Appl |
| C | 45 | 89 | 9.0 | 1971 | 14 | US-10-146-788-139 | Sequence 139, Appl |

RESULT 1

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US-09-917-265-49
: Sequence 49, Application US/09917265
: Patent No. US20020052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
: FILE REFERENCE: IM-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: CURRENT FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: PRIOR FILING DATE: 2000-08-04
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: Patentin version 3.1
: SEQ ID NO 49
: LENGTH: 591
: TYPE: DNA
: ORGANISM: Canis familiaris
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(591)
: OTHER INFORMATION:
: US-09-917-265-49

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Alignment Scores: 2.26e-120 Length: 591
Pred. No.: 994.00 Matches: 197
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 10

US-09-917-265-50 (1-197) x US-09-917-265-49 (1-591)

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QY 1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
Db 1 AGAGAGCTCCCGACAGGCTTACCGAGCCGAGATATTCAGAGCTCCAAACCTCCAA 60
QY 21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 40
Db 61 AACCTGTGAGAGCCGTCACAGCACAGCTTCAGAAAGCCAGACAACTAGATATAT 120
QY 41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
Db 121 TCCTGCACCTCCGAAAGATTCATGAAAGATATCAAAAGATAAACAGCAGCAGTG 180
QY 61 GluAlaCysLeuProLeuGlnLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
Db 181 GAGGCTGCTTACCACTGGAATTAACCATGATGAGAGTTCCTGCTCCAGAGATC 240
QY 81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
Db 241 TCCTTGTAACTAAACGGAGTTCCTGCTGCTGAAAGCCCTCTTTATGACGCTCTG 300
QY 101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
Db 301 TGCCTTAGCAGCATCTATGAGACTTGAAAGATGACAGATGGAATTCAGGCCATGAC 360
QY 121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
Db 361 GCAAGCTTTAATGATGCCAGAGGACAGATCTTCTGATCAAAACATGCTACAGCT 420
QY 141 IleAspGlnLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
Db 421 ATCGATGAGCTGTACAGGCCCTGAATTTCAACAGTGTGACTGCTGACAGAAATCCTCC 480
QY 161 LeuGlnGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
Db 481 CTGGAAGAGCCGGAATTTTAAACTAAATCAAGCTGTCGCACTTCTTCATGCTTTC 540
QY 181 ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 197
Db 541 AGAATTCGTGCGGTGACCATGATAGATGATGATGATGATGATGATGATGATGAT 591
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RESULT 2

US-09-917-265-51/c
; Sequence 51, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: 1M-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-917-265-51

Alignment Scores:

Pred. No.: 2.26e-120

Length: 591

Score: 994.00 Matches: 197
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10

US-09-917-265-50 (1-197) x US-09-917-265-51 (1-591)

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QY 1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
Db 591 AGAGAGCTCCCGACAGGCTTACCGAGCCGAGATATTCAGAGCTCCAAACCTCCAA 532
QY 21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 40
Db 531 AACCTGTGAGAGCCGTCACAGCACAGCTTCAGAAAGCCAGACAACTAGATATAT 472
QY 41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
Db 471 TCCTGCACCTCCGAAAGATTCATGAAAGATATCAAAAGATAAACAGCAGCAGTG 412
QY 61 GluAlaCysLeuProLeuGlnLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
Db 411 GAGGCTGCTTACCACTGGAATTAACCATGATGAGAGTTCCTGCTCCAGAGATC 352
QY 81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
Db 351 TCCTTGTAACTAAACGGAGTTCCTGCTGCTGAAAGCCCTCTTTATGACGCTCTG 292
QY 101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
Db 291 TGCCTTAGCAGCATCTATGAGACTTGAAAGATGACAGATGGAATTCAGGCCATGAC 232
QY 121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
Db 231 GCAAGCTTTAATGATGCCAGAGGACAGATCTTCTGATCAAAACATGCTGACAGCT 172
QY 141 IleAspGlnLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
Db 171 ATCGATGAGCTGTACAGGCCCTGAATTTCAACAGTGTGACTGCTGACAGAAATCCTCC 112
QY 161 LeuGlnGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
Db 111 CTGGAAGAGCCGGAATTTTAAACTAAATCAAGCTGTCGCACTTCTTCATGCTTTC 52
QY 181 ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 197
Db 51 AGAATTCGTGCGGTGACCATGATAGATGATGATGATGATGATGATGATGATGAT 1
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RESULT 3

US-09-917-265-46
; Sequence 46, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
; FILE REFERENCE: 1M-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(666)
; OTHER INFORMATION:
US-09-917-265-46

Alignment Scores:
Pred. No.: 2,736-120 Length: 666
Score: 994.00 Matches: 197
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-917-265-50 (1-197) x US-09-917-265-46 (1-666)

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QY 1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
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Db 76 AGGAGCCCTCCACAGCCTCCACGAGCCAGCAATATTCACGTGCTCAACCACTCCCAA 135
QY 21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuLysLeuTyr 40
    |||||||
Db 136 AACCTGCTGAGAGCGCTCAGCAACGCTTCAGAGGCGCAGCAAACTCTGAAATTATAT 195
QY 41 SerCysrhrSerGluGluIleAspHisGlnAspIleThrLysAspLysThrSerThrVal 60
    |||||||
Db 196 TCCGCACTCCGAAAGAGATTGATCATGACATACCAAAAGATAAACCAAGCAGCAGTG 255
QY 61 GluAlaCysLeuProLeuGlnLeuThrMetAsnGlnSerCysLeuAlaSerArgGluIle 80
    |||||||
Db 256 GAGCCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCTGCTTCCAGAGAGATC 315
QY 81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
    |||||||
Db 316 TCTTTGATTAACCTAACGGAGATTGCTGCTGCTTGAAAGGCTCTTTTATGACGCTCTG 375
QY 101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
    |||||||
Db 376 TGCCTTAGCAGACATCTATGAGGAGCTTGAAGATGTACCAAGATGCAATTAAGGCCATGAA 435
QY 121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
    |||||||
Db 436 GCAAAAGCTTTTAAATGATCCCAAGAGCAGATCTTTTCGATCAAAACATCTGACACACT 495
QY 141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
    |||||||
Db 496 ATGCATAGACCTTTACAGGCCCTGAAATTTCAACAGTGTGACTGTGCCACAGAAATCCCTCC 555
QY 161 LeuGlnGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
    |||||||
Db 556 CTTCAGAGCGCGGATTTTATTAATAAACAATCAAGCTCTGCATACTCTTCATGCTTTC 615
QY 181 ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 197
    |||||||
Db 616 AGAATTGCTGCGGTGACCATGATGATGATGATTATCTGAATTCTTCC 666
```

RESULT 4

US-09-917-265-48/c
: Sequence 48. Application US/09917265
: Patent No. US20020052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: APPLICANT: Boroughs, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
: FILE REFERENCE: IM-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: CURRENT FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: PRIOR FILING DATE: 2000-08-04
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 48
: LENGTH: 666
: TYPE: DNA
: ORGANISM: Canis familiaris
US-09-917-265-48

Alignment Scores: 2,736-120 Length: 666

Score: 994.00 Matches: 197
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-917-265-50 (1-197) x US-09-917-265-48 (1-666)

```
QY 1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
    |||||||
Db 591 AGGAGCCCTCCACAGCCTCCACGAGCCAGCAATATTCACGTGCTCAACCACTCCCAA 532
QY 21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuLysLeuTyr 40
    |||||||
Db 531 AACCTGCTGAGAGCGCTCAGCAACGCTTCAGAAAGCCAGCAAACTCTGAAATTATAT 472
QY 41 SerCysrhrSerGluGluIleAspHisGlnAspIleThrLysAspLysThrSerThrVal 60
    |||||||
Db 471 TCCGCACTCCGAAAGAGATTGATCATGACATACCAAAAGATAAACCAAGCAGCAGTG 412
QY 61 GluAlaCysLeuProLeuGlnLeuThrMetAsnGlnSerCysLeuAlaSerArgGluIle 80
    |||||||
Db 411 GAGCCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCTGCTTCCAGAGAGATC 352
QY 81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
    |||||||
Db 351 TCTTTGATTAACCTAACGGAGATTGCTGCTGCTTGAAAGGCTCTTTTATGACGCTCTG 292
QY 101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
    |||||||
Db 291 TGCCTTAGCAGACATCTATGAGGAGCTTGAAGATGTACCAAGATGCAATTAAGGCCATGAA 232
QY 121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
    |||||||
Db 231 GCAAAAGCTTTTAAATGATCCCAAGAGCAGATCTTTTCGATCAAAACATCTGACACACT 172
QY 141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
    |||||||
Db 171 ATGCATAGACCTTTACAGGCCCTGAAATTTCAACAGTGTGACTGTGCCACAGAAATCCCTCC 112
QY 161 LeuGlnGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
    |||||||
Db 111 CTTCAGAGCGCGGATTTTATTAATAAACAATCAAGCTCTGCATACTCTTCATGCTTTC 52
QY 181 ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 197
    |||||||
Db 51 AGAATTGCTGCGGTGACCATGATGATGATGATTATCTGAATTCTTCC 1
```

RESULT 5

US-09-917-265-104
: Sequence 104. Application US/09917265
: Patent No. US20020052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: APPLICANT: Boroughs, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
: FILE REFERENCE: IM-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: CURRENT FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: PRIOR FILING DATE: 2000-08-04
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 104
: LENGTH: 1455
: TYPE: DNA
: ORGANISM: Canis familiaris
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (232)..(897)
: OTHER INFORMATION:
US-09-917-265-104

Alignment Scores:

Pred. No.: 9.19e-120 Length: 1455
Score: 994.00 Matches: 197
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-917-265-50 (1-197) x US-09-917-265-104 (1-1455)

```
QY 1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
DB AGAGAGCTCCCGACAGCCTCACCGACCGAGAAATATTCAGTGGCTCAACCACTCCCA 366
QY 21 AsnLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuLysLeuTyr 40
DB AACCTGCTGAGAGCCGCGACAGCAACCCCTCAGAGGCCGACAAACTCTAGAAATATAT 426
QY 41 SerCysThrSerGlnGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
DB TCCTGCACCTCCGAGAGATTGATCATGAGATATCAAAAGGATMAAACGACAGCAGTG 486
QY 61 GluAlaCysLeuProLeuGlnIleuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
DB GAGGCTGCTTACCACTGGAATTAACCATGAGATGAGAGTGGCTTCCAGAGAGATC 546
QY 81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
DB TCTTGATTAACTAACGGAGATGCTGCTGCTGCTGAAAGGCTCTTTATGACGGTCTCG 606
QY 101 CysLeuSerSerIleTyrGlnAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
DB TGCCTTAGCAGCATCTATGAGGACTTGAAGATGACAGATGAGATTCAGGCCATGAC 666
QY 121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
DB GCAGAGCTTTATATGATCCCAAGAGCAGATCTTCTGATCAAAACATGCTGACAGCT 726
QY 141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
DB ATCGATGAGCTGTTACAGGCCCTGAAATTTCAACAGTGTGACTGGCCACAGAAATCTCC 786
QY 161 LeuGlnIuProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
DB CTTGAGAGCGCGATTTTATMAAACATAAATCAAGCTCTGCACTTCTTCATGCTTTC 846
QY 181 ArgIleArgAlaValThrIleAspArgMetSerTyrLeuAsnSerSer 197
DB AGAATTGCTGCGGTGACCATCGATGATGATGATGATGATGATGATGATGATGATGAT 897
```

RESULT 6

US-09-917-265-106/c
Sequence 106, Application US/09917265
Patent No. US20020052030A1
GENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/09/917,265
PRIOR FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
NUMBER OF SEQ ID NOS: 109
SOFTWARE: PatentIn version 3.1
SEQ ID NO 106
LENGTH: 1455
TYPE: DNA
ORGANISM: Canis familiaris
US-09-917-265-106

Alignment Scores:

Pred. No.: 9.19e-120

Length: 1455

Score: 994.00 Matches: 197
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-917-265-50 (1-197) x US-09-917-265-106 (1-1455)

```
QY 1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
DB AGAGAGCTCCCGACAGCCTCACCGACCGAGAAATATTCAGTGGCTCAACCACTCCCA 1090
QY 21 AsnLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuLysLeuTyr 40
DB AACCTGCTGAGAGCCGCGACAGCAACCCCTCAGAGGCCGACAAACTCTAGAAATATAT 1030
QY 41 SerCysThrSerGlnGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
DB TCCTGCACCTCCGAGAGATTGATCATGAGATATCAAAAGGATMAAACGACAGCAGTG 970
QY 61 GluAlaCysLeuProLeuGlnIleuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
DB GAGGCTGCTTACCACTGGAATTAACCATGAGATGAGAGTGGCTTCCAGAGAGATC 910
QY 81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
DB TCTTGATTAACTAACGGAGATGCTGCTGCTGCTGAAAGGCTCTTTATGACGGTCTCG 850
QY 101 CysLeuSerSerIleTyrGlnAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
DB TGCCTTAGCAGCATCTATGAGGACTTGAAGATGACAGATGAGATTCAGGCCATGAC 790
QY 121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
DB GCAGAGCTTTATATGATCCCAAGAGCAGATCTTCTGATCAAAACATGCTGACAGCT 730
QY 141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
DB ATCGATGAGCTGTTACAGGCCCTGAAATTTCAACAGTGTGACTGGCCACAGAAATCTCC 670
QY 161 LeuGlnIuProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
DB CTTGAGAGCGCGATTTTATMAAACATAAATCAAGCTCTGCACTTCTTCATGCTTTC 610
QY 181 ArgIleArgAlaValThrIleAspArgMetSerTyrLeuAsnSerSer 197
DB AGAATTGCTGCGGTGACCATCGATGATGATGATGATGATGATGATGATGATGATGAT 559
```

RESULT 7

US-09-917-265-66
Sequence 66, Application US/09917265
Patent No. US20020052030A1
GENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/09/917,265
PRIOR FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
NUMBER OF SEQ ID NOS: 109
SOFTWARE: PatentIn version 3.1
SEQ ID NO 66
LENGTH: 1533
TYPE: DNA
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: CDS
LOCATION: (1)-(1533)
OTHER INFORMATION:
US-09-917-265-66

Alignment Scores:

Pred. No.: 1,86e-116 Length: 1533
Score: 969.00 Matches: 191
Percent Similarity: 98.988 Conservative: 4
Best Local Similarity: 96.958 Mismatches: 2
Query Match: 97.488 Indels: 0
DB: 10 Gaps: 0

US-09-917-265-50 (1-197) x US-09-917-265-66 (1-1533)

```
OY 1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 943 AGAACTTGCCAAACCCCTCTCCATCCCGGGATGTGTCCAATGTTTGAACCACTCCAA 1002
OY 21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 40
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1003 ACCCTGTTGAGAGCCCTCAGCAACGCTTCAGAACGCCAGCAAACTCTAGAAATTATAT 1062
OY 41 SerCysThrSerGluLysIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1063 TCCTGCACCTCCGAGAGAGATTGATCATGAAGATATCAACAAGATAAACCAACACAGTG 1122
OY 61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1123 GAGCGCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGGCTGCTCCAGAGAGATC 1182
OY 81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1183 TCTTTGATTAACTAACGGAGGAGTTCCTCGGCTCTGGAAAGCCCTTTTATGAGGCTCTG 1242
OY 101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1243 TCCTTAGACAGCATCATGAGAGACTTGAGAGATGTACACAGATGGAATTCAGGCCATGAA 1302
OY 121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1303 GCAAAGCTTTTAAATGATCCCAAGAGCGCATCTTCTCATCAAAACATGCTGACAGCT 1362
OY 141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1363 ATCGATGACGCTTTACAGGCCCTCGAATTTCAACAGCTGACGTGCACAGAAATCTCC 1422
OY 161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1423 CTTGAAGAGCCCGGATTTTATAAACTAAATCAACGCTCGCATCTTCTCATGCTTTC 1482
OY 181 ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 197
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1483 AGAATTGTCGCGTGACATCAATGAAATGATGTCTTACTTGAACCTTCC 1533
```

RESULT 8

US-09-917-265-68/c
: Sequence 68, Application US/09917265
: Patent No. US20020052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: APPLICANT: Borouhgs, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
: FILE REFERENCE: IM-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: PRIOR APPLICATION NUMBER: 60/223,016
: PRIOR FILING DATE: 2000-08-04
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 68
: LENGTH: 1533
: TYPE: DNA
: ORGANISM: Canis familiaris
: US-09-917-265-68

Alignment Scores: 1,86e-116 Length: 1533

Score: 969.00 Matches: 191
Percent Similarity: 98.988 Conservative: 4
Best Local Similarity: 96.958 Mismatches: 2
Query Match: 97.488 Indels: 0
DB: 10 Gaps: 0

US-09-917-265-50 (1-197) x US-09-917-265-66 (1-1533)

```
OY 1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 591 AGAACTTGCCAAACCCCTCTCCATCCCGGGATGTGTCCAATGTTTGAACCACTCCAA 532
OY 21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 40
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 531 ACCCTTGTGAGAGCCCTCAGCAACGCTTCAGAACGCCAGCAAACTCTAGAAATTATAT 472
OY 41 SerCysThrSerGluLysIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 471 TCCTGCACCTCCGAGAGAGATTGATCATGAAGATATCAACAAGATAAACCAACACAGTG 412
OY 61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 411 GAGCGCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGGCTGCTCCAGAGAGATC 352
OY 81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 351 TCTTTGATTAACTAACGGAGAGTTCCTCGGCTCTGGAAAGCCCTTTTATGAGGCTCTG 292
OY 101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 291 TGCGTTAGACAGCATCATGAGAGACTTGAGAGATGTACACAGATGGAATTCAGGCCATGAA 232
OY 121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 231 GCAAAGCTTTTAAATGATCCCAAGAGCGCATCTTCTCATCAAAACATGCTGACAGCT 172
OY 141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 171 ATCGATGACGCTTTACAGGCCCTCGAATTTCAACAGCTGACGTGCACAGAAATCTCC 112
OY 161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 111 CTTGAAGAGCCCGGATTTTATAAACTAAATCAACGCTCGCATCTTCTCATGCTTTC 52
OY 181 ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 197
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 51 AGAATTGTCGCGTGACATCAATGAAATGATGTCTTACTTGAACCTTCC 1
```

RESULT 9

US-09-917-265-61
: Sequence 61, Application US/09917265
: Patent No. US20020052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: APPLICANT: Borouhgs, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
: FILE REFERENCE: IM-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: PRIOR APPLICATION NUMBER: 60/223,016
: PRIOR FILING DATE: 2000-08-04
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 61
: LENGTH: 1599
: TYPE: DNA
: ORGANISM: Canis familiaris
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(1599)
: OTHER INFORMATION:
: US-09-917-265-61

| | | | | | |
|------------------------|-----|-----|------|---------------|------|
| Pred. No.: | 1 | 98 | -116 | Length: | 1599 |
| Score: | 969 | 00 | | Matches: | 191 |
| Percent Similarity: | 98 | 98% | | Conservative: | 0 |
| Best Local Similarity: | 96 | 95% | | Mismatches: | 2 |
| Query Match: | 97 | 48% | | Indels: | 0 |
| DB: | 10 | | | Gaps: | 0 |

| | | |
|----|--|------|
| QY | ArgSerLeuProThrAlaSerProSerProGlyIleIleGlnCysLeuAsnHisSergIn | 20 |
| Db | 1009 AAAAACTGGCAACCCCTTACCTCCATCCCGGGTAGTTCCCATGTTTAAACCACTCCCAA | 1066 |
| QY | 21 AsnLeuLeuAlaAlaValSerAsnThrLeuGlnIlyAspGlnIleArgGlnThrLeuGlnLeuYr | 40 |
| Db | 1069 ACCTTGTTGAGAGCGGTGACGACACACGCTTCAGAAAGCCAGACAAACTGTGAATTAAT | 1128 |
| QY | 41 SerCysThrSerGlnGluIleAspHisGlnAspIleThrIlyAspLysThrSerThrVal | 60 |
| Db | 1129 TCCCTGCACCTCCGAGAGATGATGATCATGAAGATACACAAGAAAGAAACCAGCACACTG | 1188 |
| QY | 61 GluAlaCysLeuProLeuGlnLeuThrMetLsnGlnSerCysLeuAlaSerArgGluIle | 80 |
| Db | 1189 GAGCGCTCTTACCACTGGAATTAACCATGATGAGACTGCTCGGCTCCAGAGATC | 1248 |
| QY | 81 SerLeuIleThrAsnGlnSerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu | 100 |
| Db | 1249 TCTTTGATTAACTAACGGGAGTTGCCCTGCTGCAAAAGGCTCTTTATGAGGCTCTG | 1308 |
| QY | 101 CysLeuSerSerIleTyrGlnAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn | 120 |
| Db | 1309 TGCCTTACCAACATCTATGAGAGACTTGAAAGTATACACAGATGGAATTCAGGCCATGAC | 1368 |
| QY | 121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAsnGlnAsnMetLeuThAla | 140 |
| Db | 1369 GCAAAAGCTTTAAATGAGATCCCAAGAGCGAGATCTTCTTGATCCAAACATGCTGACACGCT | 1428 |
| QY | 141 IleAspGlnLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnIlySerSer | 160 |
| Db | 1429 ATCATGATGAGCTGTACAGGCCCTGAAATTTCAACAGTGTGACTGTGCCACAGAAATCTCTCC | 1488 |
| QY | 161 LeuGlnGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe | 180 |
| Db | 1489 CTTGAAAGAGCGGAGTTTATTAATAACATAAATCAAGCTCGCATACTTCTTCATGCTTCC | 1548 |
| QY | 181 ArgIleArgAlaValThrIleAspArgMetSerTyrLeuAsnSerSer | 197 |
| Db | 1549 AGAATTCGTGCGGAGACATCAATAGATATGATGCTACTTGAACCTCTTCC | 1599 |

```

RESULT 10
US-09-917-265-63/c
: Sequence 63, Application US/09917265
: Patent No. US20020052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: APPLICANT: Boroughs, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS,
: FILE REFERENCE: IM-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: PRIOR FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: PRIOR FILING DATE: 2000-08-04
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO: 63
: LENGTH: 1599
: TYPE: DNA
: ORGANISM: Canis familiaris
US-09-917-265-63

Alignment Scores:
Pred. No.: 1.98e-116 Length: 1599

```

| | | | |
|------------------------|--------|---------------|----|
| Score: | 969.00 | Matches: | 19 |
| Percent Similarity: | 98.98% | Conservative: | 4 |
| Best Local Similarity: | 96.95% | Mismatches: | 2 |
| Query Match: | 97.48% | Indels: | |
| DB: | 10 | Gaps: | 0 |

| | | | |
|----|-----|---|-----|
| OY | | ArgSerLeuProThrAlaSerProSerProgIyllePheGlnCysLeuSnHISerGln | 20 |
| Db | 591 | AGAACTGGACCAACCCTACTCATCCCGGGATGTTCMAATGTTTGAACCACTCCAA | 53 |
| OY | 21 | AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysLaIArgInlhrLeuGluLeuTy | 40 |
| Db | 531 | ACCTTGTTGAAGGCCGTGCAGCACACGCTTCAGAGGCCAGACAACCTTAGAATTAT | 47 |
| OY | 41 | SerCysThrSerGlutluleasPhnIslaspIleThrLysAspLysThrSerThra | 60 |
| Db | 471 | TCTGCACATCCGAAGAGATTGATCATGAGATATACCAAAGATTAACCGACAGG | 41 |
| OY | 61 | GluAlacSerProLeuGluLeuThMetAsnGluSerCysLeuAlaSerArgIule | 80 |
| Db | 411 | GAGCGCTTACCACTGGAATTAAACCATGAAGAAGTTCCTCCAGAGAGATC | 35 |
| OY | 81 | SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrAlen | 10 |
| Db | 351 | TCTTTGATTAACGGGACTTGCCTGGCCCTCGGAAGGCCCTCTTTATGACGGTCTG | 29 |
| OY | 101 | CysLeuSerSerIleTyrgLinasPLeuLysMeTyrgImetGluPheLysAlaMetAsn | 120 |
| Db | 291 | TGCCTTGACGACATCTCATGAGGACTTGAAAGTGTACCAATGATGAAATTCGAAGGCATGAAC | 23 |
| OY | 121 | AlaLysLeuLeuMetAspProLysArgInllePheLeuAspClasmeLeuThra | 140 |
| Db | 231 | GCAAGCTTTTAAATGATGCCAGAGAGGCCAGATCTTTCGATCAAAAACATGCTGCACCT | 17 |
| OY | 141 | IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer | 160 |
| Db | 171 | ATGATGAGCTGTATACAGGCCCTGAAATTTCAACAGTGTGACGTGCCACAGAAATCTCC | 11 |
| OY | 161 | LeuGlnGluProAspPheTyrgLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe | 180 |
| Db | 111 | CTTGGAAGAGCGGATTTTTATAAACATAAAACAAGCTCTGCATCTTCAAGCTTC | 52 |
| OY | 181 | ArgIlleArgAlaValThrIleAspArgMetIleSerTyrgLeuAsnSerSer | 197 |
| Db | 51 | AGAAATTCGTGGCTGCACATCATAGATGATGTCTTACTGAACCTCTCC | 1 |

RESULT 11
 US-10-079-616-9
 ? Sequence 9, Application US/10079616
 ? Publication No. US20020107366A1
 ? GENERAL INFORMATION:
 ? APPLICANT: IMADURA, Takayuki
 ? MAEDA, Hiroaki
 ? FUJITASU, Takeshi
 ? IMAGAWA, Yoshitaka
 ? TOKIYOSHI, Sachio
 ? TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
 ? NUMBER OF SEQUENCES: 26
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: BROWDY AND NEIMARK
 ? STREET: 419 Seventh Street, N.W., Suite 300
 ? CITY: Washington
 ? STATE: D.C.
 ? COUNTRY: USA
 ? ZIP: 20004
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Floppy disk
 ? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: PatentIn Release #1.0, Version #1.30
 ? CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/079,616
FILING DATE: 22-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/011,143
FILING DATE: 04-FEB-1998
APPLICATION NUMBER: PCT/JP97/01824
FILING DATE: 29-MAY-1997
APPLICATION NUMBER: JP 165249/1996
FILING DATE: 04-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: IMAMURA=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 591 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-079-616-9
Alignment Scores:
Pred. No.: 2,92e-112 Length: 591
Score: 932.00 Matches: 183
Percent Similarity: 95.94% Conservative: 6
Best Local Similarity: 92.89% Mismatches: 8
Query Match: 93.76% Indels: 0
Gaps: 0
US-09-917-265-50 (1-197) x US-10-079-616-9 (1-591)
QY 1 ArgSerLeuProThAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
Db 1 AGGAACCTCCACACCCACACCAAGCCAGAAATGTTCCAGTGCCTCACCACCTCCAA 60
QY 21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnIlySalaArgGlnThrLeuGluLeuTyr 40
Db 61 ACCCTGCTCGCAGCAGCAACACGCTTCAGAAAGCCAGCAAACTCTAGAAATTTTAC 120
QY 41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
Db 121 TCCTGCACTTCGGAAGAGATTGATCATGACAAAGATAAACCAAGCAGCAGTG 180
QY 61 GluAlaCysLeuProLeuGlnIleuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
Db 181 GAGGCTGCTTACCACTGCAATTAACATGATGAGAGTTGCTTGCCTCCAGAGAGATC 240
QY 81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
Db 241 TCTCTGATAACTAATAGGAGAGTTCCTGCGCTCCAGAAACCTCTTTATGACGACCTG 300
QY 101 CysLeuSerSerIleTyrGlnAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
Db 301 TGCCTTACAGACTATATGAGAGCTTGAAAGATGTACACAGCTGAGTTCAGGCAATGAA 360
QY 121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
Db 361 GCAAAGCTCTTAATGATCTTAAGAGCCAGATCTTTCTGATCAAAACATGCTGACAGCT 420
QY 141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
Db 421 ATTGATGAGCTGTACAGGCCCTGCAATGTCACAGTGTGACGTGCGACAGAACTCCTCC 480
QY 161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
Db 481 CTGGAAGAACAGATTTTATATAAACTAAATCAAGCTCTGATACCTTCTTCATCTTTC 540

QY 181 ArgIleArgAlaValThrIleAspArgMetSerTyrLeuAsnSerSer 197
Db 541 AGAATTCGTGCACTGACCATCATAGAAATGATGAGCTACTGTAATCTTCC 591
RESULT 12
US-10-079-616-26
Sequence 26, Application US/10079616
Publication No. US20020107366A1
GENERAL INFORMATION:
APPLICANT: IMAMURA, Takayuki
MAEDA, Hiroaki
FUJIVASU, Takeshi
IMAGAWA, Yoshitaka
TOKIYOSHI, Sachio
TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEWMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/079,616
FILING DATE: 22-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/011,143
FILING DATE: 04-FEB-1998
APPLICATION NUMBER: PCT/JP97/01824
FILING DATE: 29-MAY-1997
APPLICATION NUMBER: JP 165249/1996
FILING DATE: 04-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: IMAMURA=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 689 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-079-616-26
Alignment Scores:
Pred. No.: 3.71e-112 Length: 689
Score: 932.00 Matches: 183
Percent Similarity: 95.94% Conservative: 6
Best Local Similarity: 92.89% Mismatches: 8
Query Match: 93.76% Indels: 0
Gaps: 0
US-09-917-265-50 (1-197) x US-10-079-616-26 (1-689)
QY 1 ArgSerLeuProThAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
Db 82 AGGAACCTCCACACCCACACCAAGCCAGAAATGTTCCAGTGCCTCACCACCTCCAA 141
QY 21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnIlySalaArgGlnThrLeuGluLeuTyr 40
Db 142 ACCCTGCTCGCAGCAGCATGACCAACACGCTTCAGAAAGCCAGCAAACTCTAGAAATTTTAC 201

QY 41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
 Db 202 TCCTGACCTCCAGAGAGATGATGATCAATGAAATATACAAAGATTAACACGACAGAGT 261
 QY 61 GluAlaCysLeuProLeuGluIleuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
 Db 262 GAGGCTGCTGCGCACTGAGACTGACCATGAAATGAGAGTTGCTTCCGAGACAGATC 321
 QY 81 SerIleuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrVal 100
 Db 322 TCCTGATACATAATGGAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 381
 QY 101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
 Db 382 TCCTGATGAGATGATGAGAGCTTGAAGATGTCACAGGTGAGTTACAGGCCATGAT 441
 QY 121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
 Db 442 GCAAGCTGCTGATGATCTTAAGGCAAGATCTTCTGATCAAAACATCTGACAGCT 501
 QY 141 IleAspGluLeuLeuGlnAlaLeuAsnPhaSerValIleThrValProGlnLysSerSer 160
 Db 502 ATGTATGAGCTGTTACAGCCCTGAAATGTCAACAGTGTGACTGTGCCACAGAACTCTCC 561
 QY 161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuGlyLysLeuLeuHisAlaPhe 180
 Db 562 CTGGAAGAACCAAGATTTTATTAATAAATAAATCAAGCTCTGCAATCTCTTCATGCTTTC 621
 QY 181 ArgIleArgAlaValIleThrIleAspArgMetSerTyrIleuAsnSerSer 197
 Db 622 AGAATGCTGACGAGACCATCAATAGATGATGATGATGATGATGATGATGATGATGATG 672

RESULT 13
 US-10-079-616-8
 : Sequence 8, Application US/10079616
 : Publication No. US20020107366A1
 : GENERAL INFORMATION:
 : APPLICANT: IMAMURA, Takayuki
 : MAEDA, Hiroaki
 : FUJIYASU, Takeshi
 : IMAGAWA, Yoshitaka
 : TOKIYOSHI, Sachio
 : TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
 : NUMBER OF SEQUENCES: 26
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: BROMDY AND NEIMARK
 : STREET: 419 Seventh Street, N.W., Suite 300
 : CITY: Washington
 : STATE: D.C.
 : COUNTRY: USA
 : ZIP: 20004
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/10/079, 616
 : FILING DATE: 22-Feb-2002
 : CLASSIFICATION: <Unknown>
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 09/011,143
 : FILING DATE: 04-FEB-1998
 : APPLICATION NUMBER: PCT/JP97/01824
 : FILING DATE: 29-MAY-1997
 : APPLICATION NUMBER: JP 165249/1996
 : FILING DATE: 04-JUN-1996
 : ATTORNEY/AGENT INFORMATION:
 : NAME: BROMDY, Roger L.
 : REGISTRATION NUMBER: 25,618
 : REFERENCE/DOCKET NUMBER: IMAMURA=1
 : TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 INFORMATION FOR SEQ. ID NO: 8:
 :
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 1441 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: cDNA
 : SEQUENCE DESCRIPTION: SEQ ID NO: 8:
 US-10-079-616-8

Alignment Scores:
 Pred. No.: 1,17e-111 Length: 1441
 Score: 932.00 Matches: 183
 Percent Similarity: 95.94% Conservative: 6
 Best local Similarity: 92.89% Mismatches: 8
 Query Match: 93.76% Indels: 0
 DB: 15 Gaps: 0

US-09-917-265-50 (1-197) x US-10-079-616-8 (1-1441)

QY 1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
 Db 218 AGGAACCTCCAC 277
 QY 21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 40
 Db 278 ACCCTGCTCGAGCAGCATGACGAAACAGCGTTCAGAGGCCAGACCAACCTGAAATTTTAC 337
 QY 41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
 Db 338 TCCTGCACTCCGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 397
 QY 61 GluAlaCysLeuProLeuGluIleuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
 Db 398 GAGGCTGCTGACCTGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATG 457
 QY 81 SerIleuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
 Db 458 TCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 517
 QY 101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
 Db 518 TGCTTACAGAT 577
 QY 121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
 Db 578 GCAAGCTGTTAATGATCTTAAGGCAAGATCTTCTGATCAAAACATGCTGACAGCT 637
 QY 141 IleAspGluLeuLeuGlnAlaLeuAsnPhaSerValIleThrValProGlnLysSerSer 160
 Db 638 ATGTATGAGCTGTTACAGGCCCTGAAATGTCACAGTGTGCTGCTGCTGCTGCTGCTGCT 697
 QY 161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuGlyLysLeuLeuHisAlaPhe 180
 Db 698 CTGGAAGAACCAAGATTTTATTAATAAATAAATCAAGCTCTGCAATCTCTTCATGCTTTC 757
 QY 181 ArgIleArgAlaValIleThrIleAspArgMetSerTyrIleuAsnSerSer 197
 Db 758 AGAATGCTGACGAGACCATCAATAGATGATGATGATGATGATGATGATGATGATGATG 808

RESULT 14
 US-09-917-265-35
 : Sequence 35, Application US/09917265
 : Patent No. US20020052030A1
 : GENERAL INFORMATION:
 : APPLICANT: Wonderling, Ramani S.
 : APPLICANT: Boroughs, Karen L.
 : TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
 : FILE REFERENCE: IM-5
 : CURRENT APPLICATION NUMBER: US/09/917,265
 : CURRENT FILING DATE: 2001-07-27

```

? PRIOR APPLICATION NUMBER: 60/223,016
? PRIOR FILING DATE: 2000-08-04
? NUMBER OF SEQ ID NOS: 109
? SOFTWARE: Patentin version 3.1
? SEQ ID NO 35
? LENGTH: 591
? TYPE: DNA
? ORGANISM: Felis catus
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1)..(591)
? OTHER INFORMATION:
US-09-917-265-35

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| | |
|------------------------|-----------|
| Alignment Scores: | |
| Pred. No.: | 7,21e-112 |
| Score: | 929.00 |
| Percent Similarity: | 95.94% |
| Best Local Similarity: | 92.39% |
| Query Match: | 93.46% |
| DB: | 10 |
| | |
| Length: | 591 |
| Matches: | 182 |
| Conservative: | 7 |
| Mismatches: | 8 |
| Indels: | 0 |
| Gaps: | 0 |

US-09-917-265-50 (1-197) x US-09-917-265-35 (1-591)

| | | |
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| QY | ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln | 2 |
| Db | 1 AGCAACCTCCACACACCACCAACCCAGGAATGTTCCAGTGGCTTAACCACTCCCAA | 60 |
| QY | 21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnIlySalArgGlnThrLeuGlyLeuTr | 40 |
| Db | 61 ACCCTGCTGGAGACCATCAGCAACACGCTTGAGAAAGCCACAGCAACACTGAAATTTAC | 120 |
| QY | 41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal | 60 |
| Db | 121 TCTTGACATTCCGAAGAGATTGATCATGAAGTATACAAAAAGATAAACACGACACAGTG | 180 |
| QY | 61 GluAlaCysLeuProLeuGluLeuLeuThrLeuAsnGlySerCysLeuAlaSerArgGluIle | 80 |
| Db | 181 GAGCGCTGTTACCACTGGAATTAACCATGAATGAGAGATTGGCTGGCTCCAGAGAAATC | 240 |
| QY | 81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu | 100 |
| Db | 241 TCTCTGATTAACATAATGGAGTGGCTGGCTGCCCTCCAGAAAGACCTGTTATATAGCAACCTG | 300 |
| QY | 101 CysLeuSerSerIleTryGlnAspLeuLysMetTryGlnMetGluPheLysAlaMetAsn | 120 |
| Db | 301 TGGCTTAGACGATCATGATGAGCACTTGAAGATGTACCGAGGTGGATTCACAGCCATGAAT | 360 |
| QY | 121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla | 140 |
| Db | 361 GCACACCTTTAATGGATCTTAAAGGCGAGATCTTTCGTGATCAAAACATCGTACACAGCT | 420 |
| QY | 141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValI ThrValProGlnLysSerSer | 160 |
| Db | 421 ATTGATGAGCTGTTACAGCCCTGATGATGCACAACTGAGCTGCGCCACAAACTCTCC | 480 |
| QY | 161 LeuGluGluProAspPheTryLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe | 180 |
| Db | 481 TTGGAGAAACCGGATTTTATAAATCAAAATCAAGCTCTGCATACCTTCACAGCTTTC | 540 |
| QY | 181 ArgIleArgValAlaValThrIleAspArgMetMetSerTryPheAsnSerSer | 197 |
| Db | 541 AGAATTCGGACAGTACCATCAATACGATGAGACTATTCGAATGCTTCC | 591 |

RESULT 15
115-09-017

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: Sequence 37 Application US/09917265
: Patent No. US20020052030A1
:
: GENERAL INFORMATION:
:
: APPLICANT: Wonderling, Ramani S.
: APPLICANT: Borouhns, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
: FILE REFERENCE: 1M-5

```

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:
: CURRENT APPLICATION NUMBER: US-09/917-265-37
:
: CURRENT FILING DATE: 2001-07-27
:
: PRIOR APPLICATION NUMBER: 60/223,016
:
: PRIOR FILING DATE: 2000-08-04
:
: NUMBER OF SEQ ID NOS: 109
:
: SOFTWARE: PatentIn version 3.1
:
: SEQ ID NO 37
:
: LENGTH: 591
:
: TYPE: DNA
:
: ORGANISM: Felis catus
:
: US-09-917-265-37

```

| | |
|------------------------|-----------|
| Alignment Scores: | |
| Pred. No.: | 7,21e-112 |
| Score: | 929.00 |
| Percent Similarity: | 95.94% |
| Best Local Similarity: | 92.39% |
| Query Match: | 93.46% |
| DB: | 10 |
| | |
| length: | 591 |
| Matches: | 180 |
| Conservative: | 7 |
| Mismatches: | 8 |
| Indels: | 0 |
| Gaps: | 0 |

US-09-917-265-50 (1-197) x US-09-917-265-37 (1-591)

| | | | |
|----|-----|--|-----|
| OY | I | ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln | 20 |
| Db | 591 | AGGAACCTCCACCACCCACCACCAACCCCGAAGAATGGTTCAGTGCTTAACCACTCCAA | 532 |
| OY | 21 | AsnLeuLeuArgAlaValSerAsnThrLeuGlnIleValArgGlnThrLeuGluMetLyr | 40 |
| Db | 531 | ACCTGTCTGGAGCCATCAAGCACACGCCTTGAAAGGCCAGACAAACTCTGGATTTTAC | 472 |
| OY | 41 | SerCysThrSerGluIuileAspHisGluAspIleThrLysAspLysThrSerThrVal | 60 |
| Db | 471 | TCTCGACCTCCGAGAGAGATGATCATGAAGTATCACAAAAGATAAACACGACAGTG | 412 |
| OY | 61 | GluAlaCysLeuProLeuIleuThrMetAsnGluSerCysLeuAlaSerArgGluIle | 80 |
| Db | 411 | GAGCCGTGTACCACTGGATTAAACAAGTAAGTACGTGCTGGCTTCCAGAGATC | 352 |
| OY | 81 | SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu | 100 |
| Db | 351 | TCCTGATTAACATAATGGAGTGGCGCTCCAAAGACCTCTTTATACGACCTG | 292 |
| OY | 101 | CysLeuSerSerIleTrgIuAspLeuLysMetLyrGlnMetGluPheLysAlaMetAsn | 120 |
| Db | 291 | TGCCTTAGCAGTATCTATGAGACCTTGAAGATGTACCAGTGGAGTTCAAAGCCATGAAT | 232 |
| OY | 121 | AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThala | 140 |
| Db | 231 | GCAAACTGTAAATGGATGCTAAAGGCCAGATCTTTCGGATCAAAAACATGTCTACAGCT | 172 |
| OY | 141 | IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer | 160 |
| Db | 171 | ATTGATGAGCTGTACAGGCCCTGAATGTCAACACAGTGTGACTGTGCCACAGAACTCTCC | 112 |
| OY | 161 | LeuGluGluProAspPheTrgLysThrLysIleLysLeuCysIleLeuGlnHisAlaPhe | 180 |
| Db | 111 | TTTGAGAAACCGATTTTTATAAACTAAATCAAGCTCTGCATATCTTCAAGCTTTC | 52 |
| OY | 181 | ArgIleArgAlaValThrIleAspArgMetMetSerLyrGluAsnSerSer | 197 |
| Db | 51 | AGAAATGTGTCACTGACCTCAATGAAATGATGACCTTTCGAAATGTCTCC | 1 |

Search completed: July 17, 2003, 09:56:10
Job time : 137.587 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 13:00:49 ; Search time 2559.04 Seconds
(without alignments)
10474.108 Million cell updates/sec

Title: US-09-917-265-52

Sequence: 1 atactgggaactgcgagaaga.....gggcattctgtctctgcagt 921

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Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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2: gb_htg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
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17: em_hum: *
18: em_in: *
19: em_mu: *
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25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *
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30: em_htg_hum: *
31: em_htg_inv: *
32: em_htg_other: *
33: em_htg_mus: *
34: em_htg_pin: *
35: em_htg_fod: *
36: em_htg_mam: *
37: em_htg_vrl: *
38: em_sy: *
39: em_htg_hum: *
40: em_htg_mus: *
41: em_htg_other: *

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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| 2 | 921 | 100.0 | 990 | 6 | E15017 | E15017 Canine mRNA |
| 3 | 819 | 88.9 | 1015 | 4 | CFU049100 | U49100 Canis fam11 |
| 4 | 759 | 82.4 | 990 | 6 | AR151061 | AR151061 Sequence |
| 5 | 521 | 56.6 | 588 | 4 | AF349536 | AF349536 Canis fam |
| 6 | 444 | 48.2 | 452 | 4 | AF333121 | AF333121 Canis fam |
| 7 | 387 | 42.0 | 446 | 4 | AF091134 | AF091134 Canis fam |
| 8 | 143 | 15.5 | 990 | 6 | AX154603 | AX154603 Sequence |
| 9 | 128 | 13.9 | 984 | 6 | AX154599 | AX154599 Sequence |
| 10 | 95 | 10.3 | 984 | 6 | AX154600 | AX154600 Sequence |
| 11 | 75 | 8.1 | 969 | 6 | AX154601 | AX154601 Sequence |
| 12 | 72 | 7.8 | 975 | 6 | AX154597 | AX154597 Sequence |
| 13 | 66 | 7.2 | 431 | 4 | AF054607 | AF054607 Fells cat |
| 14 | 66 | 7.2 | 990 | 4 | FCU083184 | U83184 Fells cat |
| 15 | 66 | 7.2 | 990 | 6 | AX076200 | AX076200 Sequence |
| 16 | 66 | 7.2 | 990 | 6 | AX076482 | AX076482 Sequence |
| 17 | 66 | 7.2 | 1006 | 4 | FCU112P40 | Y07762 F. catus mRN |
| 18 | 66 | 7.2 | 4522 | 6 | AX076209 | AX076209 Sequence |
| 19 | 66 | 7.2 | 4522 | 6 | AX076476 | AX076476 Sequence |
| 20 | 47 | 5.1 | 1005 | 9 | CTU19834 | U19834 Cercopithec |
| 21 | 47 | 5.1 | 1080 | 9 | MMU19841 | AX154602 Sequence |
| 22 | 46 | 5.0 | 975 | 6 | AX154602 | AX154602 Sequence |
| 23 | 46 | 5.0 | 987 | 6 | AR008950 | AR008950 Sequence |
| 24 | 46 | 5.0 | 987 | 6 | AX154633 | AX154633 Sequence |
| 25 | 46 | 5.0 | 987 | 6 | BD007070 | BD007070 IL-12 gen |
| 26 | 46 | 5.0 | 987 | 6 | BD007076 | BD007076 Gene exp |
| 27 | 46 | 5.0 | 987 | 6 | I28591 | I28591 Sequence 1 |
| 28 | 46 | 5.0 | 1007 | 9 | AF180563 | AF180563 Homo sapi |
| 29 | 46 | 5.0 | 1018 | 6 | AR052857 | AR052857 Sequence |
| 30 | 46 | 5.0 | 1389 | 6 | AX084106 | AX084106 Sequence |
| 31 | 46 | 5.0 | 1399 | 6 | AR091391 | AR091391 Sequence |
| 32 | 46 | 5.0 | 1399 | 6 | HUWCLMF40 | M65272 Human cytot |
| 33 | 46 | 5.0 | 1560 | 6 | AR091395 | AR091395 Sequence |
| 34 | 46 | 5.0 | 1623 | 6 | AR091394 | AR091394 Sequence |
| 35 | 46 | 5.0 | 1870 | 6 | A92079 | A92079 Sequence 3 |
| 36 | 46 | 5.0 | 2318 | 6 | HUWKSPP40 | M65290 Human natur |
| 37 | 46 | 5.0 | 2362 | 6 | AR082684 | AR082684 Sequence |
| 38 | 46 | 5.0 | 2362 | 6 | ARI22960 | ARI22960 Sequence |
| 39 | 46 | 5.0 | 2362 | 6 | I28325 | I28325 Sequence 1 |
| 40 | 46 | 5.0 | 2362 | 6 | 189770 | 189770 Sequence 1 |
| 41 | 46 | 5.0 | 6139 | 6 | AR091393 | AR091393 Sequence |
| 42 | 46 | 5.0 | 15648 | 9 | AF512686 | AF512686 Homo sapi |
| 43 | 46 | 5.0 | 18340 | 9 | AY008847 | AY008847 Homo sapi |
| 44 | 46 | 5.0 | 108511 | 9 | AC011418 | AC011418 Homo sapi |
| 45 | 44 | 4.8 | 525 | 4 | CEU10160 | U10160 Cervus elap |

ALIGNMENTS

RESULT 1
AR151071
LOCUS AR151071 990 bp DNA
DEFINITION Sequence 11 from patent US 6231850.
ACCESSION AR151071
VERSION AR151071.1 GI:15117121
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 990)
AUTHORS Okano, F., Satoh, M. and Yamada, K.
TITLE Canine Interleukin 12
JOURNAL Patent: US 6231850-A 11 15-MAY-2001;
FEATURES Location/Qualifiers

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source
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/organism="unknown"
BASE COUNT 279 a 244 c 249 g 218 t
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Query Match 100.0%; Score 921; DB 6; Length 990;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATATGGAACTGGAGAAAGATGTTTATGTTGATGAGTGGAGCGACCCCTGATGCCCC 60
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QY 61 GGAGAAATGTTGCTCTCACTCCATCCCTGAGAGAGATGACATCACTTGGACCTCA 120
DB 127 GGAGAAATGTTGCTCTCACTCCATCCCTGAGAGAGATGACATCACTTGGACCTCA 186
QY 121 GGCGAGAGCAGTAAAGTCTAGTCTGGTAAACTCTGACCATCCAAAGTCAAGAAATTT 180
DB 187 GGCGAGAGCAGTAAAGTCTAGTCTGGTAAACTCTGACCATCCAAAGTCAAGAAATTT 246
QY 181 GGAGATGCTGGCAGTATACCTGCATTAAGAGGAGGAGGTTCTGAGCGCTGACTCTG 240
DB 247 GGAGATGCTGGCAGTATACCTGCATTAAGAGGAGGAGGTTCTGAGCGCTGACTCTG 306
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DB 307 TTGATTACAAAAAAGAGATGGAATTTGGTCCACTGATATCTTAAAGAGAGAGAGAA 366
QY 301 TCCAAAAATTAAGATCTTTCTGAAATGTGAGGCAAAAGATTAATCTGAGCTTCACATGC 360
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QY 361 TGGTGGCTGAGGCAATCACTAGTATGTAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
DB 427 TGGTGGCTGAGGCAATCACTAGTATGTAATTCAGTGTCAAAAGTAGCAGAGGCTTC 486
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DB 487 TCTGACCCCGAAGGGGTGACATGTGAGCAGTACACTTTCAGCAGAGAGGGTCAAGTG 546
QY 481 GACAACAGGATTTAAGAGTACAGTGAAGTACAGAGGAGGAGTGGCTCCCTCT 540
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QY 601 AACTACACGACAGCTTCTTCATCAGAGACATCATCAAAACAGACCCACCAAACTTG 660
DB 667 AACTACACGACAGCTTCTTCATCAGAGACATCATCAAAACAGACCCACCAAACTTG 726
QY 661 CACTGAAGCATTTGAAATTTCTCGGACAGTGAAGTTCGTTGGGAATCCCGGACAC 720
DB 727 CACTGAAGCATTTGAAATTTCTCGGACAGTGAAGTTCGTTGGGAATCCCGGACAC 786
QY 721 TGGAGCACCACATTCCTCTCTCTGACATTTTTCATACAGGCGCCAGGGCAAGAAC 780
DB 787 TGGAGCACCACATTCCTCTCTCTGACATTTTTCATACAGGCGCCAGGGCAAGAAC 846
QY 781 AATAGAGAAAAAGATAGACTCTGCTGAGACAGACCTCAGCCAAAGTCTGCTGACAC 840
DB 847 AATAGAGAAAAAGATAGACTCTGCTGAGACAGACCTCAGCCAAAGTCTGCTGACAC 906
QY 841 AAGGATGCCAAGATCCGCGTGAAGCCCGGAGACCGGCTACTATAGTTTCATCTGAGAGAC 900
DB 907 AAGGATGCCAAGATCCGCGTGAAGCCCGGAGACCGGCTACTATAGTTTCATCTGAGAGAC 966
QY 901 TGGGCACTGTGTCTGCTGACT 921
DB 967 TGGGCACTGTGTCTGCTGACT 987

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RESULT 2
E15017 990 bp DNA linear PAT 28-JUL-1999
LOCUS Canine mRNA for interleukin 12 40kDa subunit, complete cds.
DEFINITION E15017
ACCESSION E15017
VERSION E15017.1 GI:5709700
KEYWORDS JP 1998036397-A/1.
SOURCE Canis sp.
ORGANISM Canis sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 990)
AUTHORS Okano, F.
TITLE CANINE INTERLEUKIN 12 AND ITS PRODUCTION
JOURNAL Patent: JP 1998036397-A 1 10-FEB-1998;
TORAY IND INC
COMMENT OS Canis sp. (dog)
PN JP 1998036397-A/1
PD 10-FEB-1998
PE 08-NOV-1996 JP 1996296789
PR 08-NOV-1995 JP 95P 289729, 23-MAY-1996 JP 96P 128104 PI
OKANO FUMIYOSHI
PC C07K14/54, C07H21/04, C12N5/10, C12N15/09, C12P21/02, (C12N5/10, PC
C12R1:91);
PC (C12P21/02, C12R1:91);
CC strandedness: Double;
CC topology: Linear;
FH Key Location/Qualifiers
FT source 1. .990
FT /organism='Canis sp.'
FT /tissue-type='liver'
FT CDS 1. .990
FT /product='interleukin 12 40kDa subunit'.
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1. .990
/organism="Canis sp."
/db_xref="taxon:9616"
BASE COUNT 279 a 244 c 249 g 218 t
ORIGIN

Query Match 100.0%; Score 921; DB 6; Length 990;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATATGGAACTGGAGAAAGATGTTTATGTTGATGAGTGGAGCGACCCCTGATGCCCC 60
DB 67 ATATGGAACTGGAGAAAGATGTTTATGTTGATGAGTGGAGCGACCCCTGATGCCCC 126
QY 61 GGAGAAATGTTGCTCTCACTCCATCCCTGAGAGAGATGACATCACTTGGACCTCA 120
DB 127 GGAGAAATGTTGCTCTCACTCCATCCCTGAGAGAGATGACATCACTTGGACCTCA 186
QY 121 GGCGAGAGCAGTAAAGTCTAGTCTGGTAAACTCTGACCATCCAAAGTCAAGAAATTT 180
DB 187 GGCGAGAGCAGTAAAGTCTAGTCTGGTAAACTCTGACCATCCAAAGTCAAGAAATTT 246
QY 181 GGAGATGCTGGCAGTATACCTGCATTAAGAGGAGGAGGTTCTGAGCGCTGACTCTG 240
DB 247 GGAGATGCTGGCAGTATACCTGCATTAAGAGGAGGAGGTTCTGAGCGCTGACTCTG 306
QY 241 TTGATTACAAAAAAGAGATGGAATTTGGTCCACTGATATCTTAAAGAGAGAGAGAA 300
DB 307 TTGATTACAAAAAAGAGATGGAATTTGGTCCACTGATATCTTAAAGAGAGAGAGAA 366
QY 301 TCCAAAAATTAAGATCTTTCTGAAATGTGAGGCAAAAGATTAATCTGAGCTTCACATGC 360
DB 367 TCCAAAAATTAAGATCTTTCTGAAATGTGAGGCAAAAGATTAATCTGAGCTTCACATGC 426
QY 361 TGGTGGCTGAGGCAATCACTAGTATGTAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
DB 427 TGGTGGCTGAGGCAATCACTAGTATGTAATTCAGTGTCAAAAGTAGCAGAGGCTTC 486

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QY 421 TCTGACCCCAAGCGGTGACATGTGGACACTGTGACACTTTTCAGCAGAGAGGCTGAGAGTG 480
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Db 487 TCTGACCCCAAGCGGTGACATGTGGACACTGTGACACTTTTCAGCAGAGAGGCTGAGAGTG 546
QY 481 GACAACAGAGGATTAAGAACTACACAGTGGAGTGTGAGAGGAGGCTGCTGCCCTCT 540
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Db 547 GACAACAGAGGATTAAGAACTACACAGTGGAGTGTGAGAGGAGGCTGCTGCCCTCT 506
QY 541 GCCGAGAGAGCCCTACCCATCTGAGTGTGTGTGATGCTATTTCACAACTCAAGTATGAA 600
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Db 607 GCCGAGAGAGCCCTACCCATCTGAGTGTGTGTGATGCTATTTCACAACTCAAGTATGAA 666
QY 601 AACTACACAGCAGCTTCTTCATCAGAGACATCATCAAAACAGAGCCCAACCAACTCTG 660
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Db 667 AACTACACAGCAGCTTCTTCATCAGAGACATCATCAAAACAGAGCCCAACCAACTCTG 726
QY 661 CAGCTGAAGCCATTGAAATAATTCGCGACGCTGGAGTCACTGGGAATACCCGACAC 720
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Db 727 CAGCTGAAGCCATTGAAATAATTCGCGACGCTGGAGTCACTGGGAATACCCGACAC 786
QY 721 TGGAGCACCCACATCT 780
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Db 787 TGGAGCACCCACATCT 846
QY 781 AATAGCAAAAGAAAGATAGACTCTGCGTGAGCAAGACCTGAGCCAAAGGTGTGTGCGAC 840
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Db 847 AATAGCAAAAGAAAGATAGACTCTGCGTGAGCAAGACCTGAGCCAAAGGTGTGTGCGAC 906
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Db 907 AAGATGCCAAGATCCGCTGCCAAGCCGAGACCCGCTACTATAGTTCTCTCTGAGAGC 966
QY 901 TGGCATCTGTCTCTCTGACT 921
|||||
Db 967 TGGCATCTGTCTCTCTGACT 987

RESULT 3
CFU49100
LOCUS CFU49100 1015 bp mRNA linear MAM 13-MAR-1996
DEFINITION Canis familiaris Interleukin-12 p40 subunit mRNA, complete cds.
ACCESSION U49100
VERSION U49100.1 GI:1223907
KEYWORDS
SOURCE
ORGANISM Canis familiaris.
Canis familiaris.
Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 1015)
Belke-Louis G.F. and Bueltner, M.
Cloning and sequence analysis of the p35 and p40 subunits of canine
Interleukin-12
Unpublished
2 (bases 1 to 1015)
Belke-Louis G.F.
Direct Submission
Submitted (13-FEB-1996) Georg F. Belke-Louis, Institute of Med.
Microbiology, Veterinaerstr. 13, Muenchen, D-80539, Germany
location/Qualifiers
1..1015
/organism="Canis familiaris"
/db_xref="taxon:9615"
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/codon_start=-1
/product="Interleukin-12 p40 subunit"
/protein_id="AA092059.1"
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BASE COUNT 285 a 251 c 254 g 225 t
ORIGIN
Query Match 88.9%; Score 819; DB 4; Length 1015;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 919; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 127 GGAGAAATGGTGTGCTCACCCTGCATACCCCTGAGAGAAATGACATCACTTTGACCTCA 186
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QY 661 CAGCTGAAGCCATTGAAATAATTCGCGACGCTGGAGTCACTGGGAATACCCGACAC 720
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Db 727 CAGCTGAAGCCATTGAAATAATTCGCGACGCTGGAGTCACTGGGAATACCCGACAC 786
QY 721 TGGAGCACCCACATCT 780
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Db 787 TGGAGCACCCACATCT 846
QY 781 AATAGAGAAAGAAAGATAGACTCTGCGTGAGCAAGACCTGAGCCAAAGGTGTGTGCGAC 840
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Db 847 AATAGAGAAAGAAAGATAGACTCTGCGTGAGCAAGACCTGAGCCAAAGGTGTGTGCGAC 906
QY 841 AAGATGCCAAGATCCGCTGCCAAGCCGAGACCCGCTACTATAGTTCTCTCTGAGAGC 900
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Db 907 AAGATGCCAAGATCCGCTGCCAAGCCGAGACCCGCTACTATAGTTCTCTCTGAGAGC 966
QY 901 TGGCATCTGTCTCTCTGACT 921
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Db 967 TGGCATCTGTCTCTCTGACT 987

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RESULT 4
LOCUS AR151061 990 bp DNA Linear PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 6231850.
ACCESSION AR151061
VERSION AR151061.1 GI:15117111
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 990)
AUTHORS Okano, F., Satoh, M. and Yamada, K.
TITLE Canine Interleukin 12
JOURNAL Patent: US 6231850-A 1 15-MAY-2001;
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BASE COUNT 278 a 243 c 251 g 218 t
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Query Match 82.4%; Score 759; DB 6; Length 990;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 909; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATATGGGAACCTGGGAGAAAGATGTTTATGTTGTAGAGTTGGACCTGGATGCCCC 60
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QY 61 GGAGAAATGGTGTCTCACCCTGCCATACCCCTGAAGAAGATGATCATCTTGACCTCA 120
DB 127 GGAGAAATGGTGTCTCACCCTGCCATACCCCTGAAGAAGATGATCATCTTGACCTCA 186
QY 121 GCGCAGAGCAGTGAAGTCTAGTCTGTGTAAGAACTGTGACATCCAAAGTCAAAATTT 180
DB 187 GCGCAGAGCAGTGAAGTCTAGTCTGTGTAAGAACTGTGACATCCAAAGTCAAAATTT 246
QY 181 GGAGATCTGGCCGCTTACCTGCCATTAAGGAGGCAAGTTCTGAGCCGCTACTCTCTG 240
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DB 307 TTGATTCACAAAAAGAGATGGAATTTGGTCCACTGATATCTTAAAGAAAGAAAGAA 366
QY 301 TCCAAAAATTAAGATCTTTCTGAAATGTGAGGCAAGATTAATTTCTGAGCTTTACATGC 360
DB 367 TCCAAAAATTAAGATCTTTCTGAAATGTGAGGCAAGATTAATTTCTGAGCTTTACATGC 426
QY 361 TGGTGGCTGAGGCAATCAGTACTGATTTGAATTCAGTGTCAAAAGTACAGAGGCTTC 420
DB 427 TGGTGGCTGAGGCAATCAGTACTGATTTGAATTCAGTGTCAAAAGTACAGAGGCTTC 486
QY 421 TCTGACCCCCAAGGGGTGACATGTGAGCAGTACACTTTACAGAGAGGGTCAAGTGTG 480
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DB 667 AACTACACGACGAGCTTCTTCATCAGAGACATCATCAACACGAGCCCAACCAACTGTG 726
QY 661 CAGCTGAACCATTTGAAAAATTTCTGCGCAGTGTGAGAGTCACTGGGAATACCCGACAC 720
DB 727 CAGCTGAACCATTTGAAAAATTTCTGCGCAGTGTGAGAGTCACTGGGAATACCCGACAC 786
QY 721 TGGAGACACCCACATTTCTTCCCTTGACATTTTGCATACAGGCCCAAGGCAAGAAC 780

DB 787 TGGAGACACCCACATTTCTTCCCTTGACATTTTGCATACAGGCCCAAGGCAAGAAC 846
QY 781 AATAGAGAAAAAGAAAGATAGACTGTGCTGAGACAGACCTCAGCAGAGTGTGCTCCAC 840
DB 847 AATAGAGAAAAAGAAAGATAGACTGTGCTGAGACAGACCTCAGCAGAGTGTGCTCCAC 906
QY 841 AAGATGCCCAAGATCCGCGTGCAGAACCCGAGACCCCTACTATATGTTCACTCTGAGACGAC 900
DB 907 AAGATGCCCAAGATCCGCGTGCAGAACCCGAGACCCCTACTATATGTTCACTCTGAGACGAC 966
QY 901 TGGGATCTGTGT 912
DB 967 TGGGATCTGTGT 978

RESULT 5
LOCUS AF349536 588 bp mRNA Linear MAM 17-MAY-2001
DEFINITION Canis familiaris Interleukin-12 subunit p40 mRNA, partial cds.
ACCESSION AF349536
VERSION AF349536.1 GI:14133584
KEYWORDS
SOURCE
ORGANISM Canis familiaris.
    Canis familiaris.
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 588)
AUTHORS Fontana, S., Groene, A., Koenig, M. and Baumgaertner, W.
TITLE Sequence of canine interleukin-12-p40 mRNA in DH82-cells
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 588)
AUTHORS Fontana, S., Groene, A., Koenig, M. and Baumgaertner, W.
TITLE Direct Submission
JOURNAL Submitted (15-FEB-2001) Institute of Pathology,
    Justus-Liebig-University, Frankfurt Str. 96, Giessen 35392,
    Germany
FEATURES
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BASE COUNT 167 a 124 c 155 g 142 t
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Best Local Similarity 100.0%; Pred. No. 8.3e-280;
Matches 521; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGGGAACCTGGGAGAAAGATGTTTATGTTGTAGAGTTGGACCTGGATGCCCC 60
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QY 61 GGAGAAATGGTGTCTCACCCTGCCATACCCCTGAAGAAGATGATCATCTTGACCTCA 120
DB 120 GGAGAAATGGTGTCTCACCCTGCCATACCCCTGAAGAAGATGATCATCTTGACCTCA 179
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DB 180 GCGCAGAGCAGTGAAGTCTAGTCTGTGTAAGAACTGTGACATCCAAAGTCAAAATTT 239
QY 181 GGAGATGTGGCCAGTATACCTGCCATTAAGAGGCAAGTGTCTGAGCCGCTCACTCTG 240
DB 240 GGAGATGTGGCCAGTATACCTGCCATTAAGAGGCAAGTGTCTGAGCCGCTCACTCTG 299

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| QY | 301 | TCCAAAAAATAGATCTTCTGTAATGTGAGCCAAAGATTTATTCGAGCGTTTCAGATGC | 360 |
| Db | 360 | TCCAAAAAATAGATCTTCTGTAATGTGAGCCAAAGATTTATTCGAGCGTTTCAGATGC | 419 |
| QY | 361 | TGTGGCGTGACGGCAATCAGTACGATTTGAAATTCAGTGTCCAAAGTAGCAGAGCGTTTC | 420 |
| Db | 420 | TGTGGCGTGACGGCAATCAGTACGATTTGAAATTCAGTGTCCAAAGTAGCAGAGCGTTTC | 479 |
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| Db | 480 | TCTACCCCGCCAAAGGGGTGACATGTGACACAGTACACTTTGACGACGAGAGGGTGCAGATG | 539 |
| QY | 481 | GACAAACAGAGTTATTAAGACGTACACAGTGGAGTGTCCAGA | 521 |
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| RESULT 6 | |
| AF333121 | |
| LOCUS | 452 bp mRNA linear |
| DEFINITION | Canis familiaris interleukin 12 subunit p40 mRNA, partial cds. |
| ACCESSION | AF333121 |
| VERSION | AF333121.1 GI:12667429 |

| SOURCE ORGANISM | REFERENCE |
|--|-----------|
| <i>Canis familiaris</i> . | |
| <i>Canis familiaris</i> . | |
| <i>Eukaryotes</i> : Metazoa: Chordata: Caninata: Vertebrata: Euteleostomi: | |
| <i>Mammalia</i> : Eutheria: Carnivora: Flissipedia: Canidae: Canis. | |
| 1 (bases 1 to 452) | |

JOURNAL: *Unpublished*
REFERENCE: 2 (cases 1 to 452)
AUTHORS: Markus, S. and Baumgaertner, W.
TITLE: Direct Submission
JOURNAL: Submitted (03-JAN-2001) Department of Veterinary Pathology,
Justus-Liebig-University of Giessen, Frankfurt/Strasse 96
Giessen 35392, Germany

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FEATURES
source
location/Qualifiers
1..452
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/cell_line="DH 82"
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CDS
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/codon_start=2
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/translation="TCTHPEDDITWTSAQSSSEVIGSKTLLTVK
GGVLRSLILIKKEDQIWSTDLKEKSKNKIPLCEAKNVSGL
DKFSVSKRSGSDPGQVTCGAVTLARVRVNDNRYKKYVECEQ

```

| | | | | |
|-----------------------|----------------|-------------------|----------|------------|
| Query Match | 48.2% | Score 444 | DB 4 | Length 452 |
| Best Local Similarity | 100.0% | Pred. No. 11e-236 | | |
| Matches 444 | Conservative 0 | Mismatches 0 | Indels 0 | |

| | | |
|----|----|---|
| Qy | 78 | CACCTGCATACCCCTGAGAGAGATGACATCATCTTGAGACCTGAGCGAGAGCA |
| | | |
| Db | 1 | CACCTGCATACCCCTGAGAGAGATGACATCATCTTGAGACCTGAGCGAGAGCA |

| | | | |
|----|-----|---|-----|
| OY | 198 | TACCTGCCATAAAGCAGGCGAGTTCTGAGCCGCTACTCCCTGTTGATTCCACAAAAAGA | 257 |
| Db | 121 | TACCGCCATAAAGAGGCGAAGGTTCTGAGCCGCTACCTCCGTTGATTCCAAAAAGA | 180 |
| OY | 258 | AGATGGAAATTGGTCGCTCAGTCGATATCTTTAAAGCAGAGAAGAAATCCAAAAATTAAGATCTT | 317 |
| Db | 181 | AGATGGAAATTGGTCGCTCAGTCGATATCTTTAAAGCAGAGAAGAAATCCAAAAATTAAGATCTT | 240 |
| OY | 318 | TCCTGAATGTGAGGCAAGAAATTATCTTGAGACGTTTCACATGCTGGTGCTGACGGCAAT | 377 |
| Db | 241 | TCTGAAATGTGAGGCAAGAAATTATCTTGAGACGTTTCACATGCTGGTGCTGACGGCAAT | 300 |
| OY | 378 | CAGTTCGTATTTGAATTCAGTCGTCAAAAAGTGTGCAGAGGCTTCCTGACCCCCAAGGGGT | 437 |
| Db | 301 | CAGTTCGTATTTGAATTCAGTCGTCAAAAAGTGTGCAGAGGCTTCCTGACCCCCAAGGGGT | 360 |
| OY | 438 | GACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTTCAGAGTGGACAAACAGGGAATTATTA | 497 |
| Db | 361 | GACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTTCAGAGTGGACAAACAGGGAATTATTA | 420 |

| | |
|------------|--|
| RESULT | 7 |
| AF091134 | |
| LOCUS | 446 bp |
| DEFINITION | Canis familiaris interleukin-12 p40 mRNA, linear MAM 04-AUG-1999 |
| ACCESSION | AF091134 |
| VERSION | AF091134.1 GI:5690205 |
| KEYWORDS | . |
| SOURCE | Canis familiaris. |

ORGANISM *Canis familiaris*
 EUKARYOTA: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 1 (bases 1 to 446)
 REFERENCE German, A.-J., Helps, C. R., Harley R., Hall, E. J. and Day, M. J.
 AUTHORS Cloning and sequencing of canine IL-12 p40 mRNA
 TITLE

JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 FEATURES

Unpublished
 2 (bases 1 to 446)
 German, A. J., Helps, C. R., Harley, R., Hall, E. J. and Day, M. J.
 Direct Submission
 Submitted (12-SEP-1998) Department of Clinical Veterinary Science,
 University of Bristol, Langford House, Langford, Bristol, North
 Somerset BS40 5DU, United Kingdom
 Location/Qualifiers

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source
1. 446
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/db_xref="taxon:9615"
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/ncbi="11-12 p40"
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STDLKQEKESKNNKIFLKCEAKNNGSGFTGKMLAIATDLKFSVSKSSRSDPGVYTC
CAVTLISERVVDNRVDNRNYKTYDEDSACGSAAESLPIEVVDALP"

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| ORIGIN | 100 | 200 | 300 | 400 | 500 | 600 | 700 | 800 | 900 | 1000 |
|-----------------------|----------------|--|----------|------------|-----|-----|-----|-----|-----|------|
| Query Match | 42.0% | Score 387 | DB 4 | length 446 | | | | | | |
| Best Local Similarity | 99.8% | Pred. No. 8.8e+205 | | | | | | | | |
| Matches 437 | Conservative 0 | Mismatches 1 | Indels 0 | Gaps 0 | | | | | | |
| Q2 | 146 | CTGGTAAACCTCTACCAATCCAAAGATTGGAGATGCTGGCCAGATATACCTGCC | 205 | | | | | | | |

DB 8 CTGGTAAACCTGTGACATCCAGTCGAAGAATTGGAGATCGGCCGATTAACCTGCC b/
QY 206 ATAAAGGCGCAAGTTCTTGAGCCGCTACTCTCTTGCATTCACAAAAAGACATGGA 265
|||||

Db 68 ATAAAGGAGCGCAAGTTCGAGCCGCTCACTCCTGTTGATTCACAAAAAGAGTGA 127
QY 266 TTGGTCCACTGATATCTTAAAGAACAGAAATCAAAATTAAGATCTTCTGAAT 325
Db 128 TTGGTCCACTGATATCTTAAAGAACAGAAATCAAAATTAAGATCTTCTGAAT 187
QY 326 GTGAGCGCAAAATTAATTTCTGAGAGTTTCAATGCTGCTGAGCGCAATGACTG 385
Db 188 GTGAGCGCAAAATTAATTTCTGAGAGTTTCAATGCTGCTGAGCGCAATGACTG 247
QY 386 ATTTGAATTCAGTGTCAAAAGTAGCAGAGGCTTCTGTGACCCCAAGGGGTGACATG 445
Db 248 ATTTGAATTCAGTGTCAAAAGTAGCAGAGGCTTCTGTGACCCCAAGGGGTGACATG 307
QY 446 GAGCAGTGCACCTTTCAGCAGAGAGGCTCAGAGTGCACACAGGATTTAAGAGTACA 505
Db 308 GAGCAGTGCACCTTTCAGCAGAGAGGCTCAGAGTGCACACAGGATTTAAGAGTACA 367
QY 506 CAGTGGAGTGTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 565
Db 368 CAGTGGAGTGTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 427
QY 566 TCGTGGTGCATCTATTC 583
Db 428 TCGTGGTGCATCTATTC 445

RESULT 8
AX154603
LOCUS AX154603 990 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 7 from Patent WO0140257.
ACCESSION AX154603
VERSION AX154603.1 GI:14536186
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 990)
AUTHORS Leong,S.R. and Punnonen,J.
TITLE Cytokine polypeptides and nucleic acids
JOURNAL Patent: WO 0140257-A 7 07-JUN-2001;
Maxygen, Inc. (US)
FEATURES
source location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic Sequence"
BASE COUNT 270 a 250 c 254 g 216 t
ORIGIN

Query Match 15.5%; Score 143; DB 6; Length 990;
Best Local Similarity 100.0%; Pred. No. 3.5e-68;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 499 AAGTACACAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 558
Db 565 AAGTACACAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 624
QY 559 ATCGAGGTGCTGAGTGTGATTCATTCACACCTCAAGATGAAACTACACAGAGCTTC 618
Db 625 ATCGAGGTGCTGAGTGTGATTCATTCACACCTCAAGATGAAACTACACAGAGCTTC 684
QY 619 TTCATCAGACATCATCAACC 641
Db 685 TTCATCAGACATCATCAACC 707

RESULT 9
AX154599 984 bp DNA linear PAT 22-JUN-2001
LOCUS AX154599
DEFINITION Sequence 3 from Patent WO0140257.
ACCESSION AX154599
VERSION AX154599.1 GI:14536182

KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 984)
AUTHORS Leong,S.R. and Punnonen,J.
TITLE Cytokine polypeptides and nucleic acids
JOURNAL Patent: WO 0140257-A 3 07-JUN-2001;
Maxygen, Inc. (US)
FEATURES
source location/Qualifiers
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/organism="synthetic construct"
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/note="Synthetic Sequence"
BASE COUNT 267 a 246 c 254 g 217 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 8.7e-60;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 499 AAGTACACAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 558
Db 565 AAGTACACAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 624
QY 559 ATCGAGGTGCTGAGTGTGATTCATTCACACCTCAAGATGAAACTACACAGAGCTTC 618
Db 625 ATCGAGGTGCTGAGTGTGATTCATTCACACCTCAAGATGAAACTACACAGAGCTTC 684
QY 619 TTCATCAG 626
Db 685 TTCATCAG 692

RESULT 10
AX154600
LOCUS AX154600 984 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 4 from Patent WO0140257.
ACCESSION AX154600
VERSION AX154600.1 GI:14536183
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 984)
AUTHORS Leong,S.R. and Punnonen,J.
TITLE Cytokine polypeptides and nucleic acids
JOURNAL Patent: WO 0140257-A 4 07-JUN-2001;
Maxygen, Inc. (US)
FEATURES
source location/Qualifiers
1..984
/organism="synthetic construct"
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/note="Synthetic Sequence"
BASE COUNT 272 a 254 c 247 g 211 t
ORIGIN

Query Match 10.3%; Score 95; DB 6; Length 984;
Best Local Similarity 100.0%; Pred. No. 2.6e-41;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 520 GAGGAGAGTGCCTGCTGTGCGGAGAGAGCTACCATGAGGTGCTGTGATGCT 579
Db 586 GAGGAGAGTGCCTGCTGTGCGGAGAGAGCTACCATGAGGTGCTGTGATGCT 645
QY 580 ATTCACAGCTCAAGTATGAAACTACACAGAG 614
Db 646 ATTCACAGCTCAAGTATGAAACTACACAGAG 680

RESULT 11
AX154601 969 bp DNA linear PAT 22-JUN-2001
LOCUS AX154601

DEFINITION Sequence 5 from Patent WO0140257.
ACCESSION AX154601
VERSION AX154601.1 GI:14536184
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .969
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/note="Synthetic Sequence"
BASE COUNT 263 a 249 c 251 g 206 t
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Best Local Similarity 100.0%; Pred. No. 4; 1e-30;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 834 GTGCCACAGAGTCCAGATCCCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTG 893
Db 879 GTGCCACAGATCCAGATCCCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTG 938
OY 894 GAGCGACTGGGCATC 908
Db 939 GAGCGACTGGGCATC 953
RESULT 12
AX154597
LOCUS AX154597 975 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1 from Patent WO0140257.
ACCESSION AX154597
VERSION AX154597.1 GI:14536180
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .975
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic Sequence"
BASE COUNT 269 a 252 c 250 g 204 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2e-28;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 581 TTGCAAGCTCAAGTATGAAGCTACACGACGAGCTTCTTCATCAGACATCATCAAC 640
Db 632 TTGCAAGCTCAAGTATGAAGCTACACGACGAGCTTCTTCATCAGACATCATCAAC 691
OY 641 CACAGCCACCCA 652
Db 692 CACAGCCACCCA 703
RESULT 13
AF054607
LOCUS AF054607 431 bp mRNA linear MAM 26-JUL-2000
DEFINITION Felis catus interleukin 12 p40 subunit mRNA, partial cds.

ACCESSION AF054607
VERSION AF054607.1 GI:3126822
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
FEATURES
source
1. .431
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/note="Persistent FIV infection"
<1. .>431
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BASE COUNT 129 a 93 c 114 g 91 t 4 others
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Best Local Similarity 100.0%; Pred. No. 4; 6e-25;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 471 GGTGAGGTGACACAGGAGTTATAGAGTACACAGTGGAGTGCAGAGGCGAGTGC 530
Db 270 GGTGAGGTGACACAGGAGTTATAGAGTACACAGTGGAGTGCAGAGGCGAGTGC 329
OY 531 CTGCC 536
Db 330 CTGCC 335
RESULT 14
FCU83184
LOCUS FCU83184 990 bp mRNA linear MAM 16-JUL-1999
DEFINITION Felis catus interleukin-12 p40 subunit (IL-12) mRNA, complete cds.
ACCESSION U83184
VERSION U83184.1 GI:2735050
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
Felis catus.
Felis catus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
1 (bases 1 to 990)
Fehr, D., Dean, G. A., Huder, J., Fan, Z., Huettner, S., Higgins, J. W.,
Pedersen, N. C., and Lutz, H.
Nucleotide and predicted peptide sequence of feline interleukin-12
(IL-12)
DNA Seq. 8 (1-2), 77-82 (1997)
JOURNAL 98182592
MEDLINE 9522125
PUBMED
REFERENCE 2 (bases 1 to 990)
Fehr, D., Dean, G. A., Huder, J., Fan, Z., Huettner, S., Higgins, J. W.,

TITLE
JOURNAL

Pedersen, N.C. and Lutz, H.
Direct Submission
Submitted (24-DEC-1996) Clinical Laboratory, Department of Internal
Veterinary Medicine, University of Zurich, Winterthurerstrasse 260,
Zurich, ZH 8057, Switzerland

FEATURES

Location/Qualifiers
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CDS

/organism="Felis catus"
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/note="cytokine"
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/protein_id="AB93835.1"
/db_xref="GI:2735051"

BASE COUNT
ORIGIN

283 a 251 c 249 g 207 t

Query Match

Best Local Similarity 7.2%; Score 66; DB 4; Length 990;
Best Local Similarity 100.0%; Pred. No. 4.5e-25;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 471 GGTACAGTGGACACAGGATTATTAAGTACACAGTGTGACAGAGGCGAGTGC 530
|||||

Db 537 GGTACAGTGGACACAGGATTATTAAGTACACAGTGTGACAGAGGCGAGTGC 596
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OY 531 CTGCCC 536
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Db 597 CTGCCC 602

RESULT 15
AX076200

LOCUS AX076200 990 bp DNA Linear PAT 06-FEB-2001
DEFINITION Sequence 1 from Patent WO0104155.
ACCESSION AX076200
VERSION AX076200.1 GI:12710825

KEYWORDS

synthetic construct.
synthetic construct.

SOURCE

synthetic construct.
artificial sequences.

REFERENCE

1 (bases 1 to 990)

AUTHORS Lutz, H., Leutenegger, C., Pedersen, N., Schrott, M. and Wittig, B.
TITLE Feline Interleukin-12 as an immune stimulant
JOURNAL Patent: WO 0104155-A 1 18-JAN-2001;
Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE);
Universitaet Zurich (CH); THE REGENTS OF THE UNIVERSITY OF
CALIFORNIA (US)

FEATURES

Location/Qualifiers
1..990

/organism="synthetic construct"
/db_xref="taxon:32630"

BASE COUNT 283 a 249 c 248 g 210 t
ORIGIN

Query Match

Best Local Similarity 7.2%; Score 66; DB 6; Length 990;
Best Local Similarity 100.0%; Pred. No. 4.5e-25;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 471 GGTACAGTGGACACAGGATTATTAAGTACACAGTGTGACAGAGGCGAGTGC 530
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Db 537 GGTACAGTGGACACAGGATTATTAAGTACACAGTGTGACAGAGGCGAGTGC 596
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OY 531 CTGCCC 536
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Db 597 CTGCCC 602

Search completed: July 16, 2003, 19:39:14
Job time : 2561.24 secs

DR P-PSDB; AAW41791.

PT Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT veterinary medicine, e.g. antitumour, antiviral and vaccine adjuvant
PT activities are expected

PS Claim 10; Pages 10-11; 12pp; Japanese.

CC The present sequence encodes a canine interleukin-12 (IL-12) p40
CC subunit. A canine IL-12 comprising a p40 and p35 subunit is capable
CC of inducing an antiviral activating factor and the expression of
CC class II MHC molecules in canine tumour cells, stimulating
CC proliferation of canine blastogenic lymphocytes and activating
CC canine leukocytes to inhibit canine tumour cells. The canine IL-12
CC can be used in veterinary medicines, e.g. antitumour, antiviral and
CC vaccine adjuvant activities are expected.

SQ Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 other;

Query Match 100.0%; Score 921; DB 19; Length 990;

Matches 921; Conservative 0; Mismatches

Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

| | | | |
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| Db | 787 | TGAGACACCCCAATTCCTACTTCTCCCTGACATTTTTCATACAGGCCCAAGGCAC | 846 |
| Qy | 781 | AATAGGAAAGAAAGATAGACTCTGGGTGGCAAGACTCAGACAGGTGTGTGCCAC | 840 |
| Db | 847 | AATAGGAAAGAAAGATAGACTCTGGGTGGCAAGACTCAGCCAGGTGTGTGCCAC | 906 |
| Qy | 841 | AAGGATGCCAAGATCCGGCTGCGACGCCGAGACCCGCTACTATGTCATCTCTGAGCGAC | 900 |
| Db | 907 | AAGGATGCCAAGATCCGGCTGCGACGCCGAGACCCGCTACTATGTCATCTCTGAGCGAC | 966 |
| Qy | 901 | TGGCATCTGTGTCTCTGCAGT | 921 |
| Db | 967 | TGGCATCTGTGTCTCTGCAGT | 987 |

RESULT 2
AAK35625 standard; cDNA to mRNA: 990 BP.

RESULT 2
AAx35625
ID AAX35625 standard; cDNA to mRNA; 990 BP.

AC AAX35625;

DT 09-JUL-1999 (first entry)

DE Nucleic acid encoding canine Interleukin-12 (IL-12).

KW Interleukin-12; IL-12; dog; cat; immune disease; CatIL2; heterodimer
tumour; skin disease; infectious disease; allergic disease; ds.

OS Canis sp.

| FH | Key | Location/Qualifiers |
|----|-----|---------------------|
| 1 | 000 | |

FT
xy

/*tag= a

FT
xy

PN JP111106350-A.

PD 20-APR-1999.
yy

PF 15-MAY-1998; 98JJP-01333345.
XX

| | | |
|----|--------------|--------------|
| PR | 07-AUG-1997; | 97JP-0213/33 |
| PR | 16-MAY-1997: | 97JP-0127690 |

PR 16-MAY-1997; 97JP-0127690.

PA (TORA) TORAY IND INC.

DR WPI; 1999-308068/26-

XX
XX
E

PI for prevention and treatment of dog and cat immune diseases

XX
F2
CLAIM 1, page 14 15, 10pp, Japanese

CC The present sequence encodes canine interleukin-12 (IL-12). The
CC specification describes a method for the prevention and treatment
CC of dog and cat immune diseases. The treatment used an agent comprising
CC dog IL-12 (catil12) proteins to form a heterodimer. The agent is
CC useful for preventing and treating dog and cat immune diseases,
CC including tumours, skin diseases, infectious diseases and allergic
CC diseases.

SQ Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 other;

| Query match | Score | DB | Length |
|-------------|-------|-----|--------|
| 100.08; | 921; | 20; | 990; |

| | | | | | | | | | |
|---------|------|--------------|----|------------|----|--------|----|------|----|
| Matches | 921; | Conservative | 0; | Mismatches | 0; | Indels | 0; | Gaps | 0; |
|---------|------|--------------|----|------------|----|--------|----|------|----|

QY 1 ATATGGAACTGGAGAAATCTTATGTATGTTAGAGTTGGAACTGGACACCGTGAATGCCCC 60
Db 67 ATATGGAACTGGAGAAATCTTATGTATGTTAGAGTTGGAACTGGACACCGTGAATGCCCC 120
QY 61 GAGGAANTGTTGCTCTACCTGCATACCCCTGAAGAAGATGACATCATTGGACCTCA 120

| | | | |
|-----------|---|--|-----|
| Db | 127 | GGAGAGAAATGGTGCTCTCCATCCCTGCCATACCCTCGAAGAAGATGACATCACTTGGACCTCA | 186 |
| OY | 121 | GCGCAGACCACTGAAGTCTCTAGTTCTGGTAAAACTCTGACCAATCCAAAGTCAAAAGATTT | 180 |
| Db | 187 | GCCGAGACAGTGAAGTCTCTAGTTCTGGTAAAACTCTGACCAATCCAAAGTCAAAAGATTT | 246 |
| OY | 181 | GGAGATGCTGGCCACTATACCTGGCCATAAAGGACGCAAGCTTGTGAGCCGCTCAGTCCTG | 240 |
| Db | 247 | GGAGATGCTGGCCACTATACCTGGCCATAAAGGACGCAAGCTTGTGAGCCGCTCAGTCCTG | 306 |
| OY | 241 | TTGATTCCAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTTAAAGAACAGAAAGAA | 300 |
| Db | 307 | TTGATTCCAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTTAAAGAACAGAAAGAA | 366 |
| OY | 301 | TCGCAAAATTAAGATCTTCTTGAAATGTGAGGCAAGAATATTCTTGAGCTTTACATGC | 360 |
| Db | 367 | TCGCAAAATTAAGATCTTCTTGAAATGTGAGGCAAGAATATTCTTGAGCTTTACATGC | 426 |
| OY | 361 | TGCTGGCTGAGCGCCATCAGTACTGATTTGAAATTCAGTGTGCTGCTGCTGCTGCTGCTG | 420 |
| Db | 427 | TGCTGGCTGAGCGCCATCAGTACTGATTTGAAATTCAGTGTGCTGCTGCTGCTGCTGCTG | 486 |
| OY | 421 | TCGCAACCCCAAGGGGTGACATGTGGAGCAGTGACACTTTTCAGCAGAGAGGGTCAGAGTG | 480 |
| Db | 487 | TCGCAACCCCAAGGGGTGACATGTGGAGCAGTGACACTTTTCAGCAGAGAGGGTCAGAGTG | 546 |
| OY | 481 | GACAAACAGGGATTATTAACAGTACACAGTGGAGCTGTCAGAGAGGGCAGTCTGCTCCCTCT | 540 |
| Db | 547 | GACAAACAGGGATTATTAACAGTACACAGTGGAGCTGTCAGAGAGGGCAGTCTGCTCCCTCT | 606 |
| OY | 541 | GCCGAGAGAGACCCTACCCATCGAGGTGCTGGTGATGCTATTTCACAGCTCAAGTATGAA | 600 |
| Db | 607 | GCCGAGAGAGACCCTACCCATCGAGGTGCTGGTGATGCTATTTCACAGCTCAAGTATGAA | 666 |
| OY | 601 | AACATACACAGCAGCTTCTTCATCAGACATCATTAACACAGACCACCCACAAACTTG | 660 |
| Db | 667 | AACATACACAGCAGCTTCTTCATCAGACATCATTAACACAGACCACCCACAAACTTG | 726 |
| OY | 661 | CAGCTGAGAGCCATTAAAAATCTCGGCACGTGGAGGTGAGCGGGGAATACCCCGACAC | 720 |
| Db | 727 | CAGCTGAGAGCCATTAAAAATCTCGGCACGTGGAGGTGAGCGGGGAATACCCCGACAC | 786 |
| OY | 721 | TGCAACACCCACATTCCTACTTCCTCCCTGACATTTTGGATACAGGCCAGGCGCAAGAAC | 780 |
| Db | 787 | TGCAACACCCACATTCCTACTTCCTCCCTGACATTTTGGATACAGGCCAGGCGCAAGAAC | 846 |
| OY | 781 | AATGAGAGAAAAGAAATAGACTCTGGCGTGGACAGACACTCGAGCCAAAGTCTGTGCCAC | 840 |
| Db | 847 | AATGAGAGAAAAGAAATAGACTCTGGCGTGGACAGACACTCGAGCCAAAGTCTGTGCCAC | 906 |
| OY | 841 | AAGATGCGCAAGATCCGGTGCACAGCCCGAGACCGCTACTATAGTTCAATCTTGAGACGAC | 900 |
| Db | 907 | AAGATGCGCAAGATCCGGTGCACAGCCCGAGACCGCTACTATAGTTCAATCTTGAGACGAC | 966 |
| OY | 901 | TGGCAGTCTGTCTCTCTGCACT 921 | |
| Db | 967 | TGGCAGTCTGTCTCTCTGCACT 987 | |
| RESULT 3 | | | |
| AAOX03162 | | | |
| ID | AAOX03162 standard; cDNA to mRNA: 990 BP. | | |
| AC | AAOX03162: | | |
| XX | 30-MAR-1999 (first entry) | | |
| DE | Nucleic acid encoding canine interleukin 12. | | |
| KM | Canine: interleukin 12; IL-12; feline: immunological disease; tumour; | | |
| KM | skin disease; viral infection; allergic disease; breast tumour; | | |
| KM | oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma; | | |
| KM | othematoma; pneumoedema; skin soft pedicled soft tumour; anal tumour; | | |

| | |
|---------------------------|---|
| KM | otitis externa; dermatitis; eczema; fungal skin disease; pyoderma; |
| KW | allergic dermatitis; nettle rash; traumatic dermatitis; hair loss; |
| KV | dog parvovirus infection; distemper virus; cat plaque virus infection; |
| KX | feline leukaemia; allergy; pollinosis; ds. |
| XX | |
| OS | Canis sp. |
| FH | Key Location/Qualifiers |
| FT | CDS 1..990 |
| FT | /tag= a |
| FT | /product= interleukin_12 |
| XX | |
| PN | WO9851327-A1. |
| XX | |
| PD | 19-NOV-1998. |
| XX | |
| Pf | 07-MAY-1998; 98WO-JP02031. |
| XX | |
| PR | 16-MAY-1997; 97JP-0127690. |
| XX | |
| PA | (TORA) TORAY IND INC. |
| XX | |
| PI | Okano F, Satoh M, Yamada K; |
| DR | WPI; 1999-070100/06. |
| DR | P-P5DB; AAW84373. |
| XX | |
| PT | New therapeutic and prophylactic agents - comprise |
| PT | genetically-engineered canine Interleukin 12, used to treat, e.g. |
| PT | canine and feline immunological diseases |
| XX | |
| PS | Claim 1; Page 30-32; 45pp; Japanese. |
| CC | The present sequence encodes a canine interleukin 12 (IL-12) protein. |
| CC | The IL-12 protein can be used in therapeutic or prophylactic agents. |
| CC | The agents can be used to prevent and treat canine and feline |
| CC | immunological diseases including dog and cat tumours, skin diseases, |
| CC | viral infections and allergic diseases, especially tumours, breast |
| CC | tumour, eosinophilic granuloma, epidermoid tumour, skin tumour, lipoma, |
| CC | ottomatomas, pneumoedema, skin soft pedicled soft tumour and anal |
| CC | tumour; skin diseases, otitis externa, dermatitis, eczema, fungal |
| CC | diseases of the skin, pyoderma, allergic dermatitis, nettle rash, |
| CC | traumatic dermatitis and hair loss; infections; dog parvovirus infection |
| CC | and distemper virus; cat plaque virus infection and feline leukaemia, and |
| CC | allergic diseases, e.g. pollinosis. |
| SO | Sequence 990 BP: 279 A; 244 C; 249 G; 218 T; 0 other: |
| Query Match | 100.0%; Score 921; DB 20; Length 990; |
| Best Local Similarity | 100.0%; Pred. No. 0; |
| Matches 921; Conservative | 0; Mismatches 0; Indels 0; Gaps 0; |
| OY | I ATATGGGAACGTGAGAAAGATCTTATGCTGTACAGTTGCATCGCAACCCTGATGCCCCC 60 |
| Db | ATATGGGAACGTGAGAAAGATCTTATGCTGTACAGTTGCATCGCAACCCTGATGCCCCC 126 |
| OY | 61 GGAGAATAATGGTGTCCTCACCTGGCATACCCCTGAAGAAATGATCATTCTGGACCTCA 120 |
| Db | 127 GGAAAATAATGGTGTCCTCACCTGGCATACCCCTGAAGAAATGATCATTCTGGACCTCA 186 |
| OY | 121 GCGCAGAGCACTGAATGCTTAAGTTCTTGCTGTAAGAACTTGACATGCCAATCAAAGATT 180 |
| Db | 187 GCGCAGAGCACTGAATGCTTAAGTTCTTGCTGTAAGAACTTGACATGCCAATCAAAGATT 246 |
| OY | 181 GGAGATCTCGGCCAGTAGTACTCTGGCATTAAGAGAGCAAGGTTCTGACCCCTCACTCTG 240 |
| Db | 247 GGAGATCTCGGCCAGTAGTACTCTGGCATTAAGAGAGCAAGGTTCTGACCCCTCACTCTG 306 |
| OY | 241 TTGATTTCACAATAAAGAAGATGGAATTTGGTCTCACTGATATCTTAAAGAACAAGAA 300 |
| Db | 307 TTGATTTCACAATAAAGAAGATGGAATTTGGTCTCACTGATATCTTAAAGAACAAGAA 366 |
| OY | 301 TTCAAAAATAAGATCTTCTGAAAATGAGGCAAGAAATATATCTGGAAGTTCACATGC 360 |


```
OY 721 TGGAGCACCCACATTCCTACTCTCCCTGACATTTTCATACAGGCCAGGCAAGAAC 780
DB 787 TGGAGCACCCACATTCCTACTCTCCCTGACATTTTCATACAGGCCAGGCAAGAAC 846
OY 781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAGGTCGTGTGCCAC 840
DB 847 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAGGTCGTGTGCCAC 906
OY 841 AAGGATGCCAAGATCCCGGTGCAGACCCGCGTACTATAGTTCACTTGGAGCGAC 900
DB 907 AAGGATGCCAAGATCCCGGTGCAGACCCGCGTACTATAGTTCACTTGGAGCGAC 966
OY 901 TGGGCACTGTCTCTGCAGT 921
DB 967 TGGGCACTGTCTCTGCAGT 987

RESULT 5
AAV13816
ID AAV13816 standard; cDNA to mRNA; 990 BP.
AC AAV13816:
DT 14-MAY-1998 (first entry)
XX
XX 14-MAY-1998 (first entry)
XX
XX Canine IL-12 P40 subunit cDNA.
DE
XX Canine IL-12 P40 subunit; IL-12 P40 subunit; antitumour;
KM Canine: Interleukin-12 P40 subunit; IL-12 P40 subunit; antitumour;
KW antiviral; vaccine adjuvant; ds.
XX
XX Canis sp.
OS
XX
XX Key Location/Qualifiers
FT 1..990
FT CDS /*tag= a
FT /product= Interleukin-12_P40_subunit
PN JP10036397-A.
XX
XX 10-FEB-1998.
PD
XX 08-NOV-1996; 96JP-0296789.
PE
XX 23-MAY-1996; 96JP-0128104.
PR 08-NOV-1995; 95JP-0289729.
XX
XX (TORA ) TORAY IND INC.
PA
XX WPI: 1998-174914/16.
DR P-PSDB: AAM41790.
XX
XX Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT veterinary medicine, e.g. antitumour, antiviral and vaccine adjuvant
PT activities are expected
XX
XX Claim 8; Page 8; 12pp; Japanese.
XX
XX The present sequence encodes a canine interleukin-12 (IL-12) P40
XX subunit. A canine IL-12 comprising a P40 and P35 subunit is capable
XX of inducing an antiviral activating factor and the expression of
XX class II MHC molecules in canine tumour cells, stimulating
XX proliferation of canine blastogenic lymphocytes and activating
XX canine leukocytes to inhibit canine tumour cells. The canine IL-12
XX can be used in veterinary medicines, e.g. antitumour, antiviral and
XX vaccine adjuvant activities are expected.
XX
XX Sequence 990 BP: 278 A; 243 C; 251 G; 218 T; 0 other;
S0

Query Match 93.5%; Score 861; DB 19; Length 990;
Best Local Similarity 99.9%; Pred. NO. 0;
Matches 911; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1 ATATGGAACTGGAGAAAGATGTTATGTGTAGAGTTGAGCTGGACCCCTGATGCCCC 60
DB 67 ATATGGAACTGGAGAAAGATGTTATGTGTAGAGTTGAGCTGGACCCCTGATGCCCC 126
OY 61 GGAGAAATGTGTCTCCACCTGCCATACCCCTGAAGAAGATGACATCTTGGACCTCA 120
DB 127 GGAGAAATGTGTCTCCACCTGCCATACCCCTGAAGAAGATGACATCTTGGACCTCA 186
OY 121 GCGGACGACGATGAAGTCTGAGTCTGCTGAAACTGTCGACATCCAGTCGAAGAATTT 180
DB 187 GCGGACGACGATGAAGTCTGAGTCTGCTGAAACTGTCGACATCCAGTCGAAGAATTT 246
OY 181 GGAGATGCTGGCGCATATACCTGCCATTAAGGAGGCAAGTTCTGAGCCGCTCACTCCTG 240
DB 247 GGAGATGCTGGCGCATATACCTGCCATTAAGGAGGCAAGTTCTGAGCCGCTCACTCCTG 306
OY 241 TTGATTTCAAAAAAGAAAGATGAATTTGTCCACTGATATCTTAAAGGAAACAGAAAGAA 300
DB 307 TTGATTTCAAAAAAGAAAGATGAATTTGTCCACTGATATCTTAAAGGAAACAGAAAGAA 366
OY 301 TCCAAAAATTAAGATCTTTCTGAAATGTGAGGCAAAAGATTTATCTTGAGACGTTTCACATGC 360
DB 367 TCCAAAAATTAAGATCTTTCTGAAATGTGAGGCAAAAGATTTATCTTGAGACGTTTCACATGC 426
OY 361 TGGTGCTGACGGCAATCAGTACGTGATTTGAATTCAGTGTCCAAAGTACAGAGGCTTC 420
DB 427 TGGTGCTGACGGCAATCAGTACGTGATTTGAATTCAGTGTCCAAAGTACAGAGGCTTC 486
OY 421 TCTGACCCCAAGGGGTGACATGTGGACAGTGCACATTTTCAGCAGAGAGGTCAGAGT 480
DB 487 TCTGACCCCAAGGGGTGACATGTGGACAGTGCACATTTTCAGCAGAGAGGTCAGAGT 546
OY 481 CACAAACAGGATTTAAAGATACACAGTGCAGAGTGCAGAGGAGGAGTCTGCCCTCT 540
DB 547 GACAAACAGGATTTAAAGATACACAGTGCAGAGTGCAGAGGAGGAGTCTGCCCTCT 606
OY 541 GCCGAGGAGAGCTCCCATGAGGTGCTGGTGTGATTCATTCACAACTCAAGTATGAA 600
DB 607 GCCGAGGAGAGCTCCCATGAGGTGCTGGTGTGATTCATTCACAACTCAAGTATGAA 666
OY 601 AACTACACGACAGCTTCTTCATGACAGACATCATCAAAACGACCCACCAAACTGT 660
DB 667 AACTACACGACAGCTTCTTCATGACAGACATCATCAAAACGACCCACCAAACTGT 726
OY 661 CAGCTGAAGCCATGTAATAATTTCTGGCAGCTGGAGGTCTCACTGGGAATACCCTGACAC 720
DB 727 CAGCTGAAGCCATGTAATAATTTCTGGCAGCTGGAGGTCTCACTGGGAATACCCTGACAC 786
OY 721 TGGAGCACCCACATTCCTACTCTCCCTGACATTTTCATACAGGCCAGGCAAGAAC 780
DB 787 TGGAGCACCCACATTCCTACTCTCCCTGACATTTTCATACAGGCCAGGCAAGAAC 846
OY 781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAGGTCGTGTGCCAC 840
DB 847 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAGGTCGTGTGCCAC 906
OY 841 AAGGATGCCAAGATCCCGGTGCAGACCCGCGTACTATAGTTCACTTGGAGCGAC 900
DB 907 AAGGATGCCAAGATCCCGGTGCAGACCCGCGTACTATAGTTCACTTGGAGCGAC 966
OY 901 TGGGCACTGTGT 912
DB 967 TGGGCACTGTGT 978

RESULT 6
AAV35615
ID AAV35615 standard; cDNA to mRNA; 990 BP.
AC AAV35615:
DT 09-JUL-1999 (first entry)
XX
```

DE Nucleic acid encoding canine Interleukin-12 (IL-12).
 XX Interleukin-12; IL-12; dog; cat; immune disease; Ca112; heterodimer;
 KW tumour; skin disease; infectious disease; allergic disease; ds.
 XX
 OS Canis sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..990
 FT /*tag= a
 XX
 PN JP1106350-A.
 PD 20-APR-1999.
 XX
 PF 15-MAY-1998; 98JP-0133345.
 XX
 PR 07-AUG-1997; 97JP-0213755.
 PR 16-MAY-1997; 97JP-0127690.
 XX
 PA (TORA) TORAY IND INC.
 XX
 DR WP1; 1999-308068/26.
 DR P-PSDB; AAY02339.
 XX
 PT A prevention and treating agent containing interleukin 12 (Ca112) -
 PT for prevention and treatment of dog and cat immune diseases
 PS Claim 1; Page 12; 16pp; Japanese.
 XX
 CC The present sequence encodes canine interleukin-12 (IL-12). The
 CC specification describes a method for the prevention and treatment
 CC of dog and cat immune diseases. The treatment used an agent comprising
 CC dog IL-12 (Ca112) proteins to form a heterodimer. The agent is
 CC useful for preventing and treating dog and cat immune diseases,
 CC including tumours, skin diseases, infectious diseases and allergic
 CC diseases.
 XX
 SO Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 other:
 Query Match 93.5%; Score 861; DB 20; Length 990;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 911; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 487 TCTACCCCCCAAGGGGTGACATGTGAGCGAGTACCTTCCACAGAGAGGTCACAGTG 546
 QY 481 GACAAACAGGATTATTAAGAGTACACAGTGTGACAGAGGAGGAGTGGCTCCCTCT 540
 DB 547 GACAAACAGGATTATTAAGAGTACACAGTGTGACAGAGGAGGAGTGGCTCCCTCT 606
 QY 541 GCCGAGAGAGGCTTACCATTCGAGTGTGATGCTATTACAAAGCTCAAGTATGAA 600
 DB 607 GCCGAGAGAGGCTTACCATTCGAGTGTGATGCTATTACAAAGCTCAAGTATGAA 666
 QY 601 AACACACAGAGCTTCTTCATCAGAGCATCATCAACACAGACCCACCAAAAGCTG 660
 DB 667 AACACACAGAGCTTCTTCATCAGAGCATCATCAACACAGACCCACCAAAAGCTG 726
 QY 661 CAGCTGAAGCATTTGAAAAATTTCTGCGACGTGTGAGTGTGAGTGTGAGTGTGAG 720
 DB 727 CAGCTGAAGCATTTGAAAAATTTCTGCGACGTGTGAGTGTGAGTGTGAGTGTGAG 786
 QY 721 TGGAGCACCCCATTCCTACTCTCCGACATTTTGATACAGGCCCGGCAAGAAC 780
 DB 787 TGGAGCACCCCATTCCTACTCTCCGACATTTTGATACAGGCCCGGCAAGAAC 846
 QY 781 AATAGAGAAAAAGAGTAGACTCTGCGACAGACCTCAGCCAAAGGTCTGTGCCAC 840
 DB 847 AATAGAGAAAAAGAGTAGACTCTGCGACAGACCTCAGCCAAAGGTCTGTGCCAC 906
 QY 841 AAGGATGCCAAGATCGCGGTGCAAGCCGAGACCCGCTACTATAGTTCACTCTGAGCCAC 900
 DB 907 AAGGATGCCAAGATCGCGGTGCAAGCCGAGACCCGCTACTATAGTTCACTCTGAGCCAC 966
 QY 901 TGGGATCTGTG 912
 DB 967 TGGGATCTGTG 978
 QY
 DB
 DE
 XX
 AC AAX03152;
 XX
 DT 30-MAR-1999 (first entry)
 XX
 DE Nucleic acid encoding canine Interleukin 12.
 XX
 OS Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
 FH skin disease; viral infection; allergic disease; breast tumour;
 FT othematoma; pneumonodema; skin soft pedicled soft tumour; anal tumour;
 FT oclitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
 FT allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
 FT dog Parvovirus infection; distemper virus; cat plaque virus infection;
 FT feline leukaemia; allergy; pollinosis; ds.
 XX
 OS Canis sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..990
 FT /*tag= a
 FT /product= interleukin_12
 XX
 PN W09851327-A1.
 PD 19-NOV-1998.
 XX
 PF 07-MAY-1998; 98WO-JP02031.
 XX
 PR 16-MAY-1997; 97JP-0127690.
 PR (TORA) TORAY IND INC.
 PA
 XX
 PI Okano F, Satoh M, Yamada K;

XX WPI: 1999-070100/06.
 DR P-PSDB: AAM84371.
 XX
 PT New therapeutic and prophylactic agents - comprise
 PT genetically-engineered canine interleukin 12, used to treat, e.g.
 PT canine and feline immunological diseases
 XX
 PS Claim 1: Page 23-25; 45pp; Japanese.
 XX
 CC The present sequence encodes a canine interleukin 12 (IL-12) protein.
 CC The IL-12 protein can be used in therapeutic or prophylactic agents.
 CC The agents can be used to prevent and treat canine and feline
 CC immunological diseases including dog and cat tumours, skin diseases,
 CC viral infections and allergic diseases, especially tumours, breast,
 CC tumour, eosinophilic granuloma, epidermoid tumour, skin tumour, lipoma,
 CC osteoma, pneumoedema, skin soft pedicled soft tumour and anal
 CC tumour; skin diseases, otitis externa, dermatitis, eczema, fungal
 CC diseases of the skin, pyoderma, allergic dermatitis, nettle rash,
 CC traumatic dermatitis and hair loss; infections; dog parvovirus infection
 CC and distemper virus, cat plaque virus infection and feline leukaemia, and
 CC allergic diseases, e.g. pollinosis.
 XX
 S0 Sequence 990 BP: 278 A; 243 C; 251 G; 218 T; 0 other:

Query Match 93.5%; Score 861; DB 20; Length 990;
 Best Local Similarity 99.9%; Pred. No. 0;

Matches 911: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATATGGAGACTGGAGAAAGATGTTATGTTGTAGAGTTGACCTGGACCTCGATGCCCC 60
 DB 67 ATATGGAGACTGGAGAAAGATGTTATGTTGTAGAGTTGACCTGGACCTCGATGCCCC 126
 QY 61 GGAGAAATGGTGGTCCCTCACCCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 120
 DB 127 GGAGAAATGGTGGTCCCTCACCCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 186
 QY 121 GCGCAGACAGTGAAGTCTAGTTCGTGTAAGTCTGACCATTCGAAGTCAAGAAATTT 180
 DB 187 GCGCAGACAGTGAAGTCTAGTTCGTGTAAGTCTGACCATTCGAAGTCAAGAAATTT 246
 QY 181 GGAGATCTGGCCAGTATACCTGCCATTAAGAGGCAAGTTCTGAGCCGCTCACTCTG 240
 DB 247 GGAGATCTGGCCAGTATACCTGCCATTAAGAGGCAAGTTCTGAGCCGCTCACTCTG 306
 QY 241 TTGATTTCACAAAAAAGAGATGGAATTTGGTCCACTGATFATCTTTAAGGAACAGAA 300
 DB 307 TTGATTTCACAAAAAAGAGATGGAATTTGGTCCACTGATFATCTTTAAGGAACAGAA 366
 QY 301 TCCAAAAATTAAGATCTTCTGAATGTGAGGCAAAAGATTTCTGAGCGTTTCACATGC 360
 DB 367 TCCAAAAATTAAGATCTTCTGAATGTGAGGCAAAAGATTTCTGAGCGTTTCACATGC 426
 QY 361 TGGTGGCTGAGCGCAATCAGTACTGATTTGAATTTCAAGTCAAGAGGCTTTC 420
 DB 427 TGGTGGCTGAGCGCAATCAGTACTGATTTGAATTTCAAGTCAAGAGGCTTTC 486
 QY 421 TCTGACCCCAAGGGGTGACATGTGAGCACTGACACTTTAGACAGAGGGTCAAGTG 480
 DB 487 TCTGACCCCAAGGGGTGACATGTGAGCACTGACACTTTAGACAGAGGGTCAAGTG 546
 QY 481 GACAAACAGGATTTAAGAGATACAGTGAAGTGTGAGAGGCGAGTGGCCCTCT 540
 DB 547 GACAAACAGGATTTAAGAGATACAGTGAAGTGTGAGAGGCGAGTGGCCCTCT 606
 QY 541 GCGCAGAGAGCTACCATTCGAGGTCGTGTGATGCTATTCACAAGCTCAAGTATGAA 600
 DB 607 GCGCAGAGAGCTACCATTCGAGGTCGTGTGATGCTATTCACAAGCTCAAGTATGAA 666
 QY 601 AACTACACCGACCTCTTCATCAGACACTCAATCAAAACAGACCCCAACCAACTG 660
 DB 667 AACTACACCGACCTCTTCATCAGACACTCAATCAAAACAGACCCCAACCAACTG 726

QY 661 CAGCTGAAGCCATTGAAAAATTCGCGCAGCTGGAGGTACAGTGGGAATACCCGACACC 720
 DB 727 CAGCTGAAGCCATTGAAAAATTCGCGCAGCTGGAGGTACAGTGGGAATACCCGACACC 786
 QY 721 TGGAGACCCCGACATTCCTACTCTCTCCCTGACATTTTGCAATACAGGCCAGGCAAGAC 780
 DB 787 TGGAGACCCCGACATTCCTACTCTCTCCCTGACATTTTGCAATACAGGCCAGGCAAGAC 846
 QY 781 AATAGAGAAAAGAAAGATAGACTGTGCTGGACAAAGACTAGCCAGGTGTGTGCCAC 840
 DB 847 AATAGAGAAAAGAAAGATAGACTGTGCTGGACAAAGACTAGCCAGGTGTGTGCCAC 906
 QY 841 AAGGATGCAAGATCCCGCTCAAGCCGAGACCGCTACTATGTTATCCTGGAGCGAC 900
 DB 907 AAGGATGCAAGATCCCGCTCAAGCCGAGACCGCTACTATGTTATCCTGGAGCGAC 966
 QY 901 TGGGCATCTGTG 912
 DB 967 TGGGCATCTGTG 978

RESULT 8

AA164378
 ID AA164378 standard: DNA: 990 BP.

AC AA164378;

DT 23-NOV-2001 (first entry)

DE Canine coding sequence #1.

DE Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.

OS Canis familiaris.

FH Key Location/Qualifiers

FT CDS 1..990

FT sig_peptide /product= "Canine protein #1"

FT mat_peptide /tag= b

FT /tag= c

PN JP2001161378-A.

PD 19-JUN-2001.

PF 26-SEP-2000; 2000JP-0292946.

PR 01-OCT-1999; 99JP-0281234.

PA (TORA) TORAY IND INC.

DR WPI: 2001-592466/67.

DR P-PSDB: AAG66480.

PT Preparation of a highly pure protein, interleukin 12, a protein

PT inhibiting the activity of interleukin 12, and a treating agent and a

PT treating method for immunopathy of mammalian

PS Claim 6: Page 14; 21pp; Japanese.

CC The present invention relates to a method for the preparation of a highly

CC pure protein in which interleukin 12 (IL12) and/or a protein inhibiting

CC the activity of IL12 is contacted to an ion exchanging carrier and/or a

CC pigment carrier to get IL12 and/or a protein inhibiting the activity of

CC IL12. The protein is used as a preventive agent for dog immunopathy. The

CC present sequence was used in the method of the present invention.

S0 Sequence 990 BP: 278 A; 243 C; 251 G; 218 T; 0 other:

Query Match 93.5%; Score 861; DB 22; Length 990;

Best Local Similarity 99.9%; Pred. No. 0;
Matches 911; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 ATATGGAGACTGGAGAAAGATGTTATGTTAGTGTGAGTGGACCTGACCTGATGCCCC 60
Db 67 ATATGGAGACTGGAGAAAGATGTTATGTTAGTGTGAGTGGACCTGACCTGATGCCCC 126
QY 61 GGAGAAATGGTGTCTCTACCTGCGCATACCCCTGAGAGAGATGACATCTTGAGACTCA 120
Db 127 GGAGAAATGGTGTCTCTACCTGCGCATACCCCTGAGAGAGATGACATCTTGAGACTCA 186
QY 121 GCGGAGAGAGTGAAGTCTAGGTTCTGTTGTTAAACCTGACCATCCCAAGCAAGATTT 180
Db 187 GCGGAGAGAGTGAAGTCTAGGTTCTGTTGTTAAACCTGACCATCCCAAGCAAGATTT 246
QY 181 GGAGATGCTGGCCAGTATACCTGCGCATAAAGAGAGCAAGGTTCTGAGCCCTCAGCTCTG 240
Db 247 GGAGATGCTGGCCAGTATACCTGCGCATAAAGAGAGCAAGGTTCTGAGCCCTCAGCTCTG 306
QY 241 TTGATTACAAAAAAGATGGAATTTGCTCCACTGATATCTTTAAAGAAAGAAAGAA 300
Db 307 TTGATTACAAAAAAGATGGAATTTGCTCCACTGATATCTTTAAAGAAAGAAAGAA 366
QY 301 TCCAAAAATAGATCTTCTGAAATGAGGCAAAAGATTTATCTGACCTTTCACATGC 360
Db 367 TCCAAAAATAGATCTTCTGAAATGAGGCAAAAGATTTATCTGACCTTTCACATGC 426
QY 361 TGTGCTGAGCGGCAATCACTGATTTGAAATTCAGTGTCAAAAATAGACAGGCTTC 420
Db 427 TGTGCTGAGCGGCAATCACTGATTTGAAATTCAGTGTCAAAAATAGACAGGCTTC 486
QY 421 TCTGACCCCAAGGGGTGACATGTGAGAGTGAACACTTTTCAGAGAGAGGGTTCAGATG 480
Db 487 TCTGACCCCAAGGGGTGACATGTGAGAGTGAACACTTTTCAGAGAGAGGGTTCAGATG 546
QY 481 GACAACAGGATTTATAGAGTACACAGTGGAGTGCAGAGAGGCAATGCTGCCCTCT 540
Db 547 GACAACAGGATTTATAGAGTACACAGTGGAGTGCAGAGAGGCAATGCTGCCCTCT 606
QY 541 GCGGAGAGAGAGCTTACCATCGAGGTCGTGTGATCTTTCACAAAGCTCAAGTATGAA 600
Db 607 GCGGAGAGAGAGCTTACCATCGAGGTCGTGTGATCTTTCACAAAGCTCAAGTATGAA 666
QY 601 AACTACACACAGAGCTTCTTCATCAGAGACATCATCAACACAGACCCACCAAACTG 660
Db 667 AACTACACACAGAGCTTCTTCATCAGAGACATCATCAACACAGACCCACCAAACTG 726
QY 661 CAGCTGAAGCATTTGAAAAATTCGSCACGTGGAGGTCAAGTGGGAATACCCCGACACC 720
Db 727 CAGCTGAAGCATTTGAAAAATTCGSCACGTGGAGGTCAAGTGGGAATACCCCGACACC 786
QY 721 TGGAGCACCCACATTCCTACTCTCCCTGACATTTTGCATPACAGGCCACAGGCAAGAC 780
Db 787 TGGAGCACCCACATTCCTACTCTCCCTGACATTTTGCATPACAGGCCACAGGCAAGAC 846
QY 781 AATAGAAAAAAGAAAGTAACTCTGCTGGAGCAAGACCTCAGCAAGGTCGTGTGCAC 840
Db 847 AATAGAAAAAAGAAAGTAACTCTGCTGGAGCAAGACCTCAGCAAGGTCGTGTGCAC 906
QY 841 AAGATGCCAAGATCCGCTGCAAGCCGAGACCGGCTACTATAGTTATCTCTGAGAGAC 900
Db 907 AAGATGCCAAGATCCGCTGCAAGCCGAGACCGGCTACTATAGTTATCTCTGAGAGAC 966
QY 901 TGGGCATCTGTG 912
Db 967 TGGGCATCTGTG 978

```

RESULT 9
AA18177
ID AA18177 standard; cDNA; 924 BP.
XX
AC AA18177;

```

XX 07-MAY-1999 (first entry)
DT Canine mature CLAF p40 subunit coding sequence.
DE
XX CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW canine infectious hepatitis; ds.
XX
XX Canis sp.
PN W0985511-A1.
XX
XX 10-DEC-1998.
PD
XX
XX 26-MAY-1998; 98MO-JP02295.
PF
XX
XX 03-JUN-1997; 97JP-0161936.
PR
XX (KAGA ) CHERO-SERO-THERAPEUTIC RES INST.
PA
XX Eda Y, Imanura T, Maeda H, Tokiyoshi S;
PI
XX WPI: 1999-070260/06.
DR
XX P-PSDB; AAM74323.
PT
XX Canine cytokine protein which activates canine cytotoxic T
PT lymphocytes - is useful for treatment of viral and autoimmune
XX diseases in dogs
XX
XX Claim 8; Page 32; 51pp; Japanese.
PS
XX
XX This sequence encodes the canine lymphocyte activation factor (CLAF) of
CC the invention. CLAF activates lymphocytes, especially canine cytotoxic
CC T cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC recognising it may be used in the treatment of viral diseases in dogs
CC (such as canine distemper, canine parvovirus and canine infectious
CC hepatitis). The antibodies may also be used in isolation of CLAF from
CC culture of the transformant host cells by affinity chromatography. The
CC p40 homodimer can be used for the treatment of autoimmune diseases in
CC dogs.
XX
XX Sequence 924 BP; 273 A; 222 C; 234 G; 195 T; 0 other;
SQ
Query Match 72.2%; Score 665; DB 20; Length 924;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 665; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 257 AAGATGAATTTGCTCCACTGATATCTTAAAGAACAGAAAGATCCAAAAATAGATCT 316
Db 260 AAGATGAATTTGCTCCACTGATATCTTAAAGAACAGAAAGATCCAAAAATAGATCT 319
QY 317 TTCTGAAATGTGAGCAAGAAATTTATCTGAGAGTTTCATGCTGTGGTGACGGCAA 376
Db 320 TTCTGAAATGTGAGCAAGAAATTTATCTGAGAGTTTCATGCTGTGGTGACGGCAA 379
QY 377 TCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGAGAGGCTTCTGACCCCAAGGG 436
Db 380 TCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGAGAGGCTTCTGACCCCAAGGG 439
QY 437 TGACATGTGAGAGAGACACTTTCAGCAGAGAGGTCAGATGAGCAACAGGATTTA 496
Db 440 TGACATGTGAGAGAGACACTTTCAGCAGAGAGGTCAGATGAGCAACAGGATTTA 499
QY 497 AGAAGTACACAGTGTGAGTGTGAGAGAGAGAGGAGGAGGAGGAGAGAGAGAGAG 556
Db 500 AGAAGTACACAGTGTGAGTGTGAGAGAGAGAGGAGGAGGAGGAGAGAGAGAGAG 559
QY 557 CCATGAGGTCGTGTGATGCTATTCACAAAGCTCAAGTATGAAATACACAGAGCT 616
Db 560 CCATGAGGTCGTGTGATGCTATTCACAAAGCTCAAGTATGAAATACACAGAGCT 619
QY 617 TCTTCATCAGAGACATCATCAACACAGACCCCAACAACTGCGAGCTGAAGCCATTGA 676

```



```
|||||
Db      620 TCTTCATGAGACATCATCAAAACGAGACCCACCAAACTGCGAGTGAAGCCATTGA 679
QY      677 AAAATTTCGCGACCTGGAGGTGACCTGGGAATACCAGCCAGACCTGGAGACCCACATTT 736
Db      680 AAAATTTCGCGACCTGGAGGTGACCTGGGAATACCAGCCAGACCTGGAGACCCACATTT 739
QY      737 CCTACTTCCTCCGATTTTGATGATACAGAGCCAGGCGAAGAAATAGAGAAAGAAAG 796
Db      740 CCTACTTCCTCCGATTTTGATGATACAGAGCCAGGCGAAGAAATAGAGAAAGAAAG 799
QY      797 ATAGACTCTGCGTGACAAAGACCTGAGCCAAAGTGTGTGCCCAAGATGCGCAAGATCC 856
Db      800 ATAGACTCTGCGTGACAAAGACCTGAGCCAAAGTGTGTGCCCAAGATGCGCAAGATCC 859
QY      857 GCGTGCAGAGCCGAGACCGCTACTACTGATCTCTCTGAGAGCAGCTGGCATCTGTGTCTCT 916
Db      860 GCGTGCAGAGCCGAGACCGCTACTACTGATCTCTCTGAGAGCAGCTGGCATCTGTGTCTCT 919
QY      917 GCAGT 921
Db      920 GCAGT 924
```

```
RESULT 10
AA18176
ID      AA18176 standard; cDNA; 2154 BP.
```

```
AC      AA18176;
```

```
DT      07-MAY-1999 (first entry)
```

```
XX      Canine full length CLAF p40 subunit coding sequence.
```

```
XX      CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KM      viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW      canine infectious hepatitis; ds.
```

```
XX      Canis sp.
```

```
PN      W09855511-A1.
```

```
PD      10-DEC-1998.
```

```
PF      26-MAY-1998; 98MO-JP02295.
```

```
PR      03-JUN-1997; 97JP-0161936.
```

```
PA      (KAGA ) CHERO-SERO-THERAPEUTIC RES INST.
```

```
PI      Eda Y, Imamura T, Maeda H, Tokiyoshi S;
```

```
DR      WPI: 1999-070260/06.
```

```
DR      P-PSDB; AAW74322.
```

```
PT      Canine cytokine protein which activates canine cytotoxic T
PT      lymphocytes - is useful for treatment of viral and autoimmune
PT      diseases in dogs
XX
```

```
PS      Claim 8; Page 30-31; 51pp; Japanese.
```

```
XX      This sequence encodes the canine lymphocyte activation factor (CLAF) of
CC      the invention. CLAF activates lymphocytes, especially canine cytotoxic
CC      T cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC      recognising it may be used in the treatment of viral diseases in dogs
CC      (such as canine distemper, canine parvovirus and canine infectious
CC      hepatitis). The antibodies may also be used in isolation of CLAF from
CC      culture of the transformant host cells by affinity chromatography. The
CC      p40 homodimer can be used for the treatment of autoimmune diseases in
CC      dogs.
```

```
Sequence 2154 BP: 663 A: 448 C: 477 G: 566 T: 0 other:
```

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Query Match      72.2%; Score 665; DB 20; Length 2154;
Best local Similarity 100.0%; Pred. No. 0;
Matches 665; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      257 AAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGATTCAAAAATTAAGATCT 316
Db      377 AAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGATTCAAAAATTAAGATCT 436
QY      317 TTCTGAAATGTGAGCGAAAGAAATTTATTTGTGACGTTTACATGCTGTGTGCTGACGGCAA 376
Db      437 TTCTGAAATGTGAGCGAAAGAAATTTATTTGTGACGTTTACATGCTGTGTGCTGACGGCAA 496
QY      437 TCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTCTGTACCCCAAGGGG 436
Db      497 TCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTCTGTACCCCAAGGGG 556
QY      497 TGACATGTGAGACAGTACACTTTTGACGAGAGAGGGTCAGAGTGGACAACAGGATTTATA 616
Db      557 TGACATGTGAGACAGTACACTTTTGACGAGAGAGGGTCAGAGTGGACAACAGGATTTATA 616
QY      617 AGAAGTACACAGTGGAGTGTCAAGAGGCGAGTCCGCCCTCTGTCCGAGGAGAGCCCTAC 556
Db      617 AGAAGTACACAGTGGAGTGTCAAGAGGCGAGTCCGCCCTCTGTCCGAGGAGAGCCCTAC 676
QY      677 CCATGAGGTCGTGGTGATGCTATTTCACAAAGCTCAAGATGAAACTACACAGCAGCT 616
Db      677 CCATGAGGTCGTGGTGATGCTATTTCACAAAGCTCAAGATGAAACTACACAGCAGCT 736
QY      677 TCTTCATGAGACATCATCAAAACGAGACCCACCAAACTGCGAGCTGAAGCCATTGA 796
Db      737 TCTTCATGAGACATCATCAAAACGAGACCCACCAAACTGCGAGCTGAAGCCATTGA 796
QY      797 AAAATTTCGCGACCTGGAGGTGACCTGGGAATACCAGCCAGACCTGGAGACCCACATTT 736
Db      797 AAAATTTCGCGACCTGGAGGTGACCTGGGAATACCAGCCAGACCTGGAGACCCACATTT 856
QY      737 CCTACTTCCTCCGATTTTGATGATACAGAGCCAGGCGAAGAAATAGAGAAAGAAAG 796
Db      857 CCTACTTCCTCCGATTTTGATGATACAGAGCCAGGCGAAGAAATAGAGAAAGAAAG 916
QY      857 GCGTGCAGAGCCGAGACCGCTACTACTGATCTCTCTGAGAGCAGCTGGCATCTGTGTCTCT 916
Db      977 GCGTGCAGAGCCGAGACCGCTACTACTGATCTCTCTGAGAGCAGCTGGCATCTGTGTCTCT 1036
QY      917 GCAGT 921
Db      1037 GCAGT 1041
```

```
RESULT 11
```

```
AAD15209
ID      AAD15209 standard; DNA; 990 BP.
```

```
AC      AAD15209;
```

```
DT      01-NOV-2001 (first entry)
```

```
XX      Modified human cytokine p40 encoding DNA from clone R16-51.
```

```
XX      Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection;
KM      AIDS; diabetic retinopathy; cancer; vaccine; cell-mediated immunity;
KW      human; p40; mutant; ds.
```

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OS      Homo sapiens.
```

```
OS      Synthetic.
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```
XX      Location/Qualifiers
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FT      1..66
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FT      mat_peptide      67..987
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XX      WO200140257-A2.
XX      07-JUN-2001.
XX      30-NOV-2000; 2000WO-US32664.
XX      02-DEC-1999; 99US-0169035.
XX      28-NOV-2000; 2000US-0169035.
XX      (MAXY-) MAXYGEN INC.
XX      Leong SR, Punnonen J;
XX      WPI; 2001-502381/55.
XX      P-PSDB; AAE08602.
XX      Nucleic acids encoding modified cytokine polypeptides (i.e. modified
PT      p40 and p35 polypeptides), useful for treating various diseases e.g.
PT      diabetic retinopathy and cancer -
XX      Claim 1; Page 137-138; 223pp; English.
XX      The invention relates to nucleic acids encoding modified cytokine
CC      polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC      cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC      gamma induction activities. The polypeptides and polynucleotides of the
CC      invention are useful for treating various diseases e.g. bacterial
CC      infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC      polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC      vaccinated host's cell-mediated immunity for protective response to a
CC      pathogen. The present sequence is a modified human p40 protein encoding
CC      DNA.
XX      Sequence 990 BP; 270 A; 250 C; 254 G; 216 T; 0 other;
XX      Query Match      15.5%; Score 143; DB 22; Length 990;
XX      Best Local Similarity 100.0%; Pred. No. 2.6e-62;
XX      Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      499 AAGTACACAGTGTGATGCTCAGAGGAGGAGTGCCTGCTGCGGAGAGAGCTTACC 558
DB      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB      565 AAGTACACAGTGTGATGCTCAGAGGAGGAGTGCCTGCTGCGGAGAGAGCTTACC 624
QY      559 ATCGAGGTGCTGTGATGCTATTTCACAGCTCAAGTATGAAAACTACACAGCAGCTTC 618
DB      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB      625 ATCGAGGTGCTGTGATGCTATTTCACAGCTCAAGTATGAAAACTACACAGCAGCTTC 684
QY      619 TTCATCAGAGCATCATCAAAACC 641
DB      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB      685 TTCATCAGAGCATCATCAAAACC 707
XX      RESULT 12
XX      AAD15205
XX      ID AAD15205 standard; DNA; 984 BP.
XX      AAD15205;
XX      01-NOV-2001 (first entry)
XX      Modified human cytokine p40 encoding DNA from clone B2-52.
XX      Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection;
XX      AIDS; diabetic retinopathy; cancer; vaccine; cell-mediated immunity;
XX      human; p40; mutant; ds.
XX
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OS      Homo sapiens.
XX      Synthetic.
XX      Key
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FT      sig_peptide      /product= "Mature modified p40 protein"
FT      /*tag= b
FT      mat_peptide      67..981
FT      /*tag= c
FT      /product= "Mature modified p40 protein"
XX      WO200140257-A2.
XX      07-JUN-2001.
XX      30-NOV-2000; 2000WO-US32664.
XX      02-DEC-1999; 99US-0169035.
XX      28-NOV-2000; 2000US-0169035.
XX      (MAXY-) MAXYGEN INC.
XX      Leong SR, Punnonen J;
XX      WPI; 2001-502381/55.
XX      P-PSDB; AAE08598.
XX      Nucleic acids encoding modified cytokine polypeptides (i.e. modified
PT      p40 and p35 polypeptides), useful for treating various diseases e.g.
PT      diabetic retinopathy and cancer -
XX      Claim 1; Page 136-137; 223pp; English.
XX      The invention relates to nucleic acids encoding modified cytokine
CC      polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC      cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC      gamma induction activities. The polypeptides and polynucleotides of the
CC      invention are useful for treating various diseases e.g. bacterial
CC      infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC      polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC      vaccinated host's cell-mediated immunity for protective response to a
CC      pathogen. The present sequence is a modified human p40 protein encoding
CC      DNA.
XX      Sequence 984 BP; 267 A; 246 C; 254 G; 217 T; 0 other;
XX      Query Match      13.9%; Score 128; DB 22; Length 984;
XX      Best Local Similarity 100.0%; Pred. No. 1.1e-54;
XX      Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      499 AAGTACACAGTGTGATGCTCAGAGGAGGAGTGCCTGCTGCGGAGAGAGCTTACC 558
DB      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB      565 AAGTACACAGTGTGATGCTCAGAGGAGGAGTGCCTGCTGCGGAGAGAGCTTACC 624
QY      559 ATCGAGGTGCTGTGATGCTATTTCACAGCTCAAGTATGAAAACTACACAGCAGCTTC 618
DB      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB      625 ATCGAGGTGCTGTGATGCTATTTCACAGCTCAAGTATGAAAACTACACAGCAGCTTC 684
QY      619 TTCATCAG 626
DB      ||||||||
DB      685 TTCATCAG 692
XX      RESULT 13
XX      AAD15206
XX      ID AAD15206 standard; DNA; 984 BP.
XX      AAD15206;
XX      01-NOV-2001 (first entry)
XX
```

```

DE Modified human cytokine p40 encoding DNA from clone B1-81.
XX
XX Cytokine: T-cell; interferon-gamma; IFN-gamma; bacterial infection;
KW AIDS; diabetic retinopathy; cancer; vaccine; cell-mediated immunity;
KW human; p40; mutant; ds.
XX
XX Homo sapiens.
OS Synthetic.
XX
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FT /product= "Modified p40 protein precursor"
FT sig_peptide 1..66
FT /tag= b
FT mat_peptide 67..981
FT /tag= c
FT /product= "Mature modified p40 protein"
XX
XX WO200140257-A2.
XX
XX PD 07-JUN-2001.
XX
XX PF 30-NOV-2000; 2000WO-US32664.
XX
XX PR 02-DEC-1999; 99US-0169035.
XX PR 28-NOV-2000; 2000US-0169035.
XX
XX PA (MAXY-) MAXYGEN INC.
XX
XX PI Leong SR, Punnonen J;
XX
XX DR WPI: 2001-502381/55.
XX DR P-PSDB; AAE08599.
XX
XX PT Nucleic acids encoding modified cytokine polypeptides (i.e. modified
XX p40 and p35 polypeptides), useful for treating various diseases e.g.
XX diabetic retinopathy and cancer -
XX
XX PS Claim 1: Page 137; 223pp; English.
XX
XX CC The invention relates to nucleic acids encoding modified cytokine
XX polypeptides (i.e. modified p40 and p35 polypeptides). The modified
XX cytokine polypeptides have T-cell proliferative and interferon (IFN)-
XX gamma induction activities. The polypeptides and polynucleotides of the
XX invention are useful for treating various diseases e.g. bacterial
XX infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
XX polynucleotide may also be useful as a vaccine adjuvant, to enhance a
XX vaccinated host's cell-mediated immunity for protective response to a
XX pathogen. The present sequence is a modified human p40 protein encoding
XX DNA.
XX
XX SO Sequence 984 BP; 272 A; 254 C; 247 G; 211 T; 0 other:

Query Match 10.3%; Score 95; DB 22; Length 984;
Best Local Similarity 100.0%; Pred. No. 6.6e-38;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 520 GAGGGCACTGCTCCCTCTGCGGAGAGAGACCTACCCATGAGCTGGTGATCT 579
DB 586 GAGGGCACTGCTCCCTCTGCGGAGAGAGACCTACCCATGAGCTGGTGATCT 645
OY 580 ATTCAAGCTCACTATGAAGAATACACCAAGC 614
DB 646 ATTCAAGCTCACTATGAAGAATACACCAAGC 660

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```

DT 01-NOV-2001 (first entry)
XX
XX DE Modified human cytokine p40 encoding DNA from clone A3-48.
XX
XX KW Cytokine: T-cell; interferon-gamma; IFN-gamma; bacterial infection;
XX KW AIDS; diabetic retinopathy; cancer; vaccine; cell-mediated immunity;
XX KW human; p40; mutant; ds.
XX
XX OS Homo sapiens.
XX
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FT /product= "Modified p40 protein precursor"
FT sig_peptide 1..66
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XX WO200140257-A2.
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XX PD 07-JUN-2001.
XX
XX PF 30-NOV-2000; 2000WO-US32664.
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XX PR 02-DEC-1999; 99US-0169035.
XX PR 28-NOV-2000; 2000US-0169035.
XX
XX PA (MAXY-) MAXYGEN INC.
XX
XX PI Leong SR, Punnonen J;
XX
XX DR WPI: 2001-502381/55.
XX DR P-PSDB; AAE08599.
XX
XX PT Nucleic acids encoding modified cytokine polypeptides (i.e. modified
XX p40 and p35 polypeptides), useful for treating various diseases e.g.
XX diabetic retinopathy and cancer -
XX
XX PS Claim 1: Page 137; 223pp; English.
XX
XX CC The invention relates to nucleic acids encoding modified cytokine
XX polypeptides (i.e. modified p40 and p35 polypeptides). The modified
XX cytokine polypeptides have T-cell proliferative and interferon (IFN)-
XX gamma induction activities. The polypeptides and polynucleotides of the
XX invention are useful for treating various diseases e.g. bacterial
XX infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
XX polynucleotide may also be useful as a vaccine adjuvant, to enhance a
XX vaccinated host's cell-mediated immunity for protective response to a
XX pathogen. The present sequence is a modified human p40 protein encoding
XX DNA.
XX
XX SO Sequence 969 BP; 263 A; 249 C; 251 G; 206 T; 0 other:

Query Match 8.1%; Score 75; DB 22; Length 969;
Best Local Similarity 100.0%; Pred. No. 9.7e-28;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 834 GTGCCACAAGATGCGGCTGCAAGCCGAGACGCTACTAGTCATTCCTG 893
DB 879 GTGCCACAAGATGCGGCTGCAAGCCGAGACGCTACTAGTCATTCCTG 938
OY 894 GAGCGACTGGGCATC 908
DB 939 GAGCGACTGGGCATC 953

```

```

RESULT 14
AADI5207
ID AADI5207 standard; DNA: 965 BP.
XX
AC AADI5207;
XX

```

```

RESULT 15
AADI5203
ID AADI5203 standard; DNA: 975 BP.
XX

```

```

AC  AAD15203;
XX
DT  01-NOV-2001 (first entry)
XX
DE  Modified human cytokine p40 encoding DNA from clone C2-22.
XX
KW  Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection;
XX  AIDS; diabetic retinopathy; cancer; vaccine; cell-mediated immunity;
XX  human; p40; mutant; ds.
OS  Homo sapiens.
OS  Synthetic.
XX
FH  Key
FH  CDS
FT  Location/Qualifiers
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FT  /tag= c
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XX  WO200140257-A2.
XX
XX  07-JUN-2001.
XX
XX  30-NOV-2000; 2000WO-US32664.
XX
XX  02-DEC-1999; 99US-0169035.
XX  28-NOV-2000; 2000US-0169035.
XX
XX  (MAXY-) MAXYGEN INC.
XX
XX  Leong SR, Punnonen J;
XX
XX  WPI; 2001-502381/55.
XX  P-PSDB; AAE08596.
XX
XX  Nucleic acids encoding modified cytokine polypeptides (i.e. modified
XX  p40 and p35 polypeptides), useful for treating various diseases e.g.
XX  diabetic retinopathy and cancer -
XX
XX  Claim 1; Page 136; 223pp; English.
XX
XX  The invention relates to nucleic acids encoding modified cytokine
XX  polypeptides (i.e. modified p40 and p35 polypeptides). The modified
XX  cytokine polypeptides have T-cell proliferative and interferon (IFN)-
XX  gamma induction activities. The polypeptides and polynucleotides of the
XX  invention are useful for treating various diseases e.g. bacterial
XX  infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
XX  polynucleotide may also be useful as a vaccine adjuvant, to enhance a
XX  vaccinated host's cell-mediated immunity for protective response to a
XX  pathogen. The present sequence is a modified human p40 protein encoding
XX  DNA.
XX
SQ  Sequence 975 BP; 269 A; 252 C; 250 G; 204 T; 0 other:

Query Match      7.88; Score 72; DB 22; Length 975;
Best Local Similarity 100.0%; Pred. No. 3.3e-26;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  581 TTCACAAGCTCAGTATGAAAGTACACGACGAGCTTCTCATCAGACATCATCAAC 640
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Db  632 TTCACAAGCTCAGTATGAAAGTACACGACGAGCTTCTCATCAGACATCATCAAC 691
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QY  641 CAGAGCCACCCA 652
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Db  692 CAGAGCCACCCA 703

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Search completed: July 16, 2003, 13:41:41
 Job time : 238.016 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 10:34:53 : Search time 1582.56 Seconds
(without alignments)
9425.275 Million cell updates/sec

Title: US-09-917-265-52

Perfect score: 921

Sequence: 1 atagggaactggagaaga.....gggcacgcgtgcctcgcagt 921

Scoring table: OLIGO_NUC

Gapop 60.0 , Capext 60.0

Searched: 16154066 seqs, 8057743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
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14: gb_est5:*
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22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|-------------|
| 1 | 2.4 | 662 | 17 | AG049786 | Pan trogl |
| 2 | 2.3 | 369 | 17 | AZ884788 | RPCI-23-1 |
| 3 | 2.3 | 564 | 13 | BJ030774 | BJ030774 |
| 4 | 2.3 | 571 | 13 | BJ032049 | BJ032049 |
| 5 | 2.3 | 638 | 13 | BI099266 | IP1_40_G0 |
| 6 | 2.3 | 646 | 10 | BB038225 | BB038225 |

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| 7 | 2.3 | 667 | 13 | BJ042592 | BJ042592 |
| 8 | 2.3 | 975 | 17 | CNS04MY1 | AL310995 Tetradon |
| 9 | 2.2 | 173 | 13 | BJ006287 | BJ006287 |
| 10 | 2.2 | 239 | 17 | BH870361 | BH870361 hm61b07.b |
| 11 | 2.2 | 374 | 14 | T99581 | T99581 ye6508.r.1 |
| 12 | 2.2 | 436 | 10 | AV792889 | AV792889 AV792889 |
| 13 | 2.2 | 475 | 12 | BF704417 | BF704417 MI-P-E6-a |
| 14 | 2.2 | 527 | 17 | BH780306 | BH780306 fzmb015f0 |
| 15 | 2.2 | 536 | 10 | AV554146 | AV554146 AV554146 |
| 16 | 2.2 | 550 | 17 | B75609 | B75609 RPCI11-11L1 |
| 17 | 2.2 | 569 | 17 | AZ853726 | AZ853726 2M0157M01 |
| 18 | 2.2 | 605 | 17 | AQ0544128 | AQ0544128 RPCI-11-3 |
| 19 | 2.2 | 637 | 9 | A1982112 | A1982112 pat.pK007 |
| 20 | 2.2 | 690 | 17 | AZ424475 | AZ424475 1M0204A12 |
| 21 | 2.2 | 707 | 14 | BU002016 | BU002016 OCG2012.Y |
| 22 | 2.2 | 855 | 17 | AQ893069 | AQ893069 HS_3072_A |
| 23 | 2.2 | 1637 | 14 | BQ056451 | BQ056451 ACENECOURT |
| 24 | 2.2 | 268 | 10 | BB427690 | BB427690 BB427690 |
| 25 | 2.1 | 334 | 17 | AZ396610 | AZ396610 1M0161B18 |
| 26 | 2.1 | 352 | 17 | AZ799073 | AZ799073 2M0056D24 |
| 27 | 2.1 | 360 | 14 | CA7397 | CA7397 CA7397 yuji |
| 28 | 2.1 | 380 | 17 | AQ141956 | AQ141956 HS_3173_A |
| 29 | 2.1 | 408 | 17 | AQ118163 | AQ118163 HS_3003_A |
| 30 | 2.1 | 432 | 12 | BG513467 | BG513467 de611b06. |
| 31 | 2.1 | 448 | 10 | AW513679 | AW513679 x087e09.x |
| 32 | 2.1 | 453 | 14 | BM868100 | BM868100 m6c5013x1 |
| 33 | 2.1 | 476 | 17 | AQ766175 | AQ766175 HS_5477_B |
| 34 | 2.1 | 477 | 14 | BM750317 | BM750317 K-EST0025 |
| 35 | 2.1 | 478 | 13 | BI450211 | BI450211 dae76d11. |
| 36 | 2.1 | 480 | 17 | AZ457253 | AZ457253 1M0260E06 |
| 37 | 2.1 | 481 | 9 | A1545879 | A1545879 fb76e12.Y |
| 38 | 2.1 | 505 | 17 | AZ635629 | AZ635629 1M0493D09 |
| 39 | 2.1 | 508 | 14 | BU002504 | BU002504 OCG31119. |
| 40 | 2.1 | 509 | 13 | BJ068319 | BJ068319 BJ068319 |
| 41 | 2.1 | 535 | 17 | AZ441303 | AZ441303 1M0232M24 |
| 42 | 2.1 | 537 | 12 | BF394460 | BF394460 U1-R-CA0- |
| 43 | 2.1 | 537 | 13 | BJ035542 | BJ035542 BJ035542 |
| 44 | 2.1 | 553 | 14 | BQ047017 | BQ047017 EST96135 |
| 45 | 2.1 | 563 | 10 | AW951173 | AW951173 EST363243 |

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
Pan troglodytes DNA, clone: PTB-030A07.R, genomic survey sequence.
AC049786
ACCESSION
AG049786.1 GI:16586678
VERSION
KEYWORDS
SOURCE
ORGANISM
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC library clone:PTB-030A07.R.
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE
1
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE
BAC end sequences of library PTB
JOURNAL
Unpublished
2 (bases 1 to 662)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Suehiro-chou, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimbes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.

COMMENT

PRIMERS
Sequencing: M13Rev
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI

FEATURES
source
1..662
Location/Qualifiers

/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-030A07.R"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC library"
BASE COUNT 197 a 118 c 140 g 206 t 1 others
ORIGIN

Query Match 2.48; Score 22; DB 17; Length 662;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 241 TTGATTCACAAAAGAGATG 262
|||||
Db 345 TTGATTCACAAAAGAGATG 366

RESULT 2 369 bp DNA linear GSS 05-MAR-2001
AZ884788
LOCUS
DEFINITION
RPT-23-182A5.TV RPT-23 Mus musculus genomic clone RPT-23-182A5,
DNA sequence.
ACCESSION
AZ884788
VERSION
KEYWORDS
GSS.
SOURCE
house mouse.
ORGANISM
Mus musculus

REFERENCE
AUTHORS
Eukariyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 369)
Zhao,S., Nierman,W., Felblyum,T., Malek,J., Shatsman,S., Akinret,
B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
and Fraser,C.M.

TITLE
JOURNAL
COMMENT
Mouse BAC End Sequences from Library RPT-23
Unpublished (1999)
Other_GSSs: RPT-23-182A5.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208

Email: szhao@ligr.org
Clones are derived from the mouse BAC library RPT-23. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (<http://www.choil.org/bacpac/orderingframe.htm>). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 182 row: A column: 5
Seq primer: T7
Class: BAC ends.

FEATURES
source
1..369
Location/Qualifiers

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPT-23-182A5"
/clone_lib="RPT-23"
/sex="Female"
/lab_host="DH10B"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site:1;
EcoRI; Site:2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size

selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies).
BASE COUNT 97 a 76 c 86 g 110 t
ORIGIN

Query Match 2.3%; Score 21; DB 17; Length 369;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 418 TTCTCGACCCCAAGGGTG 438
|||||
Db 121 TTCTCGACCCCAAGGGTG 141

RESULT 3 564 bp mRNA linear EST 05-DEC-2001
BU030774
LOCUS
DEFINITION
BU030774 N1BB Mochii normalized Xenopus neurula library Xenopus
laevis cDNA clone XL005c01 5', mRNA sequence.
ACCESSION
BU030774
VERSION
KEYWORDS
EST.
SOURCE
African clawed frog.
ORGANISM
Xenopus laevis

REFERENCE
AUTHORS
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 564)
Kitayama,A., Teraoka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara
Y.

Expressed genes in X. laevis embryo
Unpublished (2001)
Contact: Tadasi Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.

FEATURES
source
1..564
Location/Qualifiers

/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XL005c01"
/clone_lib="N1BB Mochii normalized Xenopus neurula
library"
/tissue_type="whole embryo"
/dev_stage="stage 15"

/note="Vector: pBSRN3; Site:1: NotI; Site:2: EcoRI; cDNAs
were oligo-dT primed and directionally cloned. Staging
according to Nieuwkoop and Faber. Library is subtracted
and was constructed by N. Garrett and A.M. Zorn,
(Wellcome/CRC Institute)."

BASE COUNT 138 a 148 c 136 g 142 t
ORIGIN

Query Match 2.3%; Score 21; DB 13; Length 564;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 184 GATGCTGGCCAGTATACCTGC 204
|||||
Db 178 GATGCTGGCCAGTATACCTGC 198

RESULT 4 571 bp mRNA linear EST 05-DEC-2001
BU032049
LOCUS
DEFINITION
BU032049 N1BB Mochii normalized Xenopus neurula library Xenopus
laevis cDNA clone XL015h03 5', mRNA sequence.
ACCESSION
BU032049
VERSION
BU032049.1 GI:17375617

KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM *Xenopus laevis*
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; *Xenopus*.
REFERENCE 1 (bases 1 to 571)
AUTHORS Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara, Y.

TITLE Expressed genes in *X. laevis* embryo
JOURNAL Unpublished (2001)
COMMENT Contact: Tadasi Shin-i
Center For Genetic Resource Information
National Institute of Genetics
111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES
source
1..571
Location/Qualifiers
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="X1015103"
/clone_lib="NIBB Mochii normalized *Xenopus* neurula library"
/library=""
/dev_stage="stage 15"
/note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; CDNAS were oligo-dT primed and directionally cloned. Subcloned according to Nieuwkoop and Faber. Library is subcloned and was constructed by N. Garrett and A.M. Zorn, (Wellcome/CRC Institute)."

BASE COUNT 142 a 142 c 143 g 144 t

ORIGIN

Query Match 2.3%; Score 21; DB 13; Length 571;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 184 GATGCTGGCCAGTACTGTC 204
|||||
140 GATCTGCGCAGTACTGTC 160

RESULT 5
BI099266/c 638 bp mRNA linear EST 26-JUN-2001
LOCUS IP1_40_G03_g1_A002 Immature pannicle 1 (IP1) *Sorghum bicolor* cDNA,
DEFINITION mRNA sequence.
ACCESSION BI099266
VERSION BI099266.1 GI:14570848
KEYWORDS EST.
SOURCE *Sorghum*.
ORGANISM *Sorghum bicolor*
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; *Sorghum*.
1 (bases 1 to 638)
Klein, R.K., Cordonnier-Pratt, M.-M., Gingle, A., Sudman, M. and Pratt, L.H.
An EST database from *Sorghum*: developing preanthesis pannicles
Unpublished (2001)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions below phred quality 16. The threshold for high quality sequence is 20. Three-prime sequences, which are obtained with PolyMix or T7 sequencing primer, are presented as the reverse complement.

TITLE JOURNAL
COMMENT

Seq primer: T7
High quality sequence start: 8
High quality sequence stop: 638
POLYA=yes.

FEATURES
source
1..638
Location/Qualifiers
/organism="Sorghum bicolor"
/cultivar="BY623"
/db_xref="taxon:4558"
/clone_lib="Immature pannicle 1 (IP1)"
/note="Organ: Developing preanthesis pannicles; Vector: pBluescript II SK(-) from Lambda Zap II; Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda Zap II. Clones to be sequenced were prepared by mass excision."

BASE COUNT 143 a 134 c 179 g 182 t

ORIGIN

Query Match 2.3%; Score 21; DB 13; Length 638;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 659 TGCAAGCTGAGCCATTGAAA 679
|||||
135 TGCAAGCTGAGCCATTGAAA 115

RESULT 6
BB038225 646 bp mRNA linear EST 18-OCT-2001
LOCUS BB038225
DEFINITION BB038225 RIKEN full-length enriched, 13 days embryo forelimb Mus
musculus cDNA clone 5930435K16 3', mRNA sequence.
ACCESSION BB038225
VERSION BB038225.2 GI:16258473
KEYWORDS EST.
SOURCE house mouse.
ORGANISM *Mus musculus*
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 646)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Horii, F., Ishii, Y., Ito, M., Kawai, J., Kono, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
On Jun 10, 2000 this sequence version replaced gi:8444611.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagii, K., Fujiwara, S., Inoue, K., Togawa, Y., Iwawa, M., Ohara, E.,
Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multichannel sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.

TITLE JOURNAL
COMMENT

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2): 281-289 (2001)
 Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, D., Shibata, K. and Hayashizaki, Y.
 Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences *Mamm. Genome*. 12, 673-677 (2001)
 Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

FEATURES

Location/Qualifiers

1. 646
 /organism="Mus musculus"
 /strain="C57BL/6j"
 /db_xref="taxon:10090"
 /clone="5930435K16"
 /clone_lib="RIKEN full-length enriched, 13 days embryo forelimb"
 /sex="mixed"
 /tissue_type="forelimb"
 /dev_stage="13 days embryo"
 /lab_host="DH10B"
 /note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer (5' GAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTT 3'), cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of 3') cDNA was cloned into the XhoI and BamHI sites. Vector: a modified Bluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."

BASE COUNT 181 a 137 c 153 g 175 t

ORIGIN

Query Match 2.3%; Score 21; DB 10; Length 646;
 Best Local Similarity 100.0%; Pred. No. 20;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 418 TTCTCTGACCCCAAGGGGTG 438
 Db 341 TTCTCTGACCCCAAGGGGTG 361

RESULT 7

BJ042592

LOCUS 667 bp mRNA linear EST 06-DEC-2001

DEFINITION BJ042592 N1BB Mochii normalized Xenopus neurula library Xenopus

ACCESSION BJ042592

VERSION BJ042592.1 GI:17392768

KEYWORDS EST.

SOURCE African clawed frog.

ORGANISM Xenopus laevis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 Xenopodinae; Xenopus.
 1 (bases 1 to 667)
 Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara, Y.

TITLE
 JOURNAL
 COMMENT
 Expressed genes in X. laevis embryo
 Unpublished (2001)
 Contact: Tadasu Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshin@genes.nig.ac.jp.

FEATURES

source

1. 667
 /organism="Xenopus laevis"
 /db_xref="taxon:8355"
 /clone="XL032c23"
 /clone_lib="N1BB Mochii normalized Xenopus neurula library"
 /tissue_type="whole embryo"
 /dev_stage="stage 15"
 /note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs were oligo-dT primed and directionally cloned. Staging according to Muewkoop and Faber. Library is subtracted and was constructed by N. Garrett and A.M. Zorn, (Wellcome/CRC Institute)."

BASE COUNT 151 a 186 c 166 g 164 t

ORIGIN

Query Match 2.3%; Score 21; DB 13; Length 667;
 Best Local Similarity 100.0%; Pred. No. 21;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 184 GATGCTGGCCAGTATACCTGC 204
 Db 281 GATGCTGGCCAGTATACCTGC 301

RESULT 8

CNS04WYI/c

LOCUS 975 bp DNA linear GSS 26-JUL-2000

DEFINITION Tetradon nigroviridis genome survey sequence T7 end of clone

053809 of library A from Tetradon nigroviridis, genomic survey

ACCESSION AL310995

VERSION AL310995.1 GI:9543863

KEYWORDS GSS: genome survey sequence.

SOURCE Tetradon nigroviridis.

ORGANISM Tetradon nigroviridis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 Tetraodontidae; Tetradon.
 1 (bases 1 to 975)
 Roest Crolius, H., Jallion, O., Dasilva, C., Bouneau, L., Fisher, C.,
 Bernot, A., Fizames, C., Wincker, P., Brothier, P., Quetier, F.,
 Saurin, W. and Weissenbach, J.
 Estimate of human gene number provided by genome-wide analysis
 using Tetradon nigroviridis DNA sequence

using Tetradon nigroviridis DNA sequence

Nat. Genet. 25 (2), 235-238 (2000)

REFERENCE 10835645

JOURNAL 2 (bases 1 to 975)

DEFINITION Crolius, H.R., Jallion, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C.,
 Bernot, A., Bouneau, L., Billault, A., Quetier, F., Saurin, W.,
 Fischer, C., and Weissenbach, J.
 Characterization and repeat analysis of the compact genome of the
 freshwater pufferfish Tetradon nigroviridis

Genome Res. 10 (7), 939-949 (2000)

ACCESSION 20359837

VERSION 10899143

REFERENCE 3 (bases 1 to 975)

JOURNAL Genoscope.

TITLE Direct Submission

COMMENT Submitted (12-APR-2000)
 This sequence is a single read and was generated as part of a large

scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.

FEATURES

SOURCE

1. 975
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="053B09"
/clone_lib="A"
/note="genoscope sequence ID : C0AA053CA05C1-end : T7"

BASE COUNT 188 a 289 c 279 g 197 t 22 others
ORIGIN

Query Match

Best Local Similarity 100.0%: Pred. No. 22;

Matches 21: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 883 AGTTCATCCTCGAGCGACTCG 903
Db 590 AGTTCATCCTCGAGCGACTCG 570

RESULT 9

LOCUS

DEFINITION BJ006287 MF01SSA cDNA Oryzias latipes cDNA clone MF01SSA091H02 5', mRNA sequence.

ACCESSION BJ006287

VERSION BJ006287.1

KEYWORDS EST.

SOURCE Japanese medaka.

ORGANISM Oryzias latipes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorphi; Acanthopterygii; Percomorphi; Atherinomorpha; Belontiiformes; Adrianiichthyidae; Oryziinae; Oryzias.

REFERENCE 1 (bases 1 to 173)

AUTHORS Kohara,Y., Shih-I,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H.

TITLE Medaka EST Project in Takeda's lab

JOURNAL Unpublished (2001)

COMMENT Contact: Tadasu Shin-I

Center For Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tsuhin@genes.nig.ac.jp.

FEATURES

SOURCE

1. 173
/organism="Oryzias latipes"
/strain="Hg-rf"
/db_xref="taxon:8090"
/clone="MF01SSA091H02"
/clone_lib="MF01SSA cDNA"
/sex="mixture of female and male"
/tissue-type="whole embryo"
/dev-stage="segmentation stage 20 - 25"
/dev_stage="segmentation stage 20 - 25"

BASE COUNT 36 a 53 c 50 g 31 t 3 others
ORIGIN

Query Match

Best Local Similarity 100.0%: Pred. No. 51;

Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 520 GAGGCACTGCTGCCCTC 539
Db 85 GAGGCACTGCTGCCCTC 104

RESULT 10

LOCUS BH870361/c

DEFINITION hm61b07.b1 WGS-zmaysf (JM107 adapted methyl filtered) Zea mays

genomic clone hm61b07 5', DNA sequence.

ACCESSION BH870361

VERSION BH870361.1

KEYWORDS GSS.

SOURCE Zea mays.

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 239)

AUTHORS Rabinowicz,P.D., O'Shaughnessy,A.L., Balija,V., Dedhia,N., Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L., Zutavern,T., McCombie,W.R. and Martienssen,R.A.

Genomic shotgun sequences from Zea mays (methyl-filtered)

JOURNAL Unpublished (2002)

COMMENT Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874

Email: mcombie@cshl.org

Plate: hm61 row: b column: 07

Seq primer: -21M13univrev

Class: shotgun

High quality sequence stop: 239.

FEATURES

SOURCE

1. 239
Location/Qualifiers

/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="hm61b07"

/clone_lib="WGS-zmaysf (JM107 adapted methyl filtered)"

/lab_host="JM107 or DH5a"

/note="Organ: immature ears; Site_1: Xba I; Site_2: Xba I; The vector was digested with XbaI and one nucleotide was added by fill in in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (x/y reads in M13mp19, b/g reads in pUC19). The same ligation was transformed in either JM107 or DH5a."

BASE COUNT 66 a 44 c 38 g 91 t

ORIGIN

Query Match

Best Local Similarity 100.0%: Pred. No. 54;

Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 243 GATTCAACAAAAAGAGATG 262
Db 31 GATTCAACAAAAAGAGATG 12

RESULT 11
T99581/c

LOCUS T99581

DEFINITION Y65d08.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:122607 5', mRNA sequence.

ACCESSION T99581

VERSION T99581.1

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 374)

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Treaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.

The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
Insert Size: 954
High quality sequence stops: 243 Source: IMAGE Consortium, LNL This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 954 Std Error: 0.00
Seq primer: M13RPI
High quality sequence stop: 243.
Location/Qualifiers
1. 374
/organism="Homo sapiens"
/db_xref="GDB:475152"
/db_xref="taxon:9606"
/clone="IMAGE:122607"
/clone_1lb="Soares fetal liver spleen INFLS"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: p773D (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; 1st strand cDNA was primed with a Pac I - Oligo(dT) primer [5' AACGTGAGAGAAATTAATTAAGATCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified p7713 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 89 a 80 c 79 g 121 t 5 others

ORIGIN

Query Match 2.2%; Score 20; DB 14; Length 374;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 322 AAATGTGAGCAAGAATTA 341
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Db 83 AAATGTGAGCAAGAATTA 64

RESULT 12
AV792889/c 436 bp mRNA linear EST 29-MAR-2002
LOCUS AV792889 RALF7 Arabidopsis thaliana cDNA clone RALF07-17-C16 3',
DEFINITION mRNA sequence.
ACCESSION AV792889
VERSION AV792889.1 GI:19826872
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 436)
Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Atakawa, T., Shidara, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y. and Shinzaki, K.
Large scale analysis of Arabidopsis full-length cDNA (2002b)
Unpublished (2002)
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI

TITLE JOURNAL
COMMENT

and XhoI was ligated to modified lambda FL-C-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.

FEATURES
source Location/Qualifiers
1. 436
/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/clone="RALF07-17-C16"
/clone_1lb="RALF7"
/dev_stage="rosette plants"
/lab_host="DH10B"
/note="Site_1: BamHI; Site_2: SalI; subjected to cold-created (1, 2, 5, 10, 24 hr)"

BASE COUNT 121 a 72 c 103 g 140 t

ORIGIN

Query Match 2.2%; Score 20; DB 10; Length 436;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 618 CTCATCAGACATCATCA 637
|||||

Db 424 CTCATCAGACATCATCA 405

RESULT 13
BF704417 475 bp mRNA linear EST 22-DEC-2000
LOCUS BF704417
DEFINITION MI-P-E6-acc-g-09-1-UM.s1 MI-P-E6 Sus scrofa cDNA clone
ACCESSION MI-P-E6-acc-g-09-1-UM 3', mRNA sequence.
VERSION BF704417
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 475)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene discovery
Genome Res. 6 (9), 791-806 (1996)
Contact: Tugue CK
97044477
Molecular Genetics Laboratory, Department of Animal Science
Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
Tel: 5152944252
Fax: 5152942401
Email: cktugue@iastate.edu
Oligo-dT track not found. Not 1 site shown in beginning of sequence is likely internal to the message. cDNA library Preparation: RJ Woods, JA Green, RS Prather S142 Animal Science Research Center, Department of Animal Science, University of Missouri-Columbia, 65211 Clone distribution: clones will be available through Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA-No.

FEATURES
source Location/Qualifiers
1. 475
/organism="Sus scrofa"
/strain="crossbred"
/db_xref="taxon:9823"
/clone="MI-P-E6-acc-g-09-1-UM"
/clone_1lb="MI-P-E6"
/lab_host="DH10B (Life Technologies)"
/note="Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-E6 library is derived from fetus at gestational day 20. For a detailed description of the library from which this clone was derived, please visit our web site at

JOURNAL
MEDLINE
COMMENT

http://pigest.genome.istate.edu/
TAG_SEQ=None found"
BASE COUNT 129 a 120 c 121 g 104 t 1 others
ORIGIN

Query Match 2.2%: Score 20; DB 12; Length 475;
Best Local Similarity 100.0%; Pred. No. 62;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 CCTGACAGATGACATCAC 110
Db 202 CCTGAAGAGATGACATCAC 221

RESULT 14
BH780306 527 bp DNA linear GSS 28-MAR-2002
LOCUS f2mb015f001a0710 f2mb filtered library Zea mays genomic clone
DEFINITION f2mb015f001a07 5', DNA sequence.
ACCESSION BH780306
VERSION BH780306.1 GI:19783255
KEYWORDS GSS.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 527)

REFERENCE
AUTHORS Budiman, M.A., Freese, R.G., Bedell, J.A., Nurnberg, A.N. and Lakey, N.D.
TITLE Genethresher methylation filtered genomic sequences from maize
JOURNAL Unpublished (2002)
COMMENT Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: f2mb015f001 row: a column: 07
Seq primer: M13 forward
Class: shougun
High quality sequence stop: 527.
Location/Qualifiers
1..527

FEATURES
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1..527
/organism="Zea mays"
/cultivar="M017"
/db_xref="taxon:4577"
/clone="f2mb015f001a07"
/note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
prepared from purified nuclei was randomly sheared,
end-repaired, size fractionated to enrich for the 0.5 to
5 kb fraction, ligated into HincII-digested pBCSK(-)
vector and electroporated into E. coli cells."

BASE COUNT 181 a 77 c 108 g 161 t
ORIGIN

Query Match 2.2%: Score 20; DB 17; Length 527;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 GATTCAACAAAAAGAGATG 262
Db 141 GATTCAACAAAAAGAGATG 160

RESULT 15
AV554146 536 bp mRNA linear EST 06-SEP-2000
LOCUS AV554146 Arabidopsis thaliana roots Columbia
DEFINITION cDNA clone R282d11R 5', mRNA sequence.
ACCESSION AV554146
VERSION AV554146.1 GI:8725559
KEYWORDS EST.

SOURCE
ORGANISM thale cress.
Arabidopsis thaliana

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 536)

Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries

Journal DNA Res. 7, 175-180 (2000)
MEDLINE 20363093
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

FEATURES
source
1..536
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/strain="Columbia"
/db_xref="taxon:3702"
/clone="R282d11R"
/clone_lib="Arabidopsis thaliana roots Columbia"
/tissue_type="roots"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 168 a 128 c 112 g 128 t
ORIGIN

Query Match 2.2%: Score 20; DB 10; Length 536;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 618 CTTCATGACAGACATCATCA 637
Db 477 CTTCATGACAGACATCATCA 496

Search completed: July 16, 2003, 15:58:25
Job time: 1587.56 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 13:16:38 ; Search time 48.9112 Seconds
(without alignments)
5774.736 Million cell updates/sec

Title: US-09-917-265-52

Perfect score: 921
Sequence: 1 atatgggaactgagaaaga.....gggcactctgtctctgcagt 921

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 15338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued_patents_NA:*
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2: /cgn2_6/prodata/1/lna/5B_COMB.seq:*
3: /cgn2_6/prodata/1/lna/6A_COMB.seq:*
4: /cgn2_6/prodata/1/lna/6B_COMB.seq:*
5: /cgn2_6/prodata/1/lna/PCtUS_COMB.seq:*
6: /cgn2_6/prodata/1/lna/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Query Length | ID | Description |
|------------|-------|-------------|--------------|----|-------------------------------------|
| 1 | 921 | 100.0 | 990 | 4 | US-09-079-984A-11 Sequence 11, Appl |
| 2 | 759 | 82.4 | 990 | 4 | US-09-079-984A-11 Sequence 1, Appl |
| 3 | 46 | 5.0 | 987 | 1 | US-08-186-529-1 Sequence 1, Appl |
| 4 | 46 | 5.0 | 987 | 1 | US-08-640-386A-1 Sequence 1, Appl |
| 5 | 46 | 5.0 | 987 | 4 | US-08-848-760B-24 Sequence 24, Appl |
| 6 | 46 | 5.0 | 1018 | 2 | US-08-184-009-194 Sequence 194, App |
| 7 | 46 | 5.0 | 1018 | 2 | US-08-458-356-194 Sequence 194, App |
| 8 | 46 | 5.0 | 1018 | 4 | US-08-460-736-194 Sequence 194, App |
| 9 | 46 | 5.0 | 1399 | 2 | US-08-751-767A-3 Sequence 3, Appl |
| 10 | 46 | 5.0 | 1560 | 2 | US-08-751-767A-11 Sequence 11, Appl |
| 11 | 46 | 5.0 | 1623 | 2 | US-08-751-767A-9 Sequence 9, Appl |
| 12 | 46 | 5.0 | 1870 | 4 | US-09-310-842-4 Sequence 4, Appl |
| 13 | 46 | 5.0 | 2318 | 4 | US-09-851-062-3 Sequence 3, Appl |
| 14 | 46 | 5.0 | 2362 | 1 | US-08-265-087-1 Sequence 1, Appl |
| 15 | 46 | 5.0 | 2362 | 1 | US-08-621-493-1 Sequence 1, Appl |
| 16 | 46 | 5.0 | 2362 | 2 | US-08-565-688-1 Sequence 1, Appl |
| 17 | 46 | 5.0 | 2362 | 4 | US-09-260-173-1 Sequence 7, Appl |
| 18 | 46 | 5.0 | 6139 | 2 | US-08-751-767A-7 Sequence 14, Appl |
| 19 | 27 | 2.9 | 39 | 4 | US-09-079-984A-14 Sequence 17, Appl |
| 20 | 27 | 2.2 | 20 | 4 | US-09-851-062-17 Sequence 23, Appl |
| 21 | 27 | 2.2 | 20 | 4 | US-09-851-062-23 Sequence 13, Appl |
| 22 | 27 | 2.2 | 20 | 4 | US-09-851-062-33 Sequence 4, Appl |
| 23 | 27 | 2.2 | 1061 | 2 | US-08-385-335A-13 Sequence 19, Appl |
| 24 | 27 | 2.2 | 6295 | 2 | US-08-659-206A-4 Sequence 3, Appl |
| 25 | 27 | 2.2 | 7287 | 2 | US-08-659-206A-1 Sequence 3, Appl |
| 26 | 19 | 2.1 | 25 | 2 | US-08-751-767A-19 Sequence 3, Appl |
| 27 | 19 | 2.1 | 1002 | 2 | US-08-359-850-3 Sequence 3, Appl |

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|----|----|-----|---------|---|--------------------------------------|
| 28 | 19 | 2.1 | 3207 | 1 | US-07-946-497-1 Sequence 1, Appl |
| 29 | 19 | 2.1 | 3207 | 1 | US-08-483-322-1 Sequence 1, Appl |
| 30 | 19 | 2.1 | 3207 | 2 | US-08-478-882-1 Sequence 2, Appl |
| 31 | 18 | 2.0 | 20 | 4 | US-09-851-062-22 Sequence 22, Appl |
| 32 | 18 | 2.0 | 926 | 4 | US-09-079-984A-8 Sequence 8, Appl |
| 33 | 18 | 2.0 | 926 | 4 | US-08-936-165A-118 Sequence 118, App |
| 34 | 18 | 2.0 | 1375 | 2 | US-08-993-738A-2 Sequence 2, Appl |
| 35 | 18 | 2.0 | 1375 | 4 | US-08-713-354C-2 Sequence 2, Appl |
| 36 | 18 | 2.0 | 1375 | 4 | US-09-241-268-2 Sequence 2, Appl |
| 37 | 18 | 2.0 | 1375 | 4 | US-09-495-562-2 Sequence 2, Appl |
| 38 | 18 | 2.0 | 1640 | 1 | US-07-807-043B-11 Sequence 11, Appl |
| 39 | 18 | 2.0 | 1640 | 1 | US-08-299-849B-11 Sequence 11, Appl |
| 40 | 18 | 2.0 | 1640 | 2 | US-08-142-368A-11 Sequence 11, Appl |
| 41 | 18 | 2.0 | 1640 | 3 | US-08-967-727-11 Sequence 11, Appl |
| 42 | 18 | 2.0 | 1640 | 4 | US-08-037-230D-11 Sequence 11, Appl |
| 43 | 18 | 2.0 | 8257 | 4 | US-09-484-970B-65 Sequence 65, Appl |
| 44 | 18 | 2.0 | 13953 | 4 | US-09-738-884-3 Sequence 3, Appl |
| 45 | 18 | 2.0 | 4403765 | 4 | US-09-103-840A-2 Sequence 2, Appl |

ALIGNMENTS

RESULT 1
US-09-079-984A-11
Sequence 11, Application US/09079984A
Patent No. 6231850
GENERAL INFORMATION:
APPLICANT: Okano, Fumiyoshi, Satoh, Massahiro,
APPLICANT: Yamada, Katsushige
TITLE OF INVENTION: Canine interleukin 12, a production method
TITLE OF INVENTION: thereof, an immune disease treatment method and preventive
TITLE OF INVENTION: method using it
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Miller & Christenbury Intellectual Property
ADDRESSEE: Department of Schnader, Harrison, Segal and Lewis, LLP
STREET: 1600 Market Street, 39th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079, 984A
FILING DATE: 15-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Austin R. Miller
REGISTRATION NUMBER: 16,602
REFERENCE/DOCKET NUMBER: 1051-98
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-1810
TELEFAX: (215) 568-6946
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 990 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: Canine IL12
LOCATION: 1 to 987
IDENTIFICATION METHOD: Similarity
US-09-079-984A-11
Query Match 100.0%; Score 921; DB 4; Length 990;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 921; Conservative 0; Mismatched

| | QY | 01 | ATATGGAACTGAGAAAGATGTTTATGTTAGTAGGTTGAGACTGGCACCTGATGCCCC | 60 |
|--|----|-----|---|-----|
| | Db | 67 | ATATGGAACTGAGAAAGATGTTTATGTTAGTAGGTTGAGACTGGCACCTGATGCCCC | 126 |
| | QY | 61 | GGAGAAATGTTGGTCTCACCCTGGCATGCCCCGTGAAGAAGTATGATCTACTTGGACCTCA | 120 |
| | Db | 127 | GGAGAAATGTTGGTCTCACCCTGGCATGCCCCGTGAAGAAGTATGATCTACTTGGACCTCA | 186 |
| | QY | 121 | GGGAGACACACTGAAAGTCTAGTTCTGGTAAAACTGTGACATATCAAGTCAAAAGATTT | 180 |
| | Db | 187 | GGGAGACACACTGAAAGTCTAGTTCTGGTAAAACTGTGACATATCAAGTCAAAAGATTT | 246 |
| | QY | 181 | GGAGATCTCGGCCAGTATACCTGGCATTAAGAGGGCAAGGTTCTGAGCCGCTCACTCTG | 240 |
| | Db | 247 | GGAGATCTCGGCCAGTATACCTGGCATTAAGAGGGCAAGGTTCTGAGCCGCTCACTCTG | 306 |
| | QY | 241 | TTGATTCACAAAAAAGAGATGAAATTTGTCACCTGATATCTTAAAGAAACGAAAGAA | 300 |
| | Db | 307 | TTGATTCACAAAAAAGAGATGAAATTTGTCACCTGATATCTTAAAGAAACGAAAGAA | 366 |
| | QY | 301 | TCCAAAATTAAGATCTTCTGAAATGTGAGGCAAAATATTTCTGACGTTTCACATGC | 360 |
| | Db | 367 | TCCAAAATTAAGATCTTCTGAAATGTGAGGCAAAATATTTCTGACGTTTCACATGC | 426 |
| | QY | 361 | TGGTGCTACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGAGAGAGGCTTC | 420 |
| | Db | 427 | TGGTGCTACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGAGAGAGGCTTC | 486 |
| | QY | 421 | TGTGACCCCCAAGGGGTGACATGTGACACAGAGACATTTACAGCAGAGAGGCTCAGATG | 480 |
| | Db | 487 | TGTGACCCCCAAGGGGTGACATGTGACACAGAGACATTTACAGCAGAGAGGCTCAGATG | 546 |
| | QY | 481 | GACAAACAGGATTTAATAAGTATACACAGTGTGTCAGAGGGGAGTGGCTGGCCCTCT | 540 |
| | Db | 547 | GACAAACAGGATTTAATAAGTATACACAGTGTGTCAGAGGGGAGTGGCTGGCCCTCT | 606 |
| | QY | 541 | GCGAGAGAGACCTTACCATGAGAGTGTGGTGGATCTCTATTCACAAAGTCTCAAGTAGAA | 600 |
| | Db | 607 | GCGAGAGAGACCTTACCATGAGAGTGTGGTGGATCTCTATTCACAAAGTCTCAAGTAGAA | 666 |
| | QY | 601 | AACACACCCGACAGCTTCTTCATCAGACATCATCAACCAAGCCACCCCAAAACCTG | 660 |
| | Db | 667 | AACACACCCGACAGCTTCTTCATCAGACATCATCAACCAAGCCACCCCAAAACCTG | 726 |
| | QY | 661 | CAGCTGAAGCCATTGAAAAATTTCTGGACAGTGTGAGAGTCAAGCTGGGAATACCCGACAC | 720 |
| | Db | 727 | CAGCTGAAGCCATTGAAAAATTTCTGGACAGTGTGAGAGTCAAGCTGGGAATACCCGACAC | 786 |
| | QY | 721 | TGGAGACCCGACATTTCTACTTCTTCCTGACATTTTGCATACAGGCCACAGGGCAAGAAC | 780 |
| | Db | 787 | TGGAGACCCGACATTTCTACTTCTTCCTGACATTTTGCATACAGGCCACAGGGCAAGAAC | 846 |
| | QY | 781 | AATTAAGAAAAAAGATATGACTGTGCGTGGGCAAGACCTCAGCCAAAGTGGTGGCCAC | 840 |
| | Db | 847 | AATTAAGAAAAAAGATATGACTGTGCGTGGGCAAGACCTCAGCCAAAGTGGTGGCCAC | 906 |
| | QY | 841 | AAGGATGCAAGATCCGGGTGCAAGCCGAGACCGCTACTATAGTTCATCTCTGAGCGAC | 900 |
| | Db | 907 | AAGGATGCAAGATCCGGGTGCAAGCCGAGACCGCTACTATAGTTCATCTCTGAGCGAC | 966 |
| | QY | 901 | TGGGCATCTGTCTCTGAGT 921 | |
| | Db | 967 | TGGGCATCTGTCTCTGAGT 987 | |

RESULT 2
US-09-079-984A-1
; Sequence 1, Application US/09079984A
; Patent No. 6231850
; GENERAL INFORMATION:

APPLICANT: Okano, Fumiyoshi, Sacho, Massachusetts,
 APPLICANT: Yamada, Katsumige
 TITLE OF INVENTION: Canine interleukin 12, a production method
 TITLE OF INVENTION: thereof, an immune disease treatment method and preventive
 TITLE OF INVENTION: method using it
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Miller & Christenbury Intellectual Property
 ADDRESSEE: Department of Schnader, Harrison, Segal and Lewis, LLP
 STREET: 1600 Market Street, 39th Floor
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy Disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Wordperfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/079,984A
 FILING DATE: 15-MAY-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Austin R. Miller
 REGISTRATION NUMBER: 16,602
 REFERENCE/DOCKET NUMBER: 1051-98
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 563-1810
 TELEFAX: (215) 568-6946
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 990 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cdna to mRNA
 ORIGINAL SOURCE:
 ORGANISM: Canis familiaris
 FEATURE:
 NAME/KEY: Canine IL12
 LOCATION: 1 to 987
 IDENTIFICATION METHOD: Similarity

| | Query Match | 82.4% | Score 759; | DB 4; | Length 990; |
|----|---|-----------------|---------------|-----------|-------------|
| | Best Local Similarity | 99.7% | Prod. No. 0; | | |
| | Matches 909; | Conservative 0; | Mismatches 3; | Indels 0; | Gaps 0; |
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| Db | 67 ATATGGAACTGAGAGAAAGATGTTTATGTTTGAAGATTGATGGATGGACACCTGATGCCCC | 60 | | | |
| Qy | 61 GGAGAAATAGTGGTCTCCACCTGACCCATACCCCTGAAGAAAGATGACATCACTTGGACCTCA | 126 | | | |
| Db | 127 GGAGAAATAGTGGTCTCCACCTGACCCATACCCCTGAAGAAAGATGACATCACTTGGACCTCA | 126 | | | |
| Qy | 121 GGCGAGAGCAGTGAAGATCCTAGTTCCTGTGTAACCTCGACACATCCAGTAAAGATTT | 180 | | | |
| Db | 187 GGCGAGAGCAGTGAAGATCCTAGTTCCTGTGTAACCTCGACACATCCAGTAAAGATTT | 180 | | | |
| Qy | 181 GGAGATGCTGGCGACATATACCTGCCATTAAGAGAGCAAGGTTCTGAGCCGCTCACTCTG | 246 | | | |
| Db | 247 GGAGATGCTGGCGACATATACCTGCCATTAAGAGAGCAAGGTTCTGAGCCGCTCACTCTG | 246 | | | |
| Qy | 241 TTGATTCACAAAAAAGAGATGGAATTTGGTCCACCTATATCTTAAAGCAACGAAAAAA | 300 | | | |
| Db | 307 TTGATTCACAAAAAAGAGATGGAATTTGGTCCACCTATATCTTAAAGCAACGAAAAAA | 300 | | | |
| Qy | 301 TCCAAAAATAGATCTTTCTGGAATGTGAGGCAAAAGATTTATCTGAGAGTTTCACATGC | 360 | | | |
| Db | 367 TCCAAAAATAGATCTTTCTGGAATGTGAGGCAAAAGATTTATCTGAGAGTTTCACATGC | 360 | | | |
| Qy | 361 TGTGGCTGACGGCAATCACTAGTATTGGAATTCAGTGCTCAAAAGTACGAGAGCTTC | 420 | | | |

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1 INFORMATION FOR SEQ ID NO: 1 :
2 SEQUENCE CHARACTERISTICS:
3 LENGTH: 987 base pairs
4 TYPE: nucleic acid
5 STRANDEDNESS: single
6 TOPOLOGY: linear
7 MOLECULE TYPE: cDNA
8 ORIGINAL SOURCE:
9 ORGANISM: Homo sapiens
10 CELL TYPE: Lymphoblast
11 CELL LINE: RPMI 8866
12 FEATURE:
13 NAME/KEY: CDS
14 LOCATION: 1..987
15 US-08-186-529-1
16
17 Query Match 5.0%, Score 46; DB 1; Length 987;
18 Best Local Similarity 100.0%; Pred. No. 9.6e-14;
19 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
20
21 Oy 581 TTTCACAGCTCAGTATGAAACTACACACAGCTTTTCATCAG 626
22 |||||||
23 Db 644 TTCCACAGCTCAGTATGAAACTACACACAGCTTTTCATCAG 689
24
25 RESULT 4
26 US-08-640-386A-1
27 Sequence 1, Application US/08640386A
28 Patent No. 5756085
29
30 GENERAL INFORMATION:
31 APPLICANT: Sykes, Megan
32 TITLE OF INVENTION: USE OF INTERLEUKIN-12 TO PREVENT
33 TITLE OF INVENTION: GRAFT-VERSUS-HOST DISEASE
34 NUMBER OF SEQUENCES: 4
35 CORRESPONDENCE ADDRESS:
36 ADDRESSEE: Genetics Institute, Inc., Legal Affairs
37 STREET: 87 Cambridgepark Drive
38 CITY: Cambridge
39 STATE: MA
40 COUNTRY: USA
41 ZIP: 02140
42
43 COMPUTER READABLE FORM:
44 MEDIUM TYPE: Floppy disk
45 COMPUTER: IBM PC compatible
46 OPERATING SYSTEM: PC-DOS/MS-DOS
47 SOFTWARE: PatentIn Release #1.0, Version #1.25
48 CURRENT APPLICATION DATA:
49 APPLICATION NUMBER: US/08/640,386A
50 FILING DATE:
51 CLASSIFICATION: 424
52 ATTORNEY/AGENT INFORMATION:
53 NAME: Brown, Scott A.
54 REGISTRATION NUMBER: 32,724
55 REFERENCE/DOCKET NUMBER: GI 5225A
56 TELECOMMUNICATION INFORMATION:
57 TELEPHONE: 617-498-8224
58 TELEFAX: 617-876-5851
59 INFORMATION FOR SEQ ID NO: 1 :
60 SEQUENCE CHARACTERISTICS:
61 LENGTH: 987 base pairs
62 TYPE: nucleic acid
63 STRANDEDNESS: single
64 TOPOLOGY: linear
65 MOLECULE TYPE: cDNA
66 ORIGINAL SOURCE:
67 ORGANISM: Homo sapiens
68 CELL TYPE: Lymphoblast
69 CELL LINE: RPMI 8866
70 FEATURE:
71 NAME/KEY: CDS
72 LOCATION: 1..987
73 US-08-640-386A-1

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Query Match 5.0%; Score 46; DB 1; Length 987;
Best Local Similarity 100.0%; Pred. No. 9.6e-14;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 581 TTCACAGCTCAAGTATGAAACTACACGACGCTTCTTCATCAG 626
|||||
Db 644 TTCACAGCTCAAGTATGAAACTACACGACGCTTCTTCATCAG 689

RESULT 5

US-08-848-760B-24
Sequence 24, Application US/08848760B
Patent No. 6248721

GENERAL INFORMATION:

APPLICANT: Chang, Lung-Ji
TITLE OF INVENTION: Animal Model For Evaluation Of Vaccines
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESSES:
ADDRESSER: Saliwanhik, Lloyd & Saliwanhik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: United States of America
ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848,760B
FILING DATE: 25-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/838,702
FILING DATE: 09-APR-1997

ATTORNEY/AGENT INFORMATION:

NAME: PACE, DORAN R.
REGISTRATION NUMBER: 38,261
REFERENCE/DOCKET NUMBER: CNG-100C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:
LENGTH: 987 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Query Match 5.0%; Score 46; DB 4; Length 987;
Best Local Similarity 100.0%; Pred. No. 9.6e-14;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 581 TTCACAGCTCAAGTATGAAACTACACGACGCTTCTTCATCAG 626
|||||
Db 644 TTCACAGCTCAAGTATGAAACTACACGACGCTTCTTCATCAG 689

RESULT 6

US-08-184-009-194
Sequence 194, Application US/08184009
Patent No. 5833975

GENERAL INFORMATION:

APPLICANT: Paoletti, Enzo
APPLICANT: Tartaglia, James
APPLICANT: Cox, William I.
TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY

NUMBER OF SEQUENCES: 217
CORRESPONDENCE ADDRESSES:

ADDRESSER: Curtlis, Morris & Safford
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/184,009
FILING DATE: 19-JAN-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712

INFORMATION FOR SEQ ID NO: 194:

SEQUENCE CHARACTERISTICS:
LENGTH: 1018 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA

US-08-184-009-194

Query Match 5.0%; Score 46; DB 2; Length 1018;
Best Local Similarity 100.0%; Pred. No. 9.6e-14;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 581 TTCACAGCTCAAGTATGAAACTACACGACGCTTCTTCATCAG 626
|||||
Db 675 TTCACAGCTCAAGTATGAAACTACACGACGCTTCTTCATCAG 720

RESULT 7

US-08-458-356-194
Sequence 194, Application US/08458356
Patent No. 5942235

GENERAL INFORMATION:

APPLICANT: Paoletti, Enzo
APPLICANT: Tartaglia, James
APPLICANT: Cox, William I.
TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
NUMBER OF SEQUENCES: 217
CORRESPONDENCE ADDRESSES:
ADDRESSER: Curtlis, Morris & Safford
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,356
FILING DATE: 02-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/184,009
FILING DATE: 19-JAN-1994
ATTORNEY/AGENT INFORMATION:

NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEX: 425066CURTMS
INFORMATION FOR SEQ ID NO: 194:
SEQUENCE CHARACTERISTICS:
LENGTH: 1018 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-458-356-194

Query Match 5.0%, Score 46; DB 2; Length 1018;
Best Local Similarity 100.0%; Pred. No. 9.6e-14;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 581 TTCACAGCTCAAGTATGAAACTACACGAGCTTCTCATCAG 626
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DB 675 TTCACAGCTCAAGTATGAAACTACACGAGCTTCTCATCAG 720

RESULT 8
US-08-460-736-194

Sequence 194, Application US/08460736
Patent No. 6265189

GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: Tartaglia, James
APPLICANT: Cox, William I.
TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
NUMBER OF SEQUENCES: 217
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,736
FILING DATE: 02-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/184,009
FILING DATE: 19-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEX: 425066CURTMS
INFORMATION FOR SEQ ID NO: 194:
SEQUENCE CHARACTERISTICS:
LENGTH: 1018 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-460-736-194

Query Match 5.0%, Score 46; DB 4; Length 1018;
Best Local Similarity 100.0%; Pred. No. 9.6e-14;

Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 581 TTCACAGCTCAAGTATGAAACTACACGAGCTTCTCATCAG 626
|||||
DB 675 TTCACAGCTCAAGTATGAAACTACACGAGCTTCTCATCAG 720

RESULT 9
US-08-751-767A-3

Sequence 3, Application US/08751767A
Patent No. 5994104

GENERAL INFORMATION:
APPLICANT: ANDERSON, ROBERT J.
APPLICANT: GRANT, HUGH
APPLICANT: MACDONALD, IAN D.
TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHIVE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,767A
FILING DATE: 08-NOV-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.

REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 117-221
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164091
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1399 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:

NAME/KEY: CDS
LOCATION: 43..1026
US-08-751-767A-3

Query Match 5.0%, Score 46; DB 2; Length 1399;
Best Local Similarity 100.0%; Pred. No. 9.6e-14;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 581 TTCACAGCTCAAGTATGAAACTACACGAGCTTCTCATCAG 626
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DB 686 TTCACAGCTCAAGTATGAAACTACACGAGCTTCTCATCAG 731

RESULT 10

US-08-751-767A-11
Sequence 11, Application US/08751767A
Patent No. 5994104

GENERAL INFORMATION:
APPLICANT: ANDERSON, ROBERT J.
APPLICANT: GRANT, HUGH
APPLICANT: MACDONALD, IAN D.
TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHIVE P.C.

```

? TELEPHONE: 7038164091
? TELEFAX: 7038164100
? INFORMATION FOR SEQ ID NO: 9:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1623 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..1620
US-08-751-767A-9

Query Match
Best Local Similarity 100.0%; Score 46; DB 2; Length 1623;
Pred. No. 9,6e-14;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 581 TTCAACAAGCTCAAGTATGAAACTACACACGACGCTTCTTCATCAG 626
DB 644 TTCAACAAGCTCAAGTATGAAACTACACACGACGCTTCTTCATCAG 689

RESULT 12
US-09-310-842-4
? Sequence 4, Application US/09310842A
? Patent No. 6451593
? GENERAL INFORMATION:
? APPLICANT: Wilety, Prof. Burghardt
? APPLICANT: Wilety, Prof. Burghardt
? TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for G
? FILE REFERENCE: XI 597/99
? CURRENT APPLICATION NUMBER: US/09/310,842A
? EARLIER APPLICATION NUMBER: DE 196 48 625.4
? EARLIER FILING DATE: 1996-11-13
? NUMBER OF SEQ ID NOS: 13
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 4
? LENGTH: 1870
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? NAME/KEY: gene
? LOCATION: (1)..(1870)
? OTHER INFORMATION: Interleukin-12 (IL-12, p40-subunit); Oligo DNA Dumbbell
? FEATURE:
? NAME/KEY: misc.binding
? LOCATION: (1)..(2)
? OTHER INFORMATION: Intramolecular binding site; the T-nucleotides at position 1 t
? OTHER INFORMATION: 2 can be modified with amino or caroxy features
? FEATURE:
? NAME/KEY: misc.binding
? LOCATION: (1869)..(1870)
? OTHER INFORMATION: Intramolecular binding site; the T-nucleotides at position 186
? OTHER INFORMATION: to 1870 can be modified with amino or caroxy features
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Strandedness: both; nuclei
? OTHER INFORMATION: acid (linear), hypothetical: No. 6451593 anti-sense: No
US-09-310-842-4

Query Match
Best Local Similarity 100.0%; Score 46; DB 4; Length 1870;
Pred. No. 9,6e-14;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 581 TTCAACAAGCTCAAGTATGAAACTACACACGACGCTTCTTCATCAG 626
DB 1276 TTCAACAAGCTCAAGTATGAAACTACACACGACGCTTCTTCATCAG 1321

RESULT 13
US-09-851-062-3

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Sequence 3, Application US/09851062
Patent No. 6448081
GENERAL INFORMATION:
APPLICANT: Brenda F. Baker
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
FILE REFERENCE: RTS-0247
CURRENT APPLICATION NUMBER: US/09/851,062
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 3
LENGTH: 2318
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (14)...(1000)
US-09-851-062-3

Query Match 5.0%; Score 46; DB 4; Length 2318;
Best Local Similarity 100.0%; Pred. No. 9,6e-14;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 581 TTCACAGCTCAAGTATGAAACTACACGACGACCTTCTTCATCAG 626
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Db 657 TTCACAGCTCAAGTATGAAACTACACGACGACCTTCTTCATCAG 702

RESULT 14
US-08-265-087-1
Sequence 1, Application US/08265087
Patent No. 5571515

GENERAL INFORMATION:

APPLICANT: Scott, Phillip

APPLICANT: Trinchiari, Giorgio

TITLE OF INVENTION: Compositions and Methods for Use of

TITLE OF INVENTION: IL-12 as an Adjuvant

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howson and Howson

STREET: Spring House Corporate Center, PO Box 457

CITY: Spring House

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19477

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/265,087

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/229,282

FILING DATE: 18-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Bak, Mary E.

REGISTRATION NUMBER: 31,215

REFERENCE/DOCKET NUMBER: WST51AUSA

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-540-9206

TELEFAX: 215-540-5818

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2362 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: unknown

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 33..1016
US-08-265-087-1

Query Match 5.0%; Score 46; DB 1; Length 2362;

Best Local Similarity 100.0%; Pred. No. 9,6e-14;

Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 581 TTCACAGCTCAAGTATGAAACTACACGACGACCTTCTTCATCAG 626
|||||
Db 676 TTCACAGCTCAAGTATGAAACTACACGACGACCTTCTTCATCAG 721

RESULT 15
US-08-621-493-1

Sequence 1, Application US/08621493
Patent No. 5723127

GENERAL INFORMATION:

APPLICANT: Scott, Phillip

APPLICANT: Trinchiari, Giorgio

TITLE OF INVENTION: Compositions and Methods for Use of

TITLE OF INVENTION: IL-12 as an Adjuvant

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howson and Howson

STREET: Spring House Corporate Center, PO Box 457

CITY: Spring House

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19477

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/621,493

FILING DATE: 25-MAR-1996

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/265,087

FILING DATE: 17-JUN-1994

APPLICATION NUMBER: US 08/229,282

FILING DATE: 18-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Bak, Mary E.

REGISTRATION NUMBER: 31,215

REFERENCE/DOCKET NUMBER: WST51AUSA

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-540-9206

TELEFAX: 215-540-5818

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2362 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: unknown

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 33..1016

US-08-621-493-1

Query Match 5.0%; Score 46; DB 1; Length 2362;
Best Local Similarity 100.0%; Pred. No. 9,6e-14;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 581 TTCACAGCTCAAGTATGAAACTACACGACGACCTTCTTCATCAG 626
|||||
Db 676 TTCACAGCTCAAGTATGAAACTACACGACGACCTTCTTCATCAG 721

Search completed: July 16, 2003, 19:43:43
Job time : 50.9112 secs

Thu Jul 17 12:12:36 2003

us-09-917-265-52.oli.rni

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 13:21:13 ; Search time 174.379 Seconds
(without alignments)
8432.179 Million cell updates/sec

Title: US-09-917-265-52

Perfect score: 921

Sequence: 1 atagggaacgtgagaaga.....gggcacgtgtgtccgtcagt 921

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Gapop 60.0 , Gapext 60.0

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
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12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 3 | 921 | 100.0 | 2267 | 10 | US-09-917-265-107 |
| 4 | 921 | 100.0 | 2267 | 10 | US-09-917-265-109 |
| 5 | 914 | 99.2 | 987 | 10 | US-09-917-265-58 |
| 6 | 914 | 99.2 | 987 | 10 | US-09-917-265-60 |
| 7 | 914 | 99.2 | 1533 | 10 | US-09-917-265-66 |
| 8 | 914 | 99.2 | 1533 | 10 | US-09-917-265-68 |
| 9 | 914 | 99.2 | 1599 | 10 | US-09-917-265-61 |
| 10 | 914 | 99.2 | 1599 | 10 | US-09-917-265-63 |
| 11 | 66 | 7.2 | 921 | 10 | US-09-917-265-26 |
| 12 | 66 | 7.2 | 921 | 10 | US-09-917-265-28 |
| 13 | 66 | 7.2 | 921 | 12 | US-10-079-616-6 |
| 14 | 66 | 7.2 | 985 | 10 | US-09-917-265-55 |
| 15 | 66 | 7.2 | 985 | 10 | US-09-917-265-57 |
| 16 | 66 | 7.2 | 987 | 10 | US-09-917-265-29 |
| 17 | 66 | 7.2 | 987 | 10 | US-09-917-265-31 |
| 18 | 66 | 7.2 | 1533 | 10 | US-09-917-265-43 |
| 19 | 66 | 7.2 | 1533 | 10 | US-09-917-265-45 |

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| 20 | 66 | 7.2 | 1599 | 10 | US-09-917-265-38 | Sequence 38, Appl |
| 21 | 66 | 7.2 | 1599 | 10 | US-09-917-265-40 | Sequence 40, Appl |
| 22 | 66 | 7.2 | 2193 | 12 | US-10-079-616-5 | Sequence 5, Appl1 |
| 23 | 63 | 6.8 | 921 | 12 | US-10-079-616-7 | Sequence 7, Appl1 |
| 24 | 46 | 5.0 | 987 | 9 | US-09-826-025-24 | Sequence 24, Appl |
| 25 | 46 | 5.0 | 987 | 10 | US-09-754-014-2 | Sequence 2, Appl1 |
| 26 | 46 | 5.0 | 987 | 10 | US-09-836-866-2 | Sequence 2, Appl1 |
| 27 | 46 | 5.0 | 1870 | 9 | US-10-228-811-4 | Sequence 4, Appl1 |
| 28 | 46 | 5.0 | 2318 | 9 | US-10-172-399-7 | Sequence 7, Appl1 |
| 29 | 46 | 5.0 | 2362 | 10 | US-09-924-703-3 | Sequence 3, Appl1 |
| 30 | 46 | 5.0 | 8578 | 10 | US-09-828-825-1 | Sequence 1, Appl1 |
| 31 | 46 | 5.0 | 8578 | 10 | US-09-828-825-3 | Sequence 3, Appl1 |
| 32 | 46 | 5.0 | 8608 | 10 | US-09-828-825-7 | Sequence 7, Appl1 |
| 33 | 46 | 5.0 | 8623 | 10 | US-09-828-825-5 | Sequence 5, Appl1 |
| 34 | 46 | 5.0 | 8629 | 10 | US-09-828-825-15 | Sequence 15, Appl |
| 35 | 46 | 5.0 | 8638 | 10 | US-09-828-825-9 | Sequence 9, Appl1 |
| 36 | 46 | 5.0 | 8644 | 10 | US-09-828-825-13 | Sequence 13, Appl |
| 37 | 46 | 5.0 | 8659 | 10 | US-09-828-825-11 | Sequence 11, Appl |
| 38 | 24 | 2.6 | 987 | 10 | US-09-754-014-3 | Sequence 3, Appl1 |
| 39 | 24 | 2.6 | 987 | 10 | US-09-754-014-4 | Sequence 4, Appl1 |
| 40 | 22 | 2.4 | 22 | 10 | US-09-917-265-97 | Sequence 97, Appl |
| 41 | 21 | 2.3 | 44 | 12 | US-10-079-616-14 | Sequence 14, Appl |
| 42 | 20 | 2.2 | 1840 | 9 | US-10-172-399-3 | Sequence 3, Appl1 |
| 43 | 19 | 2.1 | 19 | 10 | US-09-917-265-98 | Sequence 98, Appl |
| 44 | 19 | 2.1 | 21 | 9 | US-10-233-117-35 | Sequence 35, Appl |
| 45 | 19 | 2.1 | 21 | 9 | US-10-233-121A-5 | Sequence 5, Appl1 |

ALIGNMENTS

RESULT 1
US-09-917-265-52
Sequence 52, Application US/09917265
Patent No. US20020052030A1
GENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Borouhgs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/09/917,265
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 109
SOFTWARE: PatentIn version 3.1
SEQ ID NO 52
LENGTH: 921
TYPE: DNA
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(921)
OTHER INFORMATION:
US-09-917-265-52
Query Match 100.0%; Score 921; DB 10; Length 921;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATATGGAACTGGAGAAAGATGTTATGTTGAGAGTTGGACCTGGACCCGATGCCCC 60
|||||
1 ATTTGGAACTGGAGAAAGATGTTATGTTGAGAGTTGGACCTGGACCCGATGCCCC 60
Db 1 ATTTGGAACTGGAGAAAGATGTTATGTTGAGAGTTGGACCTGGACCCGATGCCCC 60
QY 61 GGAGAAATGTTGCTCCTACCTGCCAATACCCCTGAAGAGATGATGATGACCTCA 120
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61 GGAGAAATGTTGCTCCTACCTGCCAATACCCCTGAAGAGATGATGATGACCTCA 120
Db 61 GGAGAAATGTTGCTCCTACCTGCCAATACCCCTGAAGAGATGATGATGACCTCA 120
QY 121 GCCCAGACGCTGAAGCTTCAAGTTCTGCTGTAATAACTCTGACCATCCAAAGTCAAGAAATTT 180
|||||
121 GCCCAGACGCTGAAGCTTCAAGTTCTGCTGTAATAACTCTGACCATCCAAAGTCAAGAAATTT 180
Db 121 GCCCAGACGCTGAAGCTTCAAGTTCTGCTGTAATAACTCTGACCATCCAAAGTCAAGAAATTT 180
QY 181 GGAGATGCTGGCCAGTATACCTGCCATTAAGAGAGCAAGGTCTGAGACCCGCTCAGTCTTG 240

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Db 181 GGAGATGCTGGCAGATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTACCTCAG 240
OY 241 TTGATTACAAAAAAGAAATGTAATTTGGTCCACTGATATCTTTAAAGACAGAAAGA 300
Db 241 TTGATTACAAAAAAGAAATGTAATTTGGTCCACTGATATCTTTAAAGACAGAAAGA 300
OY 301 TCCAAAAATAGATCTTTCTGAAATGTGAGGCAAAAGTAATTTCTGAGCTTTACATGC 360
Db 301 TCCAAAAATAGATCTTTCTGAAATGTGAGGCAAAAGTAATTTCTGAGCTTTACATGC 360
OY 361 TGGTGGCTACGGCAATCAGTACTGATTTGAAATTAAGTCAAAAGTACAGAGCTTC 420
Db 361 TGGTGGCTACGGCAATCAGTACTGATTTGAAATTAAGTCAAAAGTACAGAGCTTC 420
OY 421 TCTGACCCCAAGGGGTGACATGTGAGCAGTACACTTTCAGCAGAGAGGCTCAGAGT 480
Db 421 TCTGACCCCAAGGGGTGACATGTGAGCAGTACACTTTCAGCAGAGAGGCTCAGAGT 480
OY 481 GACAAACAGGATTTATTAAGATACACAGTGAAGTTCAGAGAGGCAAGTCCCTGCT 540
Db 481 GACAAACAGGATTTATTAAGATACACAGTGAAGTTCAGAGAGGCAAGTCCCTGCT 540
OY 541 GCGGAGAGAGCTTACCATTCGAGTCTGTGTGATGCTATTTCACAAAGCTCAAGTGA 600
Db 541 GCGGAGAGAGCTTACCATTCGAGTCTGTGTGATGCTATTTCACAAAGCTCAAGTGA 600
OY 601 AACTACACAGCAGCTTCTTCATCAGACATCATCAACAGACAGCCACCAACAACTG 660
Db 601 AACTACACAGCAGCTTCTTCATCAGACATCATCAACAGACAGCCACCAACAACTG 660
OY 661 CAGCTGAAGCCATTTGAAAAATTTCTCGCACGTGAGAGTCAAGTGGGAATACCCGAC 720
Db 661 CAGCTGAAGCCATTTGAAAAATTTCTCGCACGTGAGAGTCAAGTGGGAATACCCGAC 720
OY 721 TGGAGACACCCCATCTTCTTCTCTCCCTGACATTTTGCATACAGGCCCAAGGCAAG 780
Db 721 TGGAGACACCCCATCTTCTTCTCTCCCTGACATTTTGCATACAGGCCCAAGGCAAG 780
OY 781 AATAGAGAAAGAAAGATAGACTCTGCTGAGCAAGACATCAAGCTCGTGTCCAC 840
Db 781 AATAGAGAAAGAAAGATAGACTCTGCTGAGCAAGACATCAAGCTCGTGTCCAC 840
OY 841 AAGGATGCCAAGATCCGCTGCAAGCCGAGACCGCTACTATAGTTCAATCTGAGCGAC 900
Db 841 AAGGATGCCAAGATCCGCTGCAAGCCGAGACCGCTACTATAGTTCAATCTGAGCGAC 900
OY 901 TGGGCACTGTGTCTGCTGCAGT 921
Db 901 TGGGCACTGTGTCTGCTGCAGT 921

RESULT 2
US-09-917-265-54/C
; Sequence 54, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917, 265
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223, 016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-917-265-54
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Query Match 100.0%; Score 921; DB 10; Length 921;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AATAGGAACTGGAGAAAGATGTTATGTGTGTAAGTGGATGGACCCCTATGCCCC 60
Db 921 AATAGGAACTGGAGAAAGATGTTATGTGTGTAAGTGGATGGACCCCTATGCCCC 862
OY 61 GGAGAAATGGTGTCTCCTACCTGACATACCCCTGAAAGATAGATCAGTCTTGA 120
Db 861 GGAGAAATGGTGTCTCCTACCTGACATACCCCTGAAAGATAGATCAGTCTTGA 802
OY 121 GCGCAGAGCAGTGAAGTCTTCTGTTGTGTTAAACTCTGACATCCAAAGATTT 180
Db 801 GCGCAGAGCAGTGAAGTCTTCTGTTGTGTTAAACTCTGACATCCAAAGATTT 742
OY 181 GGAGATGCTGGCAGATACCTGCCATAAAGGAGGCAAGTCTGAGCCGCTACCTG 240
Db 741 GGAGATGCTGGCAGATACCTGCCATAAAGGAGGCAAGTCTGAGCCGCTACCTG 682
OY 241 TTGATTACAAAAAAGAAATGGAATTTGCTCCACTGATATCTTTAAAGACAGAA 300
Db 681 TTGATTACAAAAAAGAAATGGAATTTGCTCCACTGATATCTTTAAAGACAGAA 622
OY 301 TCCAAAAATAGATCTTTCTGAAATGTGAGGCAAAAGTAATTTCTGAGCTTTAC 360
Db 621 TCCAAAAATAGATCTTTCTGAAATGTGAGGCAAAAGTAATTTCTGAGCTTTAC 562
OY 361 TGGTGGCTACGGCAATCAGTACTGATTTGAAATTAAGTCAAAAGTACAGAGCTTC 420
Db 561 TGGTGGCTACGGCAATCAGTACTGATTTGAAATTAAGTCAAAAGTACAGAGCTTC 502
OY 421 TCTGACCCCAAGGGGTGACATGTGAGCAGTACACTTTCAGCAGAGAGGCTCAG 480
Db 501 TCTGACCCCAAGGGGTGACATGTGAGCAGTACACTTTCAGCAGAGAGGCTCAG 442
OY 481 GACAAACAGGATTTATTAAGATACACAGTGAAGTTCAGAGAGGCAAGTCCCT 540
Db 441 GACAAACAGGATTTATTAAGATACACAGTGAAGTTCAGAGAGGCAAGTCCCT 382
OY 541 GCGGAGAGAGCTTACCATTCGAGTCTGTGTGATGCTATTTCACAAAGCTCA 600
Db 381 GCGGAGAGAGCTTACCATTCGAGTCTGTGTGATGCTATTTCACAAAGCTCA 322
OY 601 AACTACACAGCAGCTTCTTCATCAGACATCATCAACAGACAGCCACCAAACTG 660
Db 321 AACTACACAGCAGCTTCTTCATCAGACATCATCAACAGACAGCCACCAAACTG 262
OY 661 CAGCTGAAGCCATTTGAAAAATTTCTCGCACGTGAGAGTCAAGTGGGAATAC 720
Db 261 CAGCTGAAGCCATTTGAAAAATTTCTCGCACGTGAGAGTCAAGTGGGAATAC 202
OY 721 TGGAGACACCCCATCTTCTTCTCTCCCTGACATTTTGCATACAGGCCCAAG 780
Db 201 TGGAGACACCCCATCTTCTTCTCTCCCTGACATTTTGCATACAGGCCCAAG 142
OY 781 AATAGAGAAAGAAAGATAGACTCTGCTGAGCAAGACATCAAGCTCGTGTCCAC 840
Db 141 AATAGAGAAAGAAAGATAGACTCTGCTGAGCAAGACATCAAGCTCGTGTCCAC 82
OY 841 AAGGATGCCAAGATCCGCTGCAAGCCGAGACCGCTACTATAGTTCAATCTGAG 900
Db 81 AAGGATGCCAAGATCCGCTGCAAGCCGAGACCGCTACTATAGTTCAATCTGAG 22
OY 901 TGGGCACTGTGTCTGCTGCAGT 921
Db 21 TGGGCACTGTGTCTGCTGCAGT 1

RESULT 3
US-09-917-265-107
; Sequence 107, Application US/09917265
; Patent No. US20020052030A1
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GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: APPLICANT: Borouhgs, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
: FILE REFERENCE: IM-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: CURRENT FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: PRIOR FILING DATE: 2000-08-04
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO: 107
: LENGTH: 2267
: TYPE: DNA
: ORGANISM: Canis familiaris
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (154)..(1140)
: OTHER INFORMATION:
US-09-917-265-107

Query Match 100.0% Score 921: DB 10: Length 2267:
Best Local Similarity 100.0%: Pred. No. 0:
Matches 921: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 1 ATATGGAACTGGAGAAAGATGTTTATGTTGAGCTGGAGCCCGTATGCCCCC 60
DB 220 ATATGGAACTGGAGAAAGATGTTTATGTTGAGCTGGAGCCCGTATGCCCCC 279
OY 61 GGAGAAATGCTGCTCCTCAGCTCCATACCCCTGAAGAGATGACATTCAGCTGCA 120
DB 280 GGAGAAATGCTGCTCCTCAGCTCCATACCCCTGAAGAGATGACATTCAGCTGCA 339
OY 121 GGCCAGAGAGTGAAGTCTAGCTTGTGTTAAACTCTGACCATCCAAAGTCAAGATTT 180
DB 340 GGCCAGAGAGTGAAGTCTAGCTTGTGTTAAACTCTGACCATCCAAAGTCAAGATTT 399
OY 181 GGAGATGCTGGCCAGATACCTGCGATTAAGAGAGAGAGTGTGAGCCGCTACCTG 240
DB 400 GGAGATGCTGGCCAGATACCTGCGATTAAGAGAGAGAGTGTGAGCCGCTACCTG 459
OY 241 TTGATTCACAAAAAAGAGATGGAATTTGCTCAGTATCTTAAAGAAAGAAAGAA 300
DB 460 TTGATTCACAAAAAAGAGATGGAATTTGCTCAGTATCTTAAAGAAAGAAAGAA 519
OY 301 TCCAAAAATTAAGATCTTTCTGAATGTGAGGCAAAATTTATCTGAGCTTCACATGC 360
DB 520 TCCAAAAATTAAGATCTTTCTGAATGTGAGGCAAAATTTATCTGAGCTTCACATGC 579
OY 361 TGGTGGCTGAGCGCAATCAGTACTGATTTGAATTCAGTGTCAAAAGTACGACAGGCTTC 420
DB 580 TGGTGGCTGAGCGCAATCAGTACTGATTTGAATTCAGTGTCAAAAGTACGACAGGCTTC 639
OY 421 TCTGACCCCAAGGGGTGACATGTGAGAGAGTGCACCTTTCAGCAGAGAGGCTCAGAGTG 480
DB 640 TCTGACCCCAAGGGGTGACATGTGAGAGAGTGCACCTTTCAGCAGAGAGGCTCAGAGTG 699
OY 481 GACACAGCGATTATTAAGAAAGTACACAGTGTGAGAGTGTGAGAGGCGAGTGCCTCT 540
DB 700 GACACAGCGATTATTAAGAAAGTACACAGTGTGAGAGTGTGAGAGGCGAGTGCCTCT 759
OY 541 GCGGAGAGAGGCTACCCATCAGAGTGTGAGAGTGTGATTTACAAAGCTCAAGTATGAA 600
DB 760 GCGGAGAGAGGCTACCCATCAGAGTGTGAGAGTGTGATTTACAAAGCTCAAGTATGAA 819
OY 601 AACTACACAGAGCTTTCTTCATCAGAGACATCATCAACACAGACCCACCAACACTG 660
DB 820 AACTACACAGAGCTTTCTTCATCAGAGACATCATCAACACAGACCCACCAACACTG 879
OY 661 CAGCTGAAGCCATTGAAAAATTTCTGGGACAGTGTGAGAGTGTGAGAGTGTGAGAGTGT 720
DB 880 CAGCTGAAGCCATTGAAAAATTTCTGGGACAGTGTGAGAGTGTGAGAGTGTGAGAGTGT 939

OY 721 TGGAGCACCCACATTCCTACTTCTCCCTGACATTTTGACATACAGCCCAAGGCAAGAC 780
DB 940 TGGAGCACCCACATTCCTACTTCTCCCTGACATTTTGACATACAGCCCAAGGCAAGAC 999
OY 781 AATAGAAAAAAGAAAGATAGACTCTGCTGAGCAAGACCTGAGCAAGGTGTGCTGCAC 840
DB 1000 AATAGAAAAAAGAAAGATAGACTCTGCTGAGCAAGACCTGAGCAAGGTGTGCTGCAC 1059
OY 841 AAGATGCCAAGATCCCGCTGCAAGCCCGAGACCGCTACTATAGTTATCTTGAAGGAC 900
DB 1060 AAGATGCCAAGATCCCGCTGCAAGCCCGAGACCGCTACTATAGTTATCTTGAAGGAC 1119
OY 901 TGGCATCTGTGCTGCTGAGT 921
DB 1120 TGGCATCTGTGCTGCTGAGT 1140

RESULT 4
US-09-917-265-109/c
: Sequence 109, Application US/09917265
: Patent No. US2002052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: APPLICANT: Borouhgs, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
: FILE REFERENCE: IM-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: CURRENT FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: PRIOR FILING DATE: 2000-08-04
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO: 109
: LENGTH: 2267
: TYPE: DNA
: ORGANISM: Canis familiaris
US-09-917-265-109

Query Match 100.0% Score 921: DB 10: Length 2267:
Best Local Similarity 100.0%: Pred. No. 0:
Matches 921: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 1 ATATGGAACTGGAGAAAGATGTTTATGTTGAGCTGGAGCCCGTATGCCCCC 60
DB 2048 ATATGGAACTGGAGAAAGATGTTTATGTTGAGCTGGAGCCCGTATGCCCCC 1989
OY 61 GGAGAAATGCTGCTCCTCAGCTCCATACCCCTGAAGAGATGACATTCAGCTGCA 120
DB 1988 GGAGAAATGCTGCTCCTCAGCTCCATACCCCTGAAGAGATGACATTCAGCTGCA 1929
OY 121 GGCCAGAGAGTGAAGTCTAGCTTGTGTTAAACTCTGACCATCCAAAGTCAAGATTT 180
DB 1928 GGCCAGAGAGTGAAGTCTAGCTTGTGTTAAACTCTGACCATCCAAAGTCAAGATTT 1869
OY 181 GGAGATGCTGGCCAGATACCTGCGATTAAGAGAGAGAGTGTGAGCCGCTACCTG 240
DB 1868 GGAGATGCTGGCCAGATACCTGCGATTAAGAGAGAGAGTGTGAGCCGCTACCTG 1809
OY 241 TTGATTCACAAAAAAGAGATGGAATTTGCTCAGTATCTTAAAGAAAGAAAGAA 300
DB 1808 TTGATTCACAAAAAAGAGATGGAATTTGCTCAGTATCTTAAAGAAAGAAAGAA 1749
OY 301 TCCAAAAATTAAGATCTTTCTGAATGTGAGGCAAAAGATTTATCTGAGCTTCACATGC 360
DB 1748 TCCAAAAATTAAGATCTTTCTGAATGTGAGGCAAAAGATTTATCTGAGCTTCACATGC 1689
OY 361 TGGTGGCTGAGCGCAATCAGTACTGATTTAAATTCAGTGTCAAAAGTACAGAGCTTC 420
DB 1688 TGGTGGCTGAGCGCAATCAGTACTGATTTAAATTCAGTGTCAAAAGTACAGAGCTTC 1629
OY 421 TCTGACCCCAAGGGGTGACATGTGAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGT 480
DB 1628 TCTGACCCCAAGGGGTGACATGTGAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGT 1569

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OY 481 GACACAGAGGATTTTAAGAAGTACACAGTGTGTCAGAGGAGGAGTGGCTGCCCTCT 540
Db 1568 GACACAGAGGATTTTAAGAAGTACACAGTGTGTCAGAGGAGGAGTGGCTGCCCTCT 1509
OY 541 GCCGAGAGAGGCTTACCCATCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1508
Db 1508 GCCGAGAGAGGCTTACCCATCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1449
OY 601 AACTACACAGCAGCTTCTTCATCAGAGACATCATCAACCCAGACCCCAACCTG 660
Db 1448 AACTACACAGCAGCTTCTTCATCAGAGACATCATCAACCCAGACCCCAACCTG 1389
OY 661 CAGCTGAGCAATTTGAAAATTTCTGGCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 720
Db 1388 CAGCTGAGCAATTTGAAAATTTCTGGCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1329
OY 721 TGGAGACCCCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 780
Db 1328 TGGAGACCCCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1269
OY 781 AATAGAGAAAAGATATGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
Db 1268 AATAGAGAAAAGATATGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1209
OY 841 AAGATGCCAAGATCCGCGTCAAGCCGAGACCGGCTACTATATGTTTCTTCTTCTTCT 900
Db 1208 AAGATGCCAAGATCCGCGTCAAGCCGAGACCGGCTACTATATGTTTCTTCTTCTTCT 1149
OY 901 TGGGATCTGTGTCTGTGAGT 921
Db 1148 TGGGATCTGTGTCTGTGAGT 1128
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RESULT 5

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US-09-917-265-58
; Sequence 58, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 987
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(987)
; OTHER INFORMATION:
US-09-917-265-58
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Query Match 99.2%; Score 914; DB 10; Length 987;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 914; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 ATATGGGAAGTGAAGAAAGATGTTTATGTGTAGTGTGACTGTGACCGACCTGATGCCCC 60
Db 67 ATATGGGAAGTGAAGAAAGATGTTTATGTGTAGTGTGACTGTGACCGACCTGATGCCCC 126
OY 61 GGAAATGTGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 120
Db 127 GGAAATGTGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 186
OY 121 GCCGAGAGCAGTGAAGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
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Db 187 GCCGAGAGCAGTGAAGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 246
OY 181 GGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
Db 247 GGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 306
OY 241 TTGATTCACAAAAGAGATGTGAATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
Db 307 TTGATTCACAAAAGAGATGTGAATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 366
OY 301 TCCAAAATTAAGATCTTTCTGAATGTGTGAAGCAAAATTTCTGTGAGCTTTTCAATGC 360
Db 367 TCCAAAATTAAGATCTTTCTGAATGTGTGAAGCAAAATTTCTGTGAGCTTTTCAATGC 426
OY 361 TGGTGTGCTACGCGCATTCATCTGATTTGAAATTCAGTGTCAAAAGTACAGAGGCTTC 420
Db 427 TGGTGTGCTACGCGCATTCATCTGATTTGAAATTCAGTGTCAAAAGTACAGAGGCTTC 486
OY 421 TCTGACCCCAAGGGGTGACATGTGTGAGCAGTGTGAGCAGTGTGAGCAGTGTGAGCAG 480
Db 487 TCTGACCCCAAGGGGTGACATGTGTGAGCAGTGTGAGCAGTGTGAGCAGTGTGAGCAG 546
OY 481 GACAAAGAGGATTTAAGAGTACAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 540
Db 547 GACAAAGAGGATTTAAGAGTACAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 606
OY 541 GCCGAGAGAGGCTTACCCATCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
Db 607 GCCGAGAGAGGCTTACCCATCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 666
OY 601 AACTACACAGCAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 660
Db 667 AACTACACAGCAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 726
OY 661 CAGCTGAAGCCATTTGAAAATTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
Db 727 CAGCTGAAGCCATTTGAAAATTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 786
OY 721 TGGAGCAACCCCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 780
Db 787 TGGAGCAACCCCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 846
OY 781 AATAGAGAAAAGAAATATGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
Db 847 AATAGAGAAAAGAAATATGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 906
OY 841 AAGATGCCAAGATCCGCGTCAAGCCGAGACCGGCTACTATATGTTTCTTCTTCTTCTT 900
Db 907 AAGATGCCAAGATCCGCGTCAAGCCGAGACCGGCTACTATATGTTTCTTCTTCTTCTT 966
OY 901 TGGGATCTGTGTGTC 914
Db 967 TGGGATCTGTGTGTC 980
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RESULT 6

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US-09-917-265-60/c
; Sequence 60, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 987
; TYPE: DNA
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ORGANISM: Canis familiaris
US-09-917-265-60

Query Match 99.2% Score 914: DB 10: Length 987:

Best Local Similarity 100.0%: Pred. No. 0:

Matches 914: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

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OY 1 ATATGGAACTGGAGAAAGATGTTATGTTGTAGAGTTGGACTGGACCCCTGATGCCCCC 60
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Db 921 ATATGGAACTGGAGAAAGATGTTATGTTGTAGAGTTGGACTGGACCCCTGATGCCCCC 862
OY 61 GGAGAAATGTTGTTCTTCACTGCGCATACCCCTGAAGAAGATGACATCACTTTGGACCTCA 120
   |||
Db 861 GGAGAAATGTTGTTCTTCACTGCGCATACCCCTGAAGAAGATGACATCACTTTGGACCTCA 802
OY 121 GCGCAGACGAGTAAGTCCTAGAGTTCTGTTAAACTGTGACATTCGCAAGTCGAAGATTT 180
   |||
Db 801 GCGCAGACGAGTAAGTCCTAGAGTTCTGTTAAACTGTGACATTCGCAAGTCGAAGATTT 742
OY 181 GGAGATGCTGGCCAGTATACCTGCGCATAAAGAGAGCAAGGTTCTGACCCGCTCAGCTCTG 240
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Db 741 GGAGATGCTGGCCAGTATACCTGCGCATAAAGAGAGCAAGGTTCTGACCCGCTCAGCTCTG 682
OY 241 TTGATTCACAAAAAGAGATGGAATTTGCTCCACTGATATCTTAAAGGAACAGAAAGAA 300
   |||
Db 681 TTGATTCACAAAAAGAGATGGAATTTGCTCCACTGATATCTTAAAGGAACAGAAAGAA 622
OY 301 TCCAAAAATTAAGATCTTTTGTGAATGTGAGGCAAAAGATTAATCTTGACAGTTTCACATGC 360
   |||
Db 621 TCCAAAAATTAAGATCTTTTGTGAATGTGAGGCAAAAGATTAATCTTGACAGTTTCACATGC 562
OY 361 TGTGCTGCTGACGCAATCACTAGTGAATTTGAATTCAGTGCAGCAAAATAGCAGAGGCTTC 420
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Db 561 TGTGCTGCTGACGCAATCACTAGTGAATTTGAATTCAGTGCAGCAAAATAGCAGAGGCTTC 502
OY 421 TCTGACCCCCAAGGGGTGACATGTGAGCAGTGACACTTTTCAGCAGAGAGGCTCAGAGTG 480
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Db 501 TCTGACCCCCAAGGGGTGACATGTGAGCAGTGACACTTTTCAGCAGAGAGGCTCAGAGTG 442
OY 481 GACAAACAGGATTAATTAAGACTACACAGTGGAGTGTGAGAGGAGGCACTGCTGCCCTCT 540
   |||
Db 441 GACAAACAGGATTAATTAAGACTACACAGTGGAGTGTGAGAGGAGGCACTGCTGCCCTCT 382
OY 541 GCGGAGAGAGGCTTACCACATCGAGAGTGTGTTGATGCTATTTCAGAGCTCAAGTATGAA 600
   |||
Db 381 GCGGAGAGAGGCTTACCACATCGAGAGTGTGTTGATGCTATTTCAGAGCTCAAGTATGAA 322
OY 601 AACTACACGACGCTTCTTCATCAGAGACATCAAAACAGACCCACACCAAAACCTG 660
   |||
Db 321 AACTACACGACGCTTCTTCATCAGAGACATCAAAACAGACCCACACCAAAACCTG 262
OY 661 CAGCTAAGCATTTGAAAAATTTCTCGGACAGTGGAGGTGACGCTGGGAATACCCGACACC 720
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Db 261 CAGCTAAGCATTTGAAAAATTTCTCGGACAGTGGAGGTGACGCTGGGAATACCCGACACC 202
OY 721 TGGAGCAGCCCACTTCTCTCTCTGACATTTTGCAATACAGGCCCGGAGGCAAGAC 780
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Db 201 TGGAGCAGCCCACTTCTCTCTCTGACATTTTGCAATACAGGCCCGGAGGCAAGAC 142
OY 781 AATAGAGAAAAGAGATAGACTCTGCTGGAGCAAGACCTTCAGCCAAAGGTCTGTGTCCAC 840
   |||
Db 141 AATAGAGAAAAGAGATAGACTCTGCTGGAGCAAGACCTTCAGCCAAAGGTCTGTGTCCAC 82
OY 841 AAGCATGCCAAGATCCCGCTGCAAGCCCGGACAGCCGCTACTATATAGTTATCTTGAGGAC 900
   |||
Db 81 AAGCATGCCAAGATCCCGCTGCAAGCCCGGACAGCCGCTACTATATAGTTATCTTGAGGAC 22
OY 901 TGGGCATCTGTGTC 914
   |||
Db 21 TGGGCATCTGTGTC 8
```

RESULT 7

US-09-917-265-66
Sequence 66, Application us/09917265

Patent No. US20020052030A1

GENERAL INFORMATION:

APPLICANT: Wonderling, Karen S.

APPLICANT: Borroughs, Karen L.

TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH

FILE REFERENCE: IM-5

CURRENT APPLICATION NUMBER: US/09/917,265

PRIOR FILING DATE: 2001-07-27

PRIOR APPLICATION NUMBER: 60/223,016

NUMBER OF SEQ ID NOS: 109

SOFTWARE: PatentIn version 3.1

SEQ ID NO 66

LENGTH: 1533

TYPE: DNA

ORGANISM: Canis familiaris

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(1533)

OTHER INFORMATION:

US-09-917-265-66

Query Match 99.2% Score 914: DB 10: Length 1533:

Best Local Similarity 100.0%: Pred. No. 0:

Matches 914: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

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OY 1 ATATGGAACTGGAGAAAGATGTTATGTTGTAGAGTTGGACTGGACCCCTGATGCCCCC 60
   |||
Db 1 ATATGGAACTGGAGAAAGATGTTATGTTGTAGAGTTGGACTGGACCCCTGATGCCCCC 60
OY 61 GGAGAAATGTTGTTCTTCACTGCGCATACCCCTGAAGAAGATGACATCACTTTGGACCTCA 120
   |||
Db 61 GGAGAAATGTTGTTCTTCACTGCGCATACCCCTGAAGAAGATGACATCACTTTGGACCTCA 120
OY 121 GCGCAGACGAGTAAGTCCTAGAGTTCTGTTAAACTGTGACATTCGCAAGTCGAAGATTT 180
   |||
Db 121 GCGCAGACGAGTAAGTCCTAGAGTTCTGTTAAACTGTGACATTCGCAAGTCGAAGATTT 180
OY 181 GCGCAGACGAGTAAGTCCTAGAGTTCTGTTAAACTGTGACATTCGCAAGTCGAAGATTT 180
   |||
Db 181 GCGCAGACGAGTAAGTCCTAGAGTTCTGTTAAACTGTGACATTCGCAAGTCGAAGATTT 180
OY 241 TGTGCTGCTGACGCAATCACTAGTGAATTTGAATTCAGTGCAGCAAAATAGCAGAGGCTTC 420
   |||
Db 241 TGTGCTGCTGACGCAATCACTAGTGAATTTGAATTCAGTGCAGCAAAATAGCAGAGGCTTC 420
OY 241 TGTGCTGCTGACGCAATCACTAGTGAATTTGAATTCAGTGCAGCAAAATAGCAGAGGCTTC 420
   |||
Db 241 TGTGCTGCTGACGCAATCACTAGTGAATTTGAATTCAGTGCAGCAAAATAGCAGAGGCTTC 420
OY 301 TCCAAAAATTAAGATCTTTTGTGAATGTGAGGCAAAAGATTAATCTTGACAGTTTCACATGC 360
   |||
Db 301 TCCAAAAATTAAGATCTTTTGTGAATGTGAGGCAAAAGATTAATCTTGACAGTTTCACATGC 360
OY 361 TGTGCTGCTGACGCAATCACTAGTGAATTTGAATTCAGTGCAGCAAAATAGCAGAGGCTTC 420
   |||
Db 361 TGTGCTGCTGACGCAATCACTAGTGAATTTGAATTCAGTGCAGCAAAATAGCAGAGGCTTC 420
OY 421 TCTGACCCCCAAGGGGTGACATGTGAGCAGTGACACTTTTCAGCAGAGAGGCTCAGAGTG 480
   |||
Db 421 TCTGACCCCCAAGGGGTGACATGTGAGCAGTGACACTTTTCAGCAGAGAGGCTCAGAGTG 480
OY 481 GACAAACAGGATTAATTAAGACTACACAGTGGAGTGTGAGAGGAGGCACTGCTGCCCTCT 540
   |||
Db 481 GACAAACAGGATTAATTAAGACTACACAGTGGAGTGTGAGAGGAGGCACTGCTGCCCTCT 540
OY 541 GCGGAGAGAGGCTTACCACATCGAGAGTGTGTTGATGCTATTTCAGAGCTCAAGTATGAA 600
   |||
Db 541 GCGGAGAGAGGCTTACCACATCGAGAGTGTGTTGATGCTATTTCAGAGCTCAAGTATGAA 600
OY 601 AACTACACGACGCTTCTTCATCAGAGACATCAAAACAGACCCACACCAAAACCTG 660
   |||
Db 601 AACTACACGACGCTTCTTCATCAGAGACATCAAAACAGACCCACACCAAAACCTG 660
OY 661 CAGCTAAGCATTTGAAAAATTTCTCGGACAGTGGAGGTGACGCTGGGAATACCCGACACC 720
   |||
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121 GCGCAGACGAGTGAAGTCCCTAGGTTCTGTAAACTCTGACATCCCAAGTCAAGAATTT 180
187 GCGCAGACGAGTGAAGTCCCTAGGTTCTGTAAACTCTGACATCCCAAGTCAAGAATTT 246
181 GGAGATGCTGGCCAGTATACCTGCGATAAAGAGGCGAGGTTCTGAGCCGCTCAGTCCTG 240
247 GGAGATGCTGGCCAGTATACCTGCGATAAAGAGGCGAGGTTCTGAGCCGCTCAGTCCTG 306
241 TTGATTTACAAAAAAGAGATGGAATTTGGTCCACTGATATCTTTAAAGACAGAAAGAA 300
307 TTGATTTACAAAAAAGAGATGGAATTTGGTCCACTGATATCTTTAAAGACAGAAAGAA 366
301 TCCAAAAATTAAGATCTTTCTGAAATGCTGAGCCAAAGATTTATTTCTGAGCTTTACATGC 360
367 TCCAAAAATTAAGATCTTTCTGAAATGCTGAGCCAAAGATTTATTTCTGAGCTTTACATGC 426
361 TGGTGGCTGACGGCAATCAGTACTGATTTTGAATTCAGTGTCAAAAAGTACAGAGGCTTC 420
427 TGGTGGCTGACGGCAATCAGTACTGATTTTGAATTCAGTGTCAAAAAGTACAGAGGCTTC 486
421 TCTGACCCCCAAGGGGTGACATGTGAGAGCAGTACACTTTCAAGCAGAGAGGGTCAAGATG 480
487 TCTGACCCCCAAGGGGTGACATGTGAGAGCAGTACACTTTCAAGCAGAGAGGGTCAAGATG 546
481 GACACAGAGGATTTATAGAAATGACACAGTGTGAGTGTGAGAGGCGCATGCTGCCCTCT 540
547 GACACAGAGGATTTATAGAAATGACACAGTGTGAGTGTGAGAGGCGCATGCTGCCCTCT 606
541 GCGCAGAGAGGCTACCCATCGAGGTGCTGTGATGCTATTTCACAAGCTCAAGATATGAA 600
607 GCGCAGAGAGGCTACCCATCGAGGTGCTGTGATGCTATTTCACAAGCTCAAGATATGAA 666
601 AACTACACGAGAGCTTTCTTCATCAGAGCATCATATAAACCCAGACCACCAAACTTG 660
667 AACTACACGAGAGCTTTCTTCATCAGAGCATCATATAAACCCAGACCACCAAACTTG 726
661 CAGCTGAAGGCAATTTGAAAAATTTCTCGGCACGTGGAGGTCAGCGGGGAATACCCCGACAC 720
727 CAGCTGAAGGCAATTTGAAAAATTTCTCGGCACGTGGAGGTCAGCGGGGAATACCCCGACAC 786
721 TGGACACCCCAATTTCTTCTTCTCCCTGACATTTTGGCATACAGGCCCGACGGCAAGAC 780
787 TGGACACCCCAATTTCTTCTTCTCCCTGACATTTTGGCATACAGGCCCGACGGCAAGAC 846
781 AATAGAGAAAAGAAAGATAGACTCTGCGTGACAAAGACCTCAGCCCAAGGTCGTCGCAC 840
847 AATAGAGAAAAGAAAGATAGACTCTGCGTGACAAAGACCTCAGCCCAAGGTCGTCGCAC 906
841 AAGGATGCCAAGATCCGCGTGCAGGCCGAGACCGCTACTATAGTTTCATCTGGAGCGAC 900
907 AAGGATGCCAAGATCCGCGTGCAGGCCGAGACCGCTACTATAGTTTCATCTGGAGCGAC 966
901 TGGGCATCTGTGTC 914
967 TGGGCATCTGTGTC 980

RESULT 10

US-09-917-265-63/c
; Sequence 63, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Broughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 63
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-917-265-63

Query Match 99.2%; Score 914; DB 10; Length 1599;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 914; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATATGGGAAGTGGAGAAAGATGTTATGTTGTAGAGTTGAGCTGGACCCCTGATGCCCC 60
1533 ATATGGGAAGTGGAGAAAGATGTTATGTTGTAGAGTTGAGCTGGACCCCTGATGCCCC 1474
61 GGAGAAATGTTGGTCTCAGCTCCATACCCCTGAGAGAAATGATCATCTTGGACCTCA 120
1473 GGAGAAATGTTGGTCTCAGCTCCATACCCCTGAGAGAAATGATCATCTTGGACCTCA 1414
121 GCGCAGAGCGTGAAGTCTAGGTTCTGTAACCTGTGACATCCCAAGTCAAGAAATTT 180
1413 GCGCAGAGCGTGAAGTCTAGGTTCTGTAACCTGTGACATCCCAAGTCAAGAAATTT 1354
181 GGAGATGCTGGCCAGTATACCTGCAATTAAGAGGCAAGGTTCTGAGCCGCTCAGTCCTG 240
1353 GGAGATGCTGGCCAGTATACCTGCAATTAAGAGGCAAGGTTCTGAGCCGCTCAGTCCTG 1294
241 TTGATTTACAAAAAAGAGATGGAATTTGGTCCACTGATATCTTTAAAGACAGAAAGAA 300
1293 TTGATTTACAAAAAAGAGATGGAATTTGGTCCACTGATATCTTTAAAGACAGAAAGAA 1234
301 TCCAAAAATTAAGATCTTTCTGAAATGCTGAGCCAAAGATTTATTTCTGAGCTTTACATGC 360
1233 TCCAAAAATTAAGATCTTTCTGAAATGCTGAGCCAAAGATTTATTTCTGAGCTTTACATGC 1174
361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTACAGAGGCTTC 420
1173 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTACAGAGGCTTC 1114
421 TCTGACCCCCAAGGGGTGACATGTGAGAGCAGTACACTTTTCAGCAGAGAGGTCAGAGTG 480
1113 TCTGACCCCCAAGGGGTGACATGTGAGAGCAGTACACTTTTCAGCAGAGAGGTCAGAGTG 1054
481 GACACAGGAGATTTATAGAAATGACACAGTGTGAGGTCAGAGGCGAGTGCCTGCCCTCT 540
1053 GACACAGGAGATTTATAGAAATGACACAGTGTGAGGTCAGAGGCGAGTGCCTGCCCTCT 994
541 GCGCAGAGAGGCTACCCATCGAGGTCGTGTGATGCTATTTCACAAGCTCAAGATGAA 600
993 GCGCAGAGAGGCTACCCATCGAGGTCGTGTGATGCTATTTCACAAGCTCAAGATGAA 934
601 AACTACACGAGAGCTTTCTTCATCAGAGCATCATATAAACCCAGACCACCAAACTTG 660
933 AACTACACGAGAGCTTTCTTCATCAGAGCATCATATAAACCCAGACCACCAAACTTG 874
661 CAGCTGAAGGCAATTTGAAAAATTTCTCGGCACGTGGAGTGTGAGGGAATACCCCGACAC 720
873 CAGCTGAAGGCAATTTGAAAAATTTCTCGGCACGTGGAGTGTGAGGGAATACCCCGACAC 814
721 TGGAGCACCCCAATTTCTTCTTCTCCCTGACATTTTGGCATACAGGCCCGACGGCAAGAC 780
813 TGGAGCACCCCAATTTCTTCTTCTCCCTGACATTTTGGCATACAGGCCCGACGGCAAGAC 754
781 AATAGAGAAAAGAAAGATAGACTCTGCGTGACAAAGACCTCAGCCCAAGGTCGTCGCAC 840
753 AATAGAGAAAAGAAAGATAGACTCTGCGTGACAAAGACCTCAGCCCAAGGTCGTCGCAC 654
841 AAGGATGCCAAGATCCGCGTGCAGGCCGAGACCGCTACTATAGTTTCATCTGGAGCGAC 900
693 AAGGATGCCAAGATCCGCGTGCAGGCCGAGACCGCTACTATAGTTTCATCTGGAGCGAC 634
901 TGGGCATCTGTGTC 914
633 TGGGCATCTGTGTC 620

RESULT 11

US-09-917-265-26
; Sequence 26, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 26
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(921)
; OTHER INFORMATION:
US-09-917-265-26

Query Match

Best Local Similarity 100.0%; Score 66; DB 10; Length 921;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 471 GGTGAGTGGACACAGGATTATTAAGAGTACACAGTGGAGTTCAGAGGCGAGTGC 530
DB 471 GGTGAGTGGACACAGGATTATTAAGAGTACACAGTGGAGTTCAGAGGCGAGTGC 530
OY 531 CTGCC 536
DB 531 CTGCC 536

RESULT 12

US-09-917-265-28/c
; Sequence 28, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 28
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265-28

Query Match
Best Local Similarity 100.0%; Score 66; DB 10; Length 921;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 471 GGTGAGTGGACACAGGATTATTAAGAGTACACAGTGGAGTTCAGAGGCGAGTGC 530
DB 471 GGTGAGTGGACACAGGATTATTAAGAGTACACAGTGGAGTTCAGAGGCGAGTGC 530
OY 531 CTGCC 536
DB 531 CTGCC 536

RESULT 13

US-10-079-616-6
; Sequence 6, Application US/10079616
; Patent No. US20020107366A1
; GENERAL INFORMATION:
; APPLICANT: IMAMURA, Takayuki
; MAEDA, Hiroaki
; FUJIVASU, Takeshi
; IMAGAWA, Yoshitaka
; TOKIYOSHI, Sachio
; TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEWMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/079,616
; FILING DATE: 22-Feb-2002
; CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/011,143
; FILING DATE: 04-FEB-1998
; APPLICATION NUMBER: PC/JP97/01824
; FILING DATE: 29-MAY-1997
; APPLICATION NUMBER: JP 165249/1996
; FILING DATE: 04-JUN-1996

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: IMAMURA=1
TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 921 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-079-616-6

Query Match

Best Local Similarity 100.0%; Score 66; DB 12; Length 921;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 471 GGTGAGTGGACACAGGATTATTAAGAGTACACAGTGGAGTTCAGAGGCGAGTGC 530
DB 471 GGTGAGTGGACACAGGATTATTAAGAGTACACAGTGGAGTTCAGAGGCGAGTGC 530
OY 531 CTGCC 536
DB 531 CTGCC 536

RESULT 14

US-09-917-265-55
; Sequence 55, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; BOROUGH, Karen L.

```
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 985
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(984)
; OTHER INFORMATION:
US-09-917-265-55
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Query Match

7.2%; Score 66; DB 10; Length 985;

Best Local Similarity 100.0%; Pred. No. 1.7e-24;

Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      471 GGTACAGTGGACACAGGATTATAGAGTACACAGTGGAGTGCAGAGGCGAGTGC 530
          |||
Db      537 GGTACAGTGGACACAGGATTATAGAGTACACAGTGGAGTGCAGAGGCGAGTGC 596
QY      531 CTGCC 536
          |||
Db      597 CTGCC 602
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RESULT 15

US-09-917-265-57/c

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; Sequence 57, Application US/09917265
; Patent No. US200200320A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
; LENGTH: 985
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265-57
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Query Match

7.2%; Score 66; DB 10; Length 985;

Best Local Similarity 100.0%; Pred. No. 1.7e-24;

Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      471 GGTACAGTGGACACAGGATTATAGAGTACACAGTGGAGTGCAGAGGCGAGTGC 530
          |||
Db      449 GGTACAGTGGACACAGGATTATAGAGTACACAGTGGAGTGCAGAGGCGAGTGC 390
QY      531 CTGCC 536
          |||
Db      389 CTGCC 384
```

Search completed: July 16, 2003, 19:58:55

Job time : 175.379 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: July 16, 2003, 15:58:34 ; Search time 2744.43 Seconds

(without alignments)
3255.531 Million cell updates/sec

Title: US-09-917-265-53

Perfect score: 1653

Sequence: 1 IWELEKDYVVELDWHDPAP.....QARDRYSSSSWDMASVSCS 307

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q/cgn2.1/USPTO_spool/US09917265/runatc.15072003_092106_1601/app_query.fasta.1.3114
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -IOOPT=0 -LOOPEXT=0
-UNITS=b1ts -START=1 -END=-1 -MATRIX=blomsun62 -TRANS=human40.cdf -LIST=45
-DOCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=plo -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=us09917265.acgn.1.1.11378 @runatc.15072003_092106_1601 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEBUFFER -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MARN_TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl: *
1: gb_ba: *
2: gb_hlg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *
15: em_da: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *

29: em_vi: *
30: em_hlg_hum: *
31: em_hlg_in: *
32: em_hlg_other: *
33: em_hlg_mus: *
34: em_hlg_pln: *
35: em_hlg_rod: *
36: em_hlg_mam: *
37: em_hlg_vtr: *
38: em_sy: *
39: em_hlgo_hum: *
40: em_hlgo_mus: *
41: em_hlgo_other: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|--------|-------------|--------|----|------------|---------------------|
| 1 | 1653 | 100.0 | 990 | 6 | AR151071 | AR151071 Sequence |
| 2 | 1653 | 100.0 | 990 | 6 | E15017 | E15017 Canine mRNA |
| 3 | 1652 | 99.9 | 1015 | 4 | CFU049100 | U49100 Canis faml |
| 4 | 1640 | 99.2 | 990 | 6 | AR151061 | AR151061 Sequence |
| 5 | 1534 | 94.0 | 990 | 6 | AX076200 | AX076200 Sequence |
| 6 | 1534 | 94.0 | 990 | 6 | AX076482 | AX076482 Sequence |
| 7 | 1554 | 94.0 | 4522 | 6 | AX076209 | AX076209 Sequence |
| 8 | 1554 | 94.0 | 4522 | 6 | AX076476 | AX076476 Sequence |
| 9 | 1552 | 93.9 | 990 | 4 | FCU83184 | U83184 Felis catus |
| 10 | 1546 | 93.5 | 1006 | 4 | FCU112P40 | U0762 F.catus mRN |
| 11 | 1484 | 89.8 | 990 | 6 | AX154603 | AX154603 Sequence |
| 12 | 1469 | 88.9 | 1058 | 4 | ECU112P40 | V11129 Equus caball |
| 13 | 1469 | 88.9 | 1626 | 12 | AF401989 | AF401989 Synthetic |
| 14 | 1451 | 87.8 | 984 | 6 | AX154600 | AX154600 Sequence |
| 15 | 1429 | 86.4 | 994 | 6 | AX154599 | AX154599 Sequence |
| 16 | 1427 | 86.3 | 993 | 4 | CEU57552 | U57552 Cervus elap |
| 17 | 1421 | 86.0 | 984 | 6 | AX154598 | AX154598 Sequence |
| 18 | 1419 | 85.9 | 1870 | 6 | A92079 | A92079 Sequence 3 |
| 19 | 1419.5 | 85.9 | 2318 | 6 | HUMNKSFP40 | M65290 Human natur |
| 20 | 1418.5 | 85.8 | 987 | 6 | AR008950 | AR008950 Sequence |
| 21 | 1418.5 | 85.8 | 987 | 6 | AX154633 | AX154633 Sequence |
| 22 | 1418.5 | 85.8 | 987 | 6 | BD007070 | BD007070 IL-12 gen |
| 23 | 1418.5 | 85.8 | 987 | 6 | BD007076 | BD007076 Gene expr |
| 24 | 1418.5 | 85.8 | 987 | 6 | BD007077 | BD007077 Gene expr |
| 25 | 1418.5 | 85.8 | 987 | 6 | BD007078 | BD007078 Gene expr |
| 26 | 1418.5 | 85.8 | 987 | 6 | 128591 | 128591 Sequence 1 |
| 27 | 1418.5 | 85.8 | 1007 | 9 | AF180563 | AF180563 Homo sapi |
| 28 | 1418.5 | 85.8 | 1018 | 6 | AR052857 | AR052857 Sequence |
| 29 | 1418.5 | 85.8 | 1389 | 6 | AX084106 | AX084106 Sequence |
| 30 | 1418.5 | 85.8 | 1399 | 6 | AR091391 | AR091391 Sequence |
| 31 | 1418.5 | 85.8 | 1399 | 6 | HUMCLMR40 | M65272 Human cytot |
| 32 | 1418.5 | 85.8 | 1560 | 6 | AR091395 | AR091395 Sequence |
| 33 | 1418.5 | 85.8 | 1623 | 6 | AR091394 | AR091394 Sequence |
| 34 | 1418.5 | 85.8 | 2362 | 6 | AR082684 | AR082684 Sequence |
| 35 | 1418.5 | 85.8 | 2362 | 6 | AR122960 | AR122960 Sequence |
| 36 | 1418.5 | 85.8 | 2362 | 6 | 128325 | 128325 Sequence 1 |
| 37 | 1418.5 | 85.8 | 2362 | 6 | 189770 | 189770 Sequence 1 |
| 38 | 1418.5 | 85.8 | 6139 | 6 | AR091393 | AR091393 Sequence |
| 39 | 1411 | 85.4 | 1012 | 4 | BTU11815 | U11815 Bos taurus |
| 40 | 1411 | 85.4 | 1019 | 6 | E35794 | E35794 Process for |
| 41 | 1407 | 85.1 | 984 | 4 | AF004024 | AF004024 Ovis arie |
| 42 | 1407 | 85.1 | 984 | 4 | AF209435 | AF209435 Ovis arie |
| 43 | 1407 | 85.1 | 1012 | 4 | AF007576 | AF007576 Capra hir |
| 44 | 1406.5 | 85.1 | 1080 | 9 | MMU19841 | U19841 Macaca mula |
| 45 | 1397.5 | 84.5 | 969 | 6 | AX154601 | AX154601 Sequence |

RESULT 1

ALIGNMENTS

AR151071
 LOCUS AR151071 990 bp DNA linear PAT 08-AUG-2001
 DEFINITION Sequence 11 from patent US 6231850.
 ACCESSION AR151071
 VERSION AR151071.1 GI:15117121
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 990)
 AUTHORS Okano, F., Satoh, M. and Yamada, K.
 TITLE Canine Interleukin 12
 JOURNAL Patent: US 6231850-A 11 15-MAY-2001;
 FEATURES
 source Location/Qualifiers
 1..990
 BASE COUNT 279 a 244 c 249 g 218 t
 ORIGIN

Alignment Scores:

Pred. No.: 1e-157 Length: 990
 Score: 1653.00 Matches: 307
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-917-265-53 (1-307) x AR151071 (1-990)

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DB 127 GGAGAAATGGTGGTCCCTCACCCTGCATACCCCTGAAGAAGATGCATCTGAGACCTCA 186
OY 41 AlaglnserSerGlulValleuglSerGlyLysThrleuThrllleglnVallysglupe 60
DB 187 GCCGAGAGCAGTGAAGTCCAGGTCTGGTAAACCTGACCATCCAAAGCAATTT 246
OY 61 GlyAspAlaGlyIntyrThrCysHisLysGlyLysValleuSerArgSerleu 80
DB 247 GGAGATGGTGGCAGATACCTGCCATTAAGAGGCAAGGTTCTGAGCCGCTCCTCCTG 306
OY 81 LeuIleHisLysLysGluAspGlyLleTrpSerThrAspIleLeuLysGluGlnLysGlu 100
DB 307 TTGATTCACAAAAGAAAGATGGAATTGGTCCACTGATATCTTAAGAGAACAGAAAGAA 366
OY 101 SerLysAsnLysIlePheLeuLysCysGlnAlaLysAsnLysSerGlyArgPheThrCys 120
DB 367 TCCAAAATTAAGATCTTCTCTGAATGTGAGGCAAGAAATTAATCTGGACGTTTCACATGC 426
OY 121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
DB 427 TGGTGGCTGACGGCAATCAGTACTGATTTGAATTCACTGCAAAAGTAGAGGGGCTTC 486
OY 141 SerAspProGlnGlyValThrCysGlyAlaValThrleuSerAlaGluArgValArgVal 160
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OY 161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProSer 180
DB 547 GACAAACAGGGGATTTAAGAACTACACAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGG 606
OY 181 AlaGluGluSerLeuProIleGluValValAspAlaIleHisLysLeuLysTyrGlu 200
DB 607 GCCGAGAGAGACCTTACCCATCGAGGTGCTGTGGATGCTATTCACAAGCTCAAGTATGA 666
OY 201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProThrAsnLeu 220
DB 667 AACACACAGCAGCTTCTTCATCAGACGACATATCAAAACCAAGCCACCAACCAACCTG 726

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OY 221 GlnleuLysProleuLysAsnSerArgHisValGluValSerTrpGluTyrProasprrh 240
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DB 847 AATAGAGAAAGAAAGATAGACTGCTGCGACAGACACTCAGCAAGAGTCTGTGCGCAC 906
OY 281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsp 300
DB 907 AAGGATGCCAAGATCCGCGCTGCAAGCCGAGACCCCTACTATAGTTATCTCGAGCGAC 966
OY 301 TrpAlaSerValSerCysSer 307
DB 967 TGGGATCTGTGTCCTCGCAGT 987

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RESULT 2

E15017 990 bp DNA linear PAT 28-JUL-1999
 LOCUS
 DEFINITION Canine mRNA for interleukin 12 40kDa subunit, complete cds.
 ACCESSION E15017
 VERSION E15017.1 GI:5709700
 KEYWORDS JP 1998036397-A/1.
 SOURCE
 ORGANISM
 Canis sp.
 Canis sp.
 Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE
 AUTHORS Okano, F.
 TITLE CANINE INTERLEUKIN 12 AND ITS PRODUCTION
 JOURNAL Patent: JP 1998036397-A 1 10-FEB-1998;
 TORAY IND INC
 OS Canis sp. (dog)
 PN JP 1998036397-A/1
 PD 10-FEB-1998
 PF 08-NOV-1996 JP 1996296789
 PR 08-NOV-1995 JP 95P 289729, 23-MAY-1996 JP 96P 128104 PI
 OKANO FUMIYOSHI
 PC C07K14/54, C07H21/04, C12N5/10, C12N15/09, C12P21/02, C12N5/10, PC
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 CC (C12P21/02, C12R1:91);
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 CC topology: Linear;
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 FT /tissue-type='liver'
 FT CDS 1..990
 FT /product='interleukin 12 40kDa subunit'.
 FT

FEATURES
 source Location/Qualifiers
 1..990
 BASE COUNT 279 a 244 c 249 g 218 t
 ORIGIN

Alignment Scores:

Pred. No.: 1e-157 Length: 990
 Score: 1653.00 Matches: 307
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-917-265-53 (1-307) x E15017 (1-990)

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| | | | |
|--|-----|---|-----|
| D | 67 | ATATGGAACTGCAGAAAGATGTTTATGTTGTAGAGTTGGACGTGACCCCTGATGCCCC | 126 |
| Q | 21 | GlyGluMetValValLeuThrCysHisThrProGluGluAspSpleThrTrpThrSer | 40 |
| D | 127 | GGAGAAATGGTGGTCTCCTCCTCCATCCCTGAAAGATGACATCCTTGACCTCA | 186 |
| Q | 41 | AlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe | 60 |
| D | 187 | GGCCACAGCAGTGAAGTCCCTAGGTTCTGGTAAAACTGTGACCATCCAAAGCAATTT | 246 |
| Q | 61 | GlyAspAlaGlyClnTrpThrCysHisLysGlyValLysValLeuSerArgSerLeuLeu | 80 |
| D | 247 | GGAGATGCTGGCCAGTATACCTCCATAAAGAGCAAGGTTCTGACCGCTCCTCTG | 306 |
| Q | 81 | LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGlu | 100 |
| D | 307 | TTGATTTCACAAAAGAGATGGAATTTGGTCCACGTATATCTTAAGAGCAAGAAAGAA | 366 |
| Q | 101 | SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTrpSerGlyArgPheThrCys | 120 |
| D | 367 | TCCAAAATATAGATCTTTCTGAATGTGAGGCAAGAAATTTATCTGACGTTTCACATGC | 426 |
| Q | 121 | TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe | 140 |
| D | 427 | TGGTGGCTGACGGCAATCACTGACTGATTTGAAATTCAGTGTCAAAAGTACAGAGGCTTC | 486 |
| Q | 141 | SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgVal | 160 |
| D | 487 | TCTGACCCCAAGGGGTGACATGTGAGCAGCAGTGACATTTTCACAGAGAGGCTCAGAGTG | 546 |
| Q | 161 | AspAsnArgAspTrpLysLysTrpThrValGluCysGlnGluLysSerAlaCysProSer | 180 |
| D | 547 | GACAAACAGGATTATAGAAAGTACAGAGTGAAGTGCAGAGGCGCTGCTGCTCTCT | 606 |
| Q | 181 | AlaGluGluSerLeuProIleGluValValAspAlaIleHisLysLeuLysTrpGlu | 200 |
| D | 607 | GCCGAGAGACGCTTACCCTCGAGCTGCTGCTGATGCTATTCACAAAGCTCAAGTATGAA | 666 |
| Q | 201 | AsnTrpThrSerSerPhePheIleArgAspIleIleLysProAspProPheThrAsnLeu | 220 |
| D | 667 | AACTACACACGACGCTTCTTCATCAGACATCATCAACCAAGCCACCAACAACTG | 726 |
| Q | 221 | GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTrpProAspThr | 240 |
| D | 727 | CAGCTGACGCATTTGAAAATTTCTCGGCAAGCTGAGGCTGAGTGGGAATACCCCGACACC | 786 |
| Q | 241 | TrpSerThrProHisSerTrpPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn | 260 |
| D | 787 | TGGAGCACCCCACTTCTCTCTCCCTGACATTTTGCAATACAGGCCCGAGGCAAGAAC | 846 |
| Q | 261 | AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValValCysHis | 280 |
| D | 847 | AATAGGAAAAAGAAATAGACTCTCGCTGACAAAGCTCAGCCAAAGGCTGCTGCGCAC | 906 |
| Q | 281 | LysAspAlaLysIleArgValGlnAlaArgAspArgTrpTrpSerSerSerTrpSerAsp | 300 |
| D | 907 | AAGGATGCCAAGATCCGGCTGCAAGCCCGAGACCGGCTACTATAGTTCATCTCTGAGCGAC | 966 |
| Q | 301 | TrpAlaSerValSerCysSer | 307 |
| D | 967 | TGGCGATCTGTCTGTCTGCACT | 987 |
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| CFU49100 | | | |
| LOCUS Canis familiaris interleukin-12 p40 subunit mRNA, linear MAM 13-MAR-1996 | | | |
| DEFINITION U49100 | | | |
| ACCESSION U49100.1 GI:1223907 | | | |
| VERSION | | | |
| KEYWORDS | | | |
| SOURCE | | | |
| ORGANISM | | | |
| Canis familiaris. | | | |
| Canis familiaris. | | | |
| Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi; | | | |
| Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis. | | | |

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| REFERENCE | 1 (bases 1 to 1015) | | |
| AUTHORS | Belke-Louis G.F. and Buettner M. | | |
| TITLE | Cloning and sequence analysis of the p35 and p40 subunits of canine interleukin-12 | | |
| JOURNAL | unpublished | | |
| REFERENCE | 2 (bases 1 to 1015) | | |
| AUTHORS | Belke-Louis G.F. | | |
| TITLE | Direct Submission | | |
| JOURNAL | Submitted (13-FEB-1996) Georg F. Belke-Louis, Institute of Med. Microbiology, Veterinaerstr. 13, Muenchen, D-80539, Germany | | |
| FEATURES | | | |
| source | 1..1015 | | |
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| | /db_xref="taxon:9615" | | |
| CDS | 1..990 | | |
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| BASE COUNT | 285 a 251 c 254 g 225 t | | |
| ORIGIN | | | |
| Alignment Scores: | | | |
| Pred. No.: | 1.3e-157 | | |
| Score: | 1652.00 | | |
| Percent Similarity: | 100.00% | | |
| Best Local Similarity: | 99.67% | | |
| Query Match: | 99.94% | | |
| DB: | 4 gaps: 0 | | |
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| D | 67 | ATATGGAACTGCAGAAAGATGTTATGTTGTAAGATTGGATGGCACCCGATGCCCC | 126 |
| Q | 21 | GlyGluMetValValLeuThrCysHisThrProGluGluAspSpleThrTrpThrSer | 40 |
| D | 127 | GGAGAAATGGTGGTGGTCTCCTCCTCCATCCCTGAAAGATGACATCCTTGACCTCA | 186 |
| Q | 41 | AlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe | 60 |
| D | 187 | GGCCACAGCAGTGAAGTCCCTAGGTTCTGGTAAAACTGTGACCATCCAAAGCAAAATTT | 246 |
| Q | 61 | GlyAspAlaGlyClnTrpThrCysHisLysGlyValLysValLeuSerArgSerLeuLeu | 80 |
| D | 247 | GGAGATGCTGGCCAGTATACCTCCATTAAGAGAGCAAGGTTCTGACCCGCTCCTG | 306 |
| Q | 81 | LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGlu | 100 |
| D | 307 | TTGATTTCACAAAAGAGATGGAATTTGGTCCACGTATATCTTAAGAGCAAGAAAGAA | 366 |
| Q | 101 | SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTrpSerGlyArgPheThrCys | 120 |
| D | 367 | TCCAAAATATAGATCTTTCTGAATGTGAGGCAAGAAATTTATCTGACGTTTCACATGC | 426 |
| Q | 121 | TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe | 140 |
| D | 427 | TGGTGGCTGACGGCAATCACTGACTGATTTGAAATTCAGTGTCAAAAGTACAGAGGCTTC | 486 |
| Q | 141 | SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgVal | 160 |
| D | 487 | TCTGACCCCAAGGGGTGACATGTGAGCAGCAGTGACATTTTCACAGAGAGGCTCAGAGTG | 546 |
| Q | 161 | AspAsnArgAspTrpLysLysTrpThrValGluCysGlnGluLysSerAlaCysProSer | 180 |
| D | 547 | GACAAACAGGATTATAGAAAGTACAGAGTGAAGTGAAGGCAAGGCTGCTGCTCTCT | 606 |

ORIGIN

Alignment Scores:

Pred. No.: 1,03e-147 Length: 990
 Score: 1554.00 Matches: 288
 Percent Similarity: 96.74% Conservative: 9
 Best Local Similarity: 93.81% Mismatches: 10
 Query Match: 94.01% Indels: 0
 DB: 6 Gaps: 0

US-09-917-265-53 (1-307) x AX076200 (1-990)

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DB 127 GGAGAAATGGCTGCTTACCTGCAATCTCTGAGAAAGATGACATCCTGACCTCT 186
OY 41 ALAGLINSERGLUVALLEUGLISERGLYSLTHRLEUTHRIEGLVALLYSGIUPHE 60
DB 187 GACCAAGACAGTGAAGCTCTAGCTCTGTAATACTGTGACCATCCAAAGCAATTT 246
OY 61 GLYASPALAGLYGINTYRTHRCYSHISLYSGLYGLYVALLEUSERARGSERLEULEU 80
DB 247 GCAGATGCTGGCCAGTATACCTGTGCAFAAGAGGCGAGCTCTGAGCCATTCTCC 306
OY 81 LEULIEHISLYSGLUASPCLYILETRPSETRHASPILLEULEULYSGIULINLYSGIU 100
DB 307 CTGATACACAAAAGAGATGGAATTGCTCCACTGATATCTTAACGACACAGAAAGAA 366
OY 101 SERLYSASNLVSLIHPHELEULYSCYGLUVALIALYSASNTYRSEGLYARPHETHRCYS 120
DB 367 TCCAAAAATAGATCTTTCTAAATGTGAGCGCAAAACATTAATCTTGAGACGTTTCA 426
OY 121 TRPTPLLEUTHRALALESERTHRASPULYSPHESERVALLYSSESERARGLYPHE 140
DB 427 TGGTGCGCTGACGCGCATACGATACGATTGGAATTCACGTGCAAAAAGCGACAGGCTCC 486
OY 141 SERASPPROGLINGLYVALTHRCYSGLYVALVALLHRLUSERALAGLUARGVALARVAL 160
DB 487 TCTACACCCCAAGGGGTACTTGTGAGCACGACACCTCTCAGCAGAGAGCTTCAGAGTG 546
OY 161 ASPASNARGASPTLYRSLYSLYSTRHVALGIUCYSGINGLUGLYSERLACYSPROSER 180
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OY 201 ASNTYRTHRSERSERPHEPHEILEARGASPILEILELYSPROASPPROBROTHRASNLEU 220
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DB 847 AACGAGAAAAAGAAAGACAGACTCTCCGTGACAAAGACCTCAGCCACGCTCTGCGCAC 906
OY 281 LYSASPALALYSILEATQVAIGLIALAARGASPARGTYRYSERSESETRPSEAR 300
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OY 301 TRPALASERVALSERCYSSER 307
  
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RESULT 6
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 Sequence 8 from Patent WO0104280.
 AX076482
 AX076482
 VERSION
 AX076482.1 GI:12711034
 KEYWORDS
 SOURCE
 ORGANISM
 synthetic construct.
 synthetic construct.
 artificial sequences.
 REFERENCE
 1 (bases 1 to 990)
 Leutenegger, C., Schroff, M., Wiltig, B. and Lutz, H.
 Vaccine against lentiviral infections, such as the feline immune
 deficiency virus of the cat.
 Patent: WO 0104280-A 8 18-JAN-2001.
 Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
 Universitaet Zuerich (CH)
 location/Qualifiers
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 BASE COUNT 283 a 249 c 248 g 210 t
 ORIGIN

Alignment Scores:
 Pred. No.: 1.03e-147 Length: 990
 Score: 1554.00 Matches: 288
 Percent Similarity: 96.74% Conservative: 9
 Best Local Similarity: 93.81% Mismatches: 10
 Query Match: 94.01% Indels: 0
 DB: 6 Gaps: 0

US-09-917-265-53 (1-307) x AX076482 (1-990)

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DB 127 GGAGAAATGGTGTCTTACCTGCAATFACTCCGGAAGAAAGATGACATCAGCTGACCTCT 186
OY 41 ALAGLINSERGLUVALLEUGLISERGLYSLTHRLEUTHRIEGLVALLYSGIUPHE 60
DB 187 GACCAAGACAGTGAAGTCCTAGGCTCTGTGTAATACTCTGACCATCCAAAGCAAAATTT 246
OY 61 GLYASPALAGLYGINTYRTHRCYSHISLYSGIULYVALLEUSERARGSERLEULEU 80
DB 247 GCAGATGCTGGCCAGATACCTGTCAFAAGAGGCGAGTGTTCGAGCCATTCTCC 306
OY 81 LEULIEHISLYSGLUASPCLYILETRPSETRHASPILLEULEULYSGIULINLYSGIU 100
DB 307 CTGATACACAAAAGAGATGGAATTGCTCCACTGATATCTTAACGACACAGAAAGAA 366
OY 101 SERLYSASNLVSLIHPHELEULYSCYGLUVALIALYSASNTYRSEGLYARPHETHRCYS 120
DB 367 TCCAAAAATAGATCTTTCTAAATGTGAGCGCAAAACATTAATCTTGAGACGTTTCA 426
OY 121 TRPTPLLEUTHRALALESERTHRASPULYSPHESERVALLYSSESERARGLYPHE 140
DB 427 TGGTGCGCTGACGCGCATACGATACGATTGGAATTTGAGTGTCAAAAGCGACAGGCTCC 486
OY 141 SERASPPROGLINGLYVALTHRCYSGLYVALVALLHRLUSERALAGLUARGVALARVAL 160
DB 487 TCTGACACCCCAAGGGGTACTTGTGAGCAGCAGACCTCTCAGCAGAAAGTACAGAGTG 546
OY 161 ASPASNARGASPTLYRSLYSLYSTRHVALGIUCYSGINGLUGLYSERLACYSPROSER 180
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BASE COUNT      1180 a      1126 c      1106 g      1110 t
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Alignment Scores:
Pred. No.:      6,74e-147      Length:      4522
Score:          1554.00      Matches:      288
Percent Similarity: 96.74%      Conservative: 9
Best Local Similarity: 93.81%      Mismatches: 10
Query Match:      94.01%      Indels:      0
DB:              Gaps:      0

US-09-917-265-53 (1-307) x AX076476 (1-4522)

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DB      3173  GGAGAAATGGTGGCTTACCTGCATCTCCTGGAAGAGATGACATCCTGGACCTCT 3232
        |||GlyGluMetValValLeuThrCysHisThrProGluGluAspAlaLeuThrTrpThrSer 40

QY      41      AlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
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DB      3233  GACCGAGACGAGTGAAGTCTAGGCTGTGTAAACTCTGACCAAGTCAAGCAAGAAATTT 3292
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QY      61      GlyAspAlaGlyGlnTyThrCysHisLysGlyGlyLysValLeuSerArgSerLeuLeu 80
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DB      3293  GCAGATGCTGCCGACGATACCTGTCTATAAGAGCGGAGGTTCTGAGCATTGCTTCCTC 3352
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QY      81      LeuIleHisLysLysGluAspCysLysIleTrpSerThrAspIleLeuLysGluGlnLysGlu 100
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QY      101     SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTySerSerGlyArgPheThrCys 120
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QY      121     TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
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DB      3473  TGTGTGCTGACGGCAATCAGTACCGATTTGAATTCTGCAAAAGCAGAGAGCTCTCC 3532
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QY      141     SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValAlaArgVal 160
        |||SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValAlaArgVal 160
DB      3533  TCTGACCCCCCAAGGGGTGACTGTGAGCAGCAGCAGCTCTCAGCAGAGAGTCAAGAGTG 3592
        |||SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValAlaArgVal 160

QY      161     AspAsnArgAspTyLysLysTyThrValGluCysGlnGluLysSerAlaCysProSer 180
        |||AspAsnArgAspTyLysLysTyThrValGluCysGlnGluLysSerAlaCysProSer 180
DB      3593  GACAACAGGAGATTATAGACAGTACAGCTGAGGTGACAGAGGCGACTGCTCCCGGCT 3652
        |||AspAsnArgAspTyLysLysTyThrValGluCysGlnGluLysSerAlaCysProSer 180

QY      181     AlaGlnGluSerLeuProIleGluValValAlaLysPalaIleHisLysLeuLysTyArgLys 200
        |||AlaGlnGluSerLeuProIleGluValValAlaLysPalaIleHisLysLeuLysTyArgLys 200
DB      3653  GCCGAGGAGAGCCTTACCATTAAGTCGTGTGACCGTATTTCACAAAGCTCAAGTACGAA 3712
        |||AlaGlnGluSerLeuProIleGluValValAlaLysPalaIleHisLysLeuLysTyArgLys 200

QY      201     AsnTyThrThrSerSerPhePheIleArgAspIleIleLysProAspProProthraAsnLeu 220
        |||AsnTyThrThrSerSerPhePheIleArgAspIleIleLysProAspProProthraAsnLeu 220
DB      3713  AACTACACGACGCTTCTTCATCAGGGCATATCAACCCGACCCACCAAGAACCTG 3772
        |||AsnTyThrThrSerSerPhePheIleArgAspIleIleLysProAspProProthraAsnLeu 220

QY      221     GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluLysTrpProAspThr 240
        |||GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluLysTrpProAspThr 240
DB      3773  CAACGGAAGCCATTAAAAATCTCGGCATGTGGAAGTACAGTGGCAATACCTGACACACC 3832
        |||GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluLysTrpProAspThr 240

QY      241     TrpSerThrProHisSerTyThrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 260
        |||TrpSerThrProHisSerTyThrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 260
DB      3833  TGGACACCCCACTTCTTCTTCTTAAACATTTGGCGTACAGGTCCAGGCGAAGAAC 3892
        |||TrpSerThrProHisSerTyThrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 260

QY      261     AsnArgGlyLysLysAspArgLeuCysValAspLysThrSerAlaLysValValLysHis 280
        |||AsnArgGlyLysLysAspArgLeuCysValAspLysThrSerAlaLysValValLysHis 280
DB      3893  AACAGAGAAAGAAAGACAGACTCTCCGTGACAGACCTCAGCCCAAGGTCGTGTCAC 3952
        |||AsnArgGlyLysLysAspArgLeuCysValAspLysThrSerAlaLysValValLysHis 280

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QY      281     LysAspAlaLysIleArgValGlnAlaArgAspArgTyTrpSerSerTrpSerAsp 300
        |||LysAspAlaLysIleArgValGlnAlaArgAspArgTyTrpSerSerTrpSerAsp 300
DB      3953  AAGATGCCAAGATCCCGCTGCAAGCCAGGAGCCGCTACTATCTATCTGAGAGCAAC 4012
        |||LysAspAlaLysIleArgValGlnAlaArgAspArgTyTrpSerSerTrpSerAsp 300

QY      301     TrpAlaSerValSerCysSer 307
        |||TrpAlaSerValSerCysSer 307
DB      4013  TGGCGATCCGCTGTCTCTGACGT 4033
        |||TrpAlaSerValSerCysSer 307

RESULT 9
FCU83184
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Felis catus.
Felis catus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE
1 (bases 1 to 990)
Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
Pedersen,N.C. and Lutz,H.
Nucleotide and predicted peptide sequence of feline interleukin-12
(IL-12)
JOURNAL
DNA Seq. 8 (1-2), 77-82 (1997)
MEDLINE
98182592
PUBMED
9522125
2 (bases 1 to 990)
Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
Pedersen,N.C. and Lutz,H.
Direct Submission
JOURNAL
Submitted (24-DEC-1996) Clinical Laboratory, Department of Internal
Veterinary Medicine, University of Zurich, Winterthurerstrasse 260,
Zurich, ZH 8057, Switzerland
LOCATION/Qualifiers
1. .990
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Pred. No.:      1.64e-147      Length:      990
Score:          1552.00      Matches:      288
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DB:              Gaps:      0

US-09-917-265-53 (1-307) x FCU83184 (1-990)

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        |||TTPGLLEUGLULYSASPVAlTYValValGluLeuAspTrpHisProAspAlaPro 20

QY      21      GlyGluMetValValLeuThrCysHisThrProGluGluAspAlaLeuThrTrpThrSer 40
        |||GlyGluMetValValLeuThrCysHisThrProGluGluAspAlaLeuThrTrpThrSer 40
DB      127  GGAGAAATGGTGGCTTACCTGCATCTCCTGGAAGAGATGACATCCTGGACCTCT 166
        |||GlyGluMetValValLeuThrCysHisThrProGluGluAspAlaLeuThrTrpThrSer 40

QY      41      AlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
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Db      187 GACCAGAGCGTAGGCTCCTAGGCTCTGTTAAACTCTGACCATCCAAAGTCAAGATTT 246
Oy      61 GLYASPALAGLGLTYTThrcysHsLysGLyLysValLeuSerArgSerLeu 80
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Oy      81 LeuLHsLysLysGLyLysGLyLLeuTrpSerThrAspLeuLysGLuLysGLu 100
Db      307 CTGATACACAAAAGAGATGAGATTTGGTCCAGCATATCTTAAGCGCAAGAAAGAA 366
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Db      367 TCCAAAAATTAAGATCTTTCTTAATGTAGAGCAAGATTAATCTGACGTTTCACCTGC 426
Oy      121 TrpTrpLeuThrAlaLLeuSerThrAspLeuLysPheSerValLysSerArgLysPhe 140
Db      427 TGGTGCTGACGGCAATCAGTACCATTTGAAATTCAGTCAAAAAGCAGCAGAGGCTCC 486
Oy      141 SerAspProGlnGlyValThrCysGLyAlaValThrLeuSerAlaGlyArgValArgVal 160
Db      487 TCTGACCCCAAGGGGTGACTGTGGAGCAGCAGCACTCTGAGCAGAAAGTCAAGAGTG 546
Oy      161 AspAsnArgAspTrpLysLysLysTrpValGluCysGlnGlnLysSerAlaCysProSer 180
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Oy      181 AlaGluGluSerLeuProLLeuValValAlaLysAlaLLeuLysLysLysLysLys 200
Db      607 GCCGAGGAGGCTTACCATTGAGTGTGGTGGACCTATTCACAAAGTCAAGTACGAA 666
Oy      201 AsnTrpTrpSerSerPhePheLLeuArgAspLLeuLysProAspProProThrAsnLeu 220
Db      667 AACTACACCCACACTCTTCTCATCAGGACATCATCAACCCGAGCCCAAGAAAGCTTG 726
Oy      221 GlnLeuLysProLeuLysAsnSerArgHsValGluValSerTrpLysTrpProAspThr 240
Db      727 CACTGAAGCCATTAAAAATTCCTCGCATGTGGAAGTGGAGGAGGGAATACCTGACACC 786
Oy      241 TrpSerThrProHsSerTrpPheSerLeuThrPheCysLLeuAlaGlnLysLysAsn 260
Db      787 TGGAGCACCCCACTTCTCTCTCTTAACTTTGGGGTACAGGTGAGGGCAAGAAC 846
Oy      261 AsnArgLysLysLysAspArgLeuLysValAspLysTrpSerAlaLysValAlaCysHs 280
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Oy      281 LysAspAlaLysLLeuArgValAlaAlaArgAspArgTrpTrpSerSerSerTrpSerAsp 300
Db      907 AAGATGCCAAGATCGCGTGCACAGCAGAGCCGCTACTATCTATCTCTGAGAGAAC 966
Oy      301 TrpAlaSerValSerCysSer 307
Db      967 TGGCATCCGTCTCTCGAGT 987

RESULT 10
FCIL12P40      1006 bp      mRNA      linear      MAM 13-MAY-1997
LOCUS          F. catus mRNA for Interleukin-12 p40 chain.
DEFINITION     Y07762.1 GI:2102664
ACCESSION      Y07762.1 GI:2102664
VERSION        Interleukin-12 p40.
KEYWORDS       cat.
SOURCE         Felis catus
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE      1 (bases 1 to 1006)
AUTHORS        Schijns,V.E., Wierda,C.M., Vahlenkamp,T.W. and Horzinek,M.C.
JOURNAL        Molecular cloning of cat interleukin-12
MEDLINE        97246745
PUBMED         Immunogenetics 45 (6), 462-463 (1997)
9089110
2 (bases 1 to 1006)
REFERENCE      Schijns,V.E.C.J.
AUTHORS

```

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TITLE          Direct Submission
JOURNAL        Submitted (03-SEP-1996) V.E.C.J. Schijns, Virology Division,
                Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL
                Utrecht, NETHERLANDS
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                GSDPOEYTGAAATLSAKRVNDKRTYVCGDSACPAEESLPLEYVVDIAHK
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ORIGIN
Alignment Scores:
Pred. No.:      6.74e-147      Length:      1006
                1546.00      Matches:      287
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                Best Local Similarity: 93.49%      Mismatches: 11
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Db      67 ATATGGCACTGGAGAAAACCTTTATTTGTGTAGAGTTGGACCTGACCTGATGCCCC 126
Oy      21 GlyGluMetValValLeuThrCysHsLysLysGLyLysValLeuSerArgSerLeu 40
Db      127 GGAGAAATGGTGTCTCTCCTGCAATATCTCTGAAAGATGATCATCACTGACCTCT 186
Oy      41 AlaGlnSerSerGluValLeuGluLysSerGlyLysThrLeuThrLLeuValLysGluPhe 60
Db      187 GACCAGACAGCTGAAGTCTAGGCTCTGTTAAACTCTGACCATCCAAAGCAATTT 246
Oy      61 GLYASPALAGLGLYNTThrcysHsLysGLyLysValLeuSerArgSerLeu 80
Db      247 GCAGATGCTGGCCAGCATATCTTCTTAATGTAGAGCAAGATTAATCTGACGTTTCACCTGC 306
Oy      81 LeuLHsLysLysGLyLysGLyLLeuTrpSerThrAspLLeuLysGLuLysGLu 100
Db      307 CTGATACACAAAAGAGATGAGATTTGGTCCAGCATATCTTAAGGGAAACAGAAAGAA 366
Oy      101 SerLysAsnLysLLeuLeuLysCysGLuAlaLysAsnTrpSerGlyArgPheTrpCys 120
Db      367 TCCAAAAATTAAGATCTTTCTTAATGTAGAGCAAGATTAATCTGACGTTTCACCTGC 426
Oy      121 TrpTrpLeuThrAlaLLeuSerThrAspLeuLysPheSerValLysSerArgLysPhe 140
Db      427 TGGTGCTGACGGCAATCAGTACCATTTGAAATTCAGTCAAAAAGCAGCAGAGCTCC 486
Oy      141 SerAspProGlnGlyValThrCysGLyAlaValThrLeuSerAlaGlyArgValArgVal 160
Db      487 TCTGACCCCAAGAGGTGACTGTGGAGCAGCAGCACTCTGAGCAGAAAGTCAAGAGTG 546
Oy      161 AspAsnArgAspTrpLysLysLysTrpValGluCysGlnGlnLysSerAlaCysProSer 180

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| Db | 547 | GACAAACAGGATTATAGAAAGTACACACTGGAGTGTACGAGGACAGTGCCTGCCGCT | 606 |
| QY | 181 | AlaGlnGlnSerLeuProIleGluValValAlaSpAlaIleHisLysLeuLysTyrGlu | 200 |
| Db | 607 | GCCGAGGAGACCTTACCATTGAAGTGTGGTGACCGTATTCCAAACCTCAAGTACGAA | 666 |
| QY | 201 | AsnTyrThrSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeu | 220 |
| Db | 667 | AACACACACACACACTTCTTCATCAGGCATCATCAACACCGACCCCAACAAACTG | 726 |
| QY | 221 | GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr | 240 |
| Db | 727 | CAACTGAACCATTTAAATAATTCTCGCATGTGGAAAGTGAAGCTGGGAATACCTGTACACC | 786 |
| QY | 241 | TrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn | 260 |
| Db | 787 | TGGAGCAACCCACATCTCTACTTCTCTCTTACATTGGCGCTACAGGTCCAGGCAAGAAC | 846 |
| QY | 261 | AsnArgGlnLysLysAspArgLeuCysValAspLysThrSerAlaLysValValCysHis | 280 |
| Db | 847 | AACAGAGAAAAGAAAGACAGACTCTCGGTGACAAAGACCTCAGCCAAAGCTGTGCAC | 906 |
| QY | 281 | LysAspAlaLysIleLeuArgValGlnAlaArgAspArgTyrTyrSerSerTrpSerAsp | 300 |
| Db | 907 | AAGATGTCACCAAGATCCCGTGCAGGCCAGAGACCGCTACTATACCTCATCTCGAGACAC | 966 |
| QY | 301 | TrpAlaSerValSerCysSer 307 | |
| Db | 967 | TGGCATTCGCTGCTCTCTCCACT 987 | |
| RESULT 11 | | | |
| AX154603 | | | |
| LOCUS | AX154603 | 990 bp | DNA |
| DEFINITION | Sequence 7 from Patent WO0140257. | | linear |
| ACCESSION | AX154603 | | |
| VERSION | AX154603.1 | | GI:14536186 |
| KEYWORDS | | | |
| SOURCE | | | |
| ORGANISM | | | |
| REFERENCE | | | |
| AUTHORS | Leong,S.R. and Punnonen,J. | | |
| TITLE | Cytokine polypeptides and nucleic acids | | |
| JOURNAL | Patent: WO 0140257-A 7 07-JUN-2001; | | |
| | Maxygen, Inc. (US) | | |
| FEATURES | | | |
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| | /db_xref="taxon:32630" | | |
| | /note="Synthetic Sequence" | | |
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| Pred. No.: | 1,23e-140 | Length: | 990 |
| Score: | 1484.00 | Matches: | 275 |
| Percent Similarity: | 93.81% | Conservative: | 13 |
| Best local Similarity: | 89.58% | Mismatches: | 19 |
| Query Match: | 89.78% | Indels: | 0 |
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| Db | 67 | ATATGGCACTGGAGAAACGTTTATGTTGTAGAAATTGACTGTGATCCCGATGCCCTT | 126 |
| QY | 21 | GlyGlnLeuValValLeuThrCysHisThrProGlnLysAspAlaIleThrTrpThrSer | 40 |
| Db | 127 | GGACAAATGTGGTCCCTCGCCTGTGACACACTCTTAACAACATGGCATTCAGTCACTCA | 186 |
| QY | 41 | AlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe | 60 |

| | | | |
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| Db | 187 | GACCAGACGACTGAGGCTCTTGGGCACTGGCAAAACCTTGACCATTCCACGTCAAAGATTT | 246 |
| Oy | 61 | GLyspAlaGLyGLnTYrThrCysHisLysGLyLysValLeuSerArgSerLeuLeu | 80 |
| Db | 247 | GGAGATGCTGGCCACTACACTGTCGCCAAAGAGGCGGAGTTCTGACGACGACTCTG | 306 |
| Oy | 81 | LeuIleHisLysLysGLuAspGlyLLeTrpSerThrAspIleLeuLysGLuLysGLu | 100 |
| Db | 307 | CTGCTTCACAAAAAGGAATGAAATTGGTCCACTGATATTTTAAAGACACAAAGAG | 366 |
| Oy | 101 | SerLysAsnLysIlePheLeuLysCysLysLysAsnTYrSerGlyArgPheThrCys | 120 |
| Db | 367 | CCCAAAACCAAGATCTTTCTGAATATGAGGCAAAAGAAATTCCTCGGACGTTTCACTGC | 426 |
| Oy | 121 | TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe | 140 |
| Db | 427 | TGGTGCGCTGACAGCATGACTACAGATTTCGAAATTCACCTGTCCAAAGACAGAGAGCTCC | 486 |
| Oy | 141 | SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgVal | 160 |
| Db | 487 | TCTGACCCCCCAAGGGGTGACTTTGGAGACCCGTTACACTCTCGACAGAGGTCAGCATG | 546 |
| Oy | 161 | AspAsnArgAspTYrLysLysTYrThrValGluCysGlnGluGlySerAlaCysProSer | 180 |
| Db | 547 | GACCACAGGGGTATTAACACAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCTCT | 606 |
| Oy | 181 | AlaGlnGluSerLeuProGlnGlyValValAlaAlaIleHisLysLeuLysTYrGlu | 200 |
| Db | 607 | GCCAGAGAGACCTTACCATCGAGGTCCTGGTGGATGCTTATTCCACAAAGCTCAAGTATAA | 666 |
| Oy | 201 | AsnTYrThrSerSerPhePheIleArgAspIleIleLysProAspProThrAsnLeu | 220 |
| Db | 667 | AACTAACACAGCAGCTTCTTCATCAGACATCATCAACACCTGACCCCAAGAACTTG | 726 |
| Oy | 221 | GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTYrProAspThr | 240 |
| Db | 727 | CAGCTGAGCCATTAAAGAAATTCTCGCACCTGGAGATCACCTGGGATACCTCGACACC | 786 |
| Oy | 241 | TrpSerThrProHisSerTYrPheSerLeuThrPheCysIleGlnAlaGlnLYsAsn | 260 |
| Db | 787 | TGGAGCATCCACACATCTCTACTTTTCCCTGATGTTTGGTGTTCAAAGTTCAAGGCCAAGAC | 846 |
| Oy | 261 | AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValAlaCysHis | 280 |
| Db | 847 | AAGAGAGAAAGAAAGATAGACTCTGCTGGACAAGACCTCAGCCAAAGCTGTCGCCAC | 906 |
| Oy | 281 | LysAspAlaLysIleArgValGlnAlaArgAspArgTYrTYrSerSerSerTrpSerAsp | 300 |
| Db | 907 | AAGATGCGCAAGATCCCGCTCCAAAGCCGAGACCCGCTACTACAGTCATCTTGGAGCGAA | 966 |
| Oy | 301 | TrpAlaSerValSerCysSer 307 | |
| Db | 967 | TGGGCATCTGTGCCCTGCAGT 987 | |
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| LOCUS | EC112P40 | 1058 bp | linear |
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| ACCESSION | Y11129 | | |
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| KEYWORDS | interleukin-12 p40. | | |
| SOURCE | Eqgus caballus. | | |
| ORGANISM | Eqgus caballus. | | |
| REFERENCE | | | |
| AUTHORS | Mammalia: Eutheria; Perissodactyla; Equidae; Eqgus: Mammalia: 1 (bases 1 to 1058) | | |
| | Nicolson, L., Penha-Gonzales, M.N., Keanle, J.L., Logan, N.A., | | |
| | Argyle, D.J. and Onions, D.E. | | |
| TITLE | Cloning and sequencing of horse interleukin-12 and interleukin-18 | | |
| JOURNAL | CDNAS | | |
| MEDLINE | Immunogenetics 50 (1-2), 94-97 (1999) | | |
| PUBMED | 20009534 | | |
| | 10541814 | | |

REFERENCE 2 (bases 1 to 1058)
 AUTHORS Nicolson, L.
 TITLE Direct Submission
 JOURNAL Submitted (04-FEB-1997) L. Nicolson, Dept. of Vet. Pathology,
 University of Glasgow Vet. School, Bearsden Rd., Glasgow G61 1QH,
 UK

FEATURES

source

Location/Qualifiers

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 GSSDPKGVTCGAATLSAEKVSVDREYKKTYYECQSGSACPAEBSLPLEIYVDVHK
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282 g

223 t

BASE COUNT

ORIGIN

Alignment Scores:

Pred. No.: 4,38e-139 Length: 1058
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 Percent Similarity: 94.14% Conservativity: 20
 Best Local Similarity: 87.62% Mismatches: 18
 Query Match: 88.87% Indels: 0
 DB: 4 Gaps: 0

US-09-917-265-53 (1-307) x ECIL12P40 (1-1058)

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 QY 21 GLYGLUMETVALLEUTHRCYSHSTHTRPROGLUGLUSAPSLIEHTRTPHRSER 40
 DB 127 GGAGAAATGCTGCTCCACCTCCATACCCCGAAGAAAGCATCACCTGACCTG 186
 QY 41 ALAGLSERSEGLUVALLEUGLYSERGLYSLTHLEUTHRIEGLINVALYSLGULPHE 60
 DB 187 GCCCAGACGATAGGCTTACGCTCTGGCAAAACCTTGACCTCCAAAGTCAAGAGTTT 246
 QY 61 GLYASPALAGLYINTYRTHRCYSHSLYSGLYGLYSLVALLEUSERARGSERLEULEU 80
 DB 247 GGAGATGCTGGCTGGATACACCTGTCACAAAGAGGAGGTCTGAGCATTCTCACCTG 306
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DB 367 TCCAAAATAAGACCTTTCTAATAATGTAGAGCCAAAGAAATTAATCCGACGTTTCACATGC 426
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 DB 427 TGGTGGCTACACGATCATGCTACTGATTTGAAATTCAGTGTCAAAAGCAGCAGAGTCC 486
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 QY 281 LYSASPALALYSILARGVALGLNALAARGASPARGYRTRYSERSETRPSEARSP 300
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 QY 301 TRPALASERVALSERCYSSER 307
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RESULT 13
 AF401989
 LOCUS AF401989 1626 bp mRNA linear SYN 14-FEB-2002
 DEFINITION Synthetic construct single chain interleukin-12 mRNA, complete cds.
 ACCESSION AF401989
 VERSION AF401989.1 GI:16656516
 KEYWORDS
 SOURCE
 ORGANISM
 synthetic construct.
 synthetic construct.
 artificial sequences.
 1 (bases 1 to 1626)
 McMonagle, E.L.J., Taylor, S., van Zullekom, H., Sanders, L.,
 Scholtes, N., Keanie, L.J., Hopkins, C.A., Logan, N.A., Balin, D.,
 Argyle, D.J., Onions, D.E., Schljns, V.E., and Nicolson, L.,
 Production of biologically active equine interleukin 12 through
 expression of p35, p40 and single chain IL-12 in mammalian and
 baculovirus expression systems
 Equine Vet. J. 33 (7), 693-698 (2001)
 MEDLINE 21626920
 PUBMED 11770992
 REFERENCE 2 (bases 1 to 1626)
 McMonagle, E.L.J., Taylor, S., Keanie, L.J., Hopkins, C.A., Logan, N.A.,
 Argyle, D.J., Onions, D.E., and Nicolson, L.,
 Direct Submission
 Submitted (24-Jul-2001) Veterinary Pathology, Glasgow Veterinary
 School, Bearsden Rd, Glasgow G61 1QH, UK
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 Location/Qualifiers
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 /organism="Synthetic construct"
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Oy      101  SERLYSASNYSLIEPHELEUYSCYSGUALALAYASNTYRSERYLARGPHERCY 120
Db      367  CCCCCAACAAAGATCTTTCTGAAATGTGAGCAAAAGAAATTAAGTCTCCGAGCTTCACTCC 426
Oy      121  TRTPRLEUTHRALLESERTHRASPLEULYSPHERSERVALYSSERARGLYPHE 140
Db      427  TGGTGGCTGACAGCATCAGTACAGATTGGAATTCACCTGCAAAAGACAGAGGCTCC 486
Oy      141  SERASPPROGLNGLYVALTHRCYSGLYALAYALTHRLUSERALAGUARGVAL 160
Db      487  TCTGACCCCAAGGGGTGACTTGTGGAGCCGTTACACTCTCTGACAGAGGGTCAAGCATG 546
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Db      667  AACTACACCCAGACAGTCTTCATCAGGAGCATCATCAACCGGACCCCAAGAACTTG 726
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Db      847  AAGAGAGAAAAAGAA-----CTCTTCATGAGCAAAACCTCAGCCAAAGTACATGAGCC 900
Oy      281  LYSASPALALYSLEARGVALGLNALARGASPARGYTRYRSESRSESRTRPSERTSP 300
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RESULT 15
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LOCUS      AX154599      984 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION Sequence 3 from Patent WO0140257.
ACCESSION AX154599
VERSION    AX154599.1 GI:14536182
KEYWORDS
SOURCE
ORGANISM   synthetic construct.
            artificial construct.
            (bases 1 to 984)
REFERENCE  1 (bases 1 to 984)
AUTHORS   Leong,S.R. and Punnonen,J.
TITLE      Cytokine polypeptides and nucleic acids
JOURNAL    Patent: WO 0140257-A 3 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES
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            location/Qualifiers
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Thu Jul 17 12:12:39 2003

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Search completed: July 17, 2003, 06:40:32
Job time : 2751.43 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: July 16, 2003, 13:41:48 ; Search time 217.05 Seconds
(without alignments)
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Title: US-09-917-265-53

Perfect score: 1653
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Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 1653 | 100.0 | 990 | 19 AAV13817 | Canine IL-12 p40 s |
| 2 | 1653 | 100.0 | 990 | 20 AAX35625 | Nucleic acid encod |
| 3 | 1653 | 100.0 | 990 | 20 AAX03162 | Nucleic acid encod |
| 4 | 1653 | 100.0 | 990 | 22 AA164388 | Canine coding sequ |
| 5 | 1644 | 99.5 | 990 | 19 AAV13816 | Canine IL-12 p40 s |
| 6 | 1644 | 99.5 | 990 | 20 AAX35615 | Nucleic acid encod |
| 7 | 1644 | 99.5 | 990 | 20 AAX03152 | Nucleic acid encod |
| 8 | 1644 | 99.5 | 990 | 22 AA164378 | Canine coding sequ |
| 9 | 1618.5 | 97.9 | 924 | 20 AAX18177 | Canine mature CLAF |
| 10 | 1618.5 | 97.9 | 2154 | 20 AAX18176 | Canine full length |
| 11 | 1554 | 94.0 | 921 | 19 AAV56626 | Feline FLAPp40 cDN |
| 12 | 1554 | 94.0 | 921 | 19 AAV56627 | Feline FLAPp40 cDN |
| 13 | 1554 | 94.0 | 990 | 22 AAF26082 | Feline IL-12p40 en |
| 14 | 1554 | 94.0 | 990 | 22 AAF26085 | Feline IL-12p40 en |
| 15 | 1554 | 94.0 | 2193 | 19 AAV56625 | Feline FLAPp40 cDN |
| 16 | 1554 | 94.0 | 4522 | 22 AAF26076 | Feline IL-12p40 en |
| 17 | 1554 | 94.0 | 4522 | 22 AAF26094 | Plasmid pMO1-f1112 |
| 18 | 1484 | 89.8 | 990 | 22 AAD15209 | Modified human cyt |
| 19 | 1451 | 87.8 | 984 | 22 AAD15206 | Modified human cyt |
| 20 | 1429 | 86.4 | 984 | 22 AAD15205 | Modified human cyt |
| 21 | 1421 | 86.0 | 984 | 22 AAD15204 | Modified human cyt |
| 22 | 1419.5 | 85.9 | 987 | 20 AAV83199 | Interleukin (IL)-1 |
| 23 | 1419.5 | 85.9 | 8578 | 24 AAD31545 | PIRES-hb7-1-IL12.1 |
| 24 | 1419.5 | 85.9 | 8578 | 24 AAD31546 | PIRES-hb7-1-IL12.1 |
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| 26 | 1419.5 | 85.9 | 8623 | 24 AAD31547 | PIRES-hb7-1-IL12.3 |
| 27 | 1419.5 | 85.9 | 8629 | 24 AAD31552 | PIRES-IL12.2-hb7-1 |
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| 29 | 1419.5 | 85.9 | 8644 | 24 AAD31551 | PIRES-IL12.3-hb7-1 |
| 30 | 1419.5 | 85.9 | 8659 | 24 AAD31550 | PIRES-IL12.4-hb7-1 |
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| 32 | 1418.5 | 85.8 | 987 | 19 AAV07273 | Human interleukin- |
| 33 | 1418.5 | 85.8 | 987 | 19 AAV07272 | DNA encoding human |
| 34 | 1418.5 | 85.8 | 987 | 20 AAZ40404 | Human interleukin |
| 35 | 1418.5 | 85.8 | 987 | 20 AAZ40405 | Human interleukin |
| 36 | 1418.5 | 85.8 | 987 | 20 AAZ40406 | Human interleukin |
| 37 | 1418.5 | 85.8 | 987 | 22 AAD15210 | Human cytokine p40 |
| 38 | 1418.5 | 85.8 | 1007 | 22 AAD18585 | Human interleukin- |
| 39 | 1418.5 | 85.8 | 1018 | 15 AAO67879 | EPV 42 kD promoter |
| 40 | 1418.5 | 85.8 | 1018 | 20 AAZ08510 | Human p40-IL-2 cod |
| 41 | 1418.5 | 85.8 | 1389 | 22 AAF76880 | 40 kDa subunit of |
| 42 | 1418.5 | 85.8 | 1397 | 18 AAV00401 | 40 kDa subunit of |
| 43 | 1418.5 | 85.8 | 1397 | 18 AAT77849 | 40 kDa subunit of |
| 44 | 1418.5 | 85.8 | 1397 | 18 AAT97969 | 40 kDa subunit of |
| 45 | 1418.5 | 85.8 | 1397 | 19 AAV37767 | Cytotoxic lymphocy |

ALIGNMENTS

| RESULT 1 | AAV13817 | standard; cDNA to mRNA; 990 bp. |
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| AC | AAV13817; | |
| XX | | |
| DT | 14-MAY-1998 | (first entry) |
| XX | | |
| DE | Canine IL-12 p40 subunit cDNA. | |
| XX | | |
| KW | Canine; interleukin-12 p40 subunit; IL-12 p40 subunit; antitumour; | |
| KW | antiviral; vaccine adjuvant; ds. | |
| XX | | |
| OS | Canis sp. | |
| XX | | |
| FH | Key | Location/Qualifiers |
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| FT | | /-*-a |

FT /product= interleukin-12_P40_subunit
 XX JP10036397-A.
 XX 10-FEB-1998.
 XX 08-NOV-1996: 96JP-0296789.
 XX 23-MAY-1996: 96JP-0128104.
 PR 08-NOV-1995: 95JP-0289729.
 XX (TORA) TORAY IND INC.
 PA WPI: 1998-174914/16.
 DR P-PSDB; AAI41791.
 PT Canine interleukin 12 - comprises P40 and P35 subunits: useful in
 PT veterinary medicine, e.g. antitumour, antiviral and vaccine adjuvant
 PT activities are expected
 XX Claim 10; Pages 10-11; 12pp; Japanese.
 XX
 CC The present sequence encodes a canine interleukin-12 (IL-12) P40
 CC subunit. A canine IL-12 comprising a P40 and P35 subunit is capable
 CC of inducing an antiviral activating factor and the expression of
 CC class II MHC molecules in canine tumour cells, stimulating
 CC proliferation of canine blastogenic lymphocytes and activating
 CC canine leukocytes to inhibit canine tumour cells. The canine IL-12
 CC can be used in veterinary medicines, e.g. antitumour, antiviral and
 CC vaccine adjuvant activities are expected.
 XX
 SQ Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 other;
 Alignment Scores:
 Pred. No.: 1, 87e-161 Length: 990
 Score: 1653.00 Matches: 307
 Percent Similarity: 100.00% Conservative: 0
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 DB: 19 Gaps: 0
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 DB 127 GGAGAAATGGTGTCTCACTGCCATACCCCTGAAGAAGATGACATCATCTGGACCTCA 186
 QY 41 AlaGlnSerSerGluValLeuGlySerGlyIleThrLeuThrIleGlnValIleGlyGluPhe 60
 DB 187 GCGCAGAGAGCAATGCTAGTCTGTGTTAAACCTGACCATCAAGTCAAAAGATTT 246
 QY 61 GlyAspAlaGlyGlnTYrThrCysHisIleGlyValLeuSerArgSerLeuLeu 80
 DB 247 GGAGATGTGGCCAGATATCTGCTCAATAAGAGCAAGATGCTGAGCGCTCCTG 306
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 QY 121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValIleSerSerArgGlyPhe 140
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DB 487 TCTGACCCCAAGGGGTGACATGTGGAGCATGACACTTTCAGCAGAGGGCTCAGAGTG 546
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 QY 221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTYrProAspThr 240
 DB 727 CAGCTGACCATTTGAAAAATTTCTCGCAGCGTGGAGAGTCACTGGGAATACCCGACAC 786
 QY 241 TrpSerThrProHisSerTYrPheSerLeuThrPheCysIleGlnAlaGlnIleLysAsn 260
 DB 787 TGGAGCACCACCATTCCTACTCTCCCTGACATTTTGCATACAGGCCAGGCAAGAAC 846
 QY 261 AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValIleCysHis 280
 DB 847 AATAGGAAAGAAAGATATGACTGTGCGGACAAAGACCTCAAGGTCGTGGCCAC 906
 QY 281 LysAspAlaLysIleArgValGlnAlaArgAspArgTYrTYrSerSerSerTrpSerAsp 300
 DB 907 AAGGATGCCAAGATCCGCTGCAAGGCCGACAGCCGCTACTATAGTTCACTGAGAGCAG 966
 QY 301 TrpAlaSerValSerCysSer 307
 DB 967 TCGCATCTGTCTCCTGCAGT 987
 RESULT 2
 AAX35625
 ID AAX35625 standard; cDNA to mRNA; 990 BP.
 AC AAX35625;
 DT 09-JUL-1999 (first entry)
 DE Nucleic acid encoding canine Interleukin-12 (IL-12).
 DE Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
 KW tumour; skin disease; infectious disease; allergic disease; ds.
 OS Canis sp.
 FH Key Location/Qualifiers
 FT CDS 1..990
 FT /tag= a
 PN JP11106350-A.
 PD 20-APR-1999.
 PF 15-MAY-1998: 98JP-0133345.
 PR 07-AUG-1997: 97JP-0213755.
 PR 16-MAY-1997: 97JP-0127690.
 PA (TORA) TORAY IND INC.
 XX WPI: 1999-308068/26.
 XX P-PSDB; AAI02342.
 DR A prevention and treating agent containing interleukin 12 (CaIL12) -
 PT for prevention and treatment of dog and cat immune diseases
 XX Claim 1; Page 14-15; 16pp; Japanese.
 CC The present sequence encodes canine Interleukin-12 (IL-12). The

CC specification describes a method for the prevention and treatment
 CC of dog and cat immune diseases. The treatment used an agent comprising
 CC dog IL-12 (CaIl12) proteins to form a heterodimer. The agent is
 CC useful for preventing dog and cat immune diseases,
 CC including tumours, skin diseases, infectious diseases and allergic
 CC diseases.

XX Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 other;

Alignment Scores:

| Pred. No.: | 1,87e-161 | Length: | 990 |
|------------------------|-----------|---------------|-----|
| Score: | 1653.00 | Matches: | 307 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
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US-09-917-265-53 (1-307) x AAX35625 (1-990)

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OY 41 A1aGlnSerSerGluValLeuGlnSerGlyLysThrLeuThrIleGlnValLysGluPhe 60
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OY 81 Leu11eHisLysLysGluAspGly11eTrpSerThrAspIleLeuLysGluGlnGlu 100
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OY 181 AlaGlnLysLeuProIleGluValValValAspAlaIleHisLysLeuLysTrpGlu 200
DB 607 GCCCAGAGAGAGCTTACCCTGAGGTCGTGATGCTATTCACAGAGCTCAAGTATGAA 666
OY 201 AsnTrpThrSerSerPhePheIleArqAspIleIleLysProAspProThrAsnLeu 220
DB 667 AACTACACAGCAGCTTCTTCATCAGAGCATCATCAACCCAGACCACCAAAACCTG 726
OY 221 GlnLeuLysProLeuLysAsnSerArqHisValGluValSerTrpGlnTrpProAspTrp 240
DB 727 CAGCTGAAGCCATTGAAAAATTTCTGGCGACGTGGAGGTAGCTGGGAATTAACCCGACAC 786
OY 241 TrpSerThrProHisSerTrpPheSerLeuThrPheCysIleGlnAlaGlnLysLysAsn 260
DB 787 TGGACACACCCACATTCCTACTTCTCCGACATTTTGGCATACAGGCCCAAGCAAGAAC 846
OY 261 AsnArqGluLysLysAspArqLeuCysValAspLysThrSerAlaLysValValCysHis 280

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DB 847 AATAGAGAAAAGAAAGATAGACTTCGCTGGAGCAAGACCTCAGCAAGTCTGTCGCCAC 906
OY 281 LysAspAlaLysIleArqValGlnAlaArqAspArqTrpTrpSerSerTrpSerAsp 300
DB 907 AAGATGCCAAGATCCCGCGCAAGCCGAGACCGCTACTATAGTTGATCTCTGAGAGGAC 966
OY 301 TrpAlaSerValSerCysSer 307
DB 967 TGGGCATCTGTCCTCTGCACT 987

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RESULT 3

AAX03162

ID AAX03162 standard; cDNA to mRNA; 990 BP.

XX

AC AAX03162;

XX

DE 30-MAR-1999 (first entry)

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Alignment Scores:

Pred. No.: 1.87e-161 Length: 990
 Score: 1653.00 Matches: 307
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 20 Gaps: 0

US-09-917-265-53 (1-307) x AAX03162 (1-990)

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QY 1 ILETTPGLULEUGLULYSASPVALTYRVALVGLIULEUASPTRPHISPROASPLAPRO 20
DB 67 ATATGGAACTGGAGAAAGATGTTATGTTGAGAGTTGAGCTGGACCCCTGATGCCCCC 126
QY 21 GYGLUMETVALVLEUETHRCYSHSTHRPROGLUGUASPAPLIEHTTRPTHRSER 40
DB 127 GGAGAAATGGTGTCTCCATCCCTGACATACCCTGAAGAAGATGACATCTGGACCTCA 186
QY 41 ALAGINSERSEGLUVALLEUGLYSERGLYSTRLEUTHRLIEGLNVALYSGLUPE 60
DB 187 GCGCAGACGAGTGAAGTCTAGTCTGTAAACCTGACCATCCAACTCAAGCAATTT 246
QY 61 GLYASPALAGLYGLNTHYRTHRCYSHSLYSGLYGLYVALLEUSERARGSERLEUEN 80
DB 247 GGAGATGCTGGCCAGTATACCTGCCATAAGAGGCAAGGTTCTGAGCCGCTCACTCTG 306
QY 81 LEULIEHISLYSLYSGLUASPLIYLETSPSERTHRASPILIEULYSGLUINLYSGLU 100
DB 307 TTGATTCACAAAAAAGAAAGATGGAATTGGTCCACATGATATCTTAAAGSAGACAAAGAA 366
QY 101 SERLYSASNLYSILIEPHEULYSCYSGUVALYASNTYSESGLYARGHETHRCYS 120
DB 367 TCCAAAAATAGATCTTCTGAAATGTGAGGCAAAATATCTGGAGGTTTCACATGC 426
QY 121 TPTPTPLEUTHRALIESESTRHASPULYSPHSESERVALYSSERARGLYPHE 140
DB 427 TGTGTGCTACCGCAATCAGTACTGATTGAAATTCAGTGTCAAAAAGTAGCAGAGGCTTC 486
QY 141 SERASPPROGLINGLYVALTHRCYSGLYALVALTHRLEUSERALAGLUARGVAL 160
DB 487 TCTGACCCCAAGGGGTGACATGTGAGCAGTGCACCTTTCAGCAGAGGAGGCTCAGAGTG 546
QY 161 ASPAANARGASPTRYLYSTYRTHRVALLIGUCYSGINGLYSERLACYSPROSER 180
DB 547 GACACACAGGATTTATAGAAATGACAGTGCAGAGGAGGAGGAGTCCCTGCTCT 606
QY 181 ALAGLUGUSERLEUPROILEGLUVALVALLASPALALIEHISLYSEULYSTYRGLU 200
DB 607 GCGCAGAGACGCTACCCATCGAGGCGTGTGAGTGTATTCACAAAGCTCAAGTATGAA 666
QY 201 ASNTYRTHRSERSETPHEPHEILEARGASPILEILELYSPROASPPROPTHASNLEU 220
DB 667 AACTACACCCAGCAGCTTCTTCATCAGACATCAATCAACCAAGCCACCAACCAACCTG 726
QY 221 GINLEULYSPROLEULYSASNSERARGHISVALIGUVALSERTRPGLUJYRPROASPTHR 240
DB 727 CAGCTGAACCATTTGAAAAATTTCTCGCACGTGAGAGTGTGCTGGAAATACCCCGACAC 786
QY 241 TRPSERTHRPROHISSETRYRPHESERLEUTHRPHECYSILIEGLNALAGINLYLSASN 260
DB 787 TGGAGACCCCAACATTCCTACTTCTCCCTGACATTTTGTGATACAGGCCCAAGGCAAGAAC 846
QY 261 ASNAARGULYLYSASPARGLEUCYSVALASPLYSTHRSERLALYSLVALYCYSHIS 280
DB 847 AATAGAGAAAAGAAAGATAGACTCTGCGGACAGACACTCAGCCAAAGTCTGTCGCCAC 906
QY 281 LYSASPALALYSILIEARGVALGINLAARGASPARGTYRYSERSESERTRPSERASP 300
DB 907 AAGGATGCCAAGATCCGCTGCAAGCCGAGACCCCTACTATAGTTTCATCTGGAGCGAC 966
QY 301 TRPALASERVALSERCYSSER 307
DB 967 TGGGCATCTGTCTCTGCAGT 987

```

RESULT 4
 ID AAI64388
 XX AAI64388 standard; DNA; 990 BP.
 AC AAI64388;
 XX

DT 23-NOV-2001 (first entry)
 DE Canine coding sequence #3.
 XX
 KW Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
 XX
 OS Canis familiaris.

XX
 FH Key Location/Qualifiers
 FT CDS 1..990
 FT sig_peptide 1..66 /product= "Canine protein #1"
 FT mat_peptide 67..987 /tag= b
 FT /tag= c
 PN JP2001161378-A.

XX
 PD 19-JUN-2001.
 XX
 PF 26-SEP-2000; 2000JP-0292946.
 XX
 PR 01-OCT-1999; 990P-0281234.

XX
 PA (TORA) TORAY IND INC.
 XX
 DR WPI: 2001-592466/67.
 DR P-PSDB: AAG66482.

PT Preparation of a highly pure protein, interleukin 12, a protein
 PT inhibiting the activity of interleukin 12, and a treating agent and a
 PT treating method for immunopathy of mammalian
 PS
 XX Claim 6; Page 16-17; 21pp; Japanese.

CC The present invention relates to a method for the preparation of a highly
 CC pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
 CC the activity of IL12 is contacted to an ion exchanging carrier and/or a
 CC pigment carrier to get IL12 and/or a protein inhibiting the activity of
 CC IL12. The protein is used as a preventive agent for dog immunopathy. The
 CC present sequence was used in the method of the present invention.

XX Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 other;

Alignment Scores:
 Pred. No.: 1.87e-161 Length: 990
 Score: 1653.00 Matches: 307
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0

US-09-917-265-53 (1-307) x AAI64388 (1-990)

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QY 1 ILETTPGLULEUGLULYSASPVALTYRVALVGLIULEUASPTRPHISPROASPLAPRO 20
DB 67 ATATGGAACTGGAGAAAGATGTTATGTTGAGAGTTGAGCTGGACCCCTGATGCCCCC 126
QY 21 GYGLUMETVALVLEUETHRCYSHSTHRPROGLUGUASPAPLIEHTTRPTHRSER 40
DB 127 GGAGAAATGGTGTCTCCATCCCTGACATACCCTGAAGAAGATGACATCTGGACCTCA 186
QY 41 ALAGINSERSEGLUVALLEUGLYSERGLYSTRLEUTHRLIEGLNVALYSGLUPE 60
DB 187 GCGCAGACGAGTGAAGTCTAGTCTGTGTAATAACTGACCATCCAAAGTCAAAATTT 246

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QY 61 GlyAspAlaGlyGlnTyrThrCysHisLysGlyLysValLeuSerArgSerLeuLeu 80
Db 247 GGAGATGCTGGCCAGTATACCTGCCATAAAGCAGCAAGTTTCGAGCCCTCACTCTG 306
QY 81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGlu 100
Db 307 TTGATTCACAAAAGAAAGATGAGAAATTGGTCCACTGATATCTTAAAGCAACAGAAAGAA 366
QY 101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
Db 367 TCCAAAATATAGATCTTCTGAAATGTGAGCAAGAAATATCTTGACGTTTCAACATGC 426
QY 121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
Db 427 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGCACAAAGAGCAGAGCCCTC 486
QY 141 SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgVal 160
Db 487 TCTGACCCCAAGGGGTGACATGTGAGACACTTTCAGCAGAGCGTCAGAGTG 546
QY 161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGlnLysSerAlaCysProSer 180
Db 547 GACACACGGGATTATTAAGAGTACACAGTGGAGGTGAGGAGGAGGAGTGCCTGCCCTCT 606
QY 181 AlaGlnGluSerLeuProIleGlyValValAlaAspAlaIleHisLysLeuLysTyrGlu 200
Db 607 GCCGAGCAGAGCCATACCAGCTGAGCTGCTGGATGTATTACAAACCTCAAGTATGAA 666
QY 201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProThrAsnLeu 220
Db 667 AACTACACACGACACTTCTTCATCAGACATCATCAAAACAGACCCACCAAAACCTG 726
QY 221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGlnTyrProAspThr 240
Db 727 CAGCTGAAGCCATTGAATAAATTCGCGCAGCTGGAGGTCACCTGGAAATACCCGACACC 786
QY 241 TrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 260
Db 787 TGGAGCACCCACACTTCTCTACTCTCCCTGACATTTTGCAATACAGGCCACAGGCACAG 846
QY 261 AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValAlaCysHis 280
Db 847 AATGAGCAAAAAGAAAGATAGACTCTGCGTGCAGCAAGCCTCAGCCAGGTGCTGCAC 906
QY 281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTrpSerSerSerTrpSerAsp 300
Db 907 AAGGATCCAGAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCTGGAAGCCAC 966
QY 301 TrpAlaSerValSerCysSer 307
Db 967 TGGGCATCTGCTCTCTGCAGT 987

RESULT 5
AAV13816
ID AAV13816 standard; cDNA to mRNA; 990 BP.
XX
AC AAV13816;
XX
DT 14-MAY-1998 (first entry)
XX
DE Canine IL-12 P40 subunit cDNA.
XX
KW Canine: interleukin-12 P40 subunit; IL-12 P40 subunit; antitumour;
antiviral; vaccine adjuvant; ds.
XX
OS Canis sp.
XX
FH Key location/Qualifiers
FT CDS 1..990 /*tag= a
FT /product= interleukin-12_P40_subunit
XX
PN JP10036397-A.
```

```
XX 10-FEB-1998.
PD 10-NOV-1996; 96JP-0296789.
XX
PF 08-NOV-1996; 96JP-0296789.
XX
PR 23-MAY-1996; 96JP-0128104.
PR 08-NOV-1995; 95JP-0289729.
XX
PA (TORA ) TORAY IND INC.
XX
DR WPI: 1998-174914/16.
DR P-PSDB: AAW41790.
XX
PT Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT veterinary medicine, e.g. antitumour, antiviral and vaccine adjuvant
PT activities are expected
XX
PS Claim 8: Page 8; 12pp; Japanese.
XX
CC The present sequence encodes a canine interleukin-12 (IL-12) P40
CC subunit. A canine IL-12 comprising a P40 and P35 subunit is capable
CC of inducing an antiviral activating factor and the expression of
CC class II MHC molecules in canine tumour cells, stimulating
CC proliferation of canine blastogenic lymphocytes and activating
CC canine leukocytes to inhibit canine tumour cells. The canine IL-12
CC can be used in veterinary medicines, e.g. antitumour, antiviral and
CC vaccine adjuvant activities are expected.
XX
SQ Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 other;
Alignment Scores:
Pred. No.: 1,66-160 Length: 990
Score: 1644.00 Matches: 305
Percent Similarity: 99.67% Conservative: 1
Best Local Similarity: 99.35% Mismatches: 1
Query Match: 99.46% Indels: 0
Gaps: 0
DB: 19
US-09-917-265-53 (1-307) x AAV13816 (1-990)
QY 1 IleTrpGluLeuGluLysAspValTyrValValGluLeuAspTrpHisProAspAlaPro 20
Db 67 ATATGGCAACTGAGCAAAAGATGTTATGTTGTAGAGTTGACCTGGACCCCTGATGCCCC 126
QY 21 GlyLuuMetValValLeuThrCysHisThrProGluGluAspAspIleThrTrpThrSer 40
Db 127 GGAGAAATGGTGGTCTCACCCTGCCATACCCCTGAAGAAGTGAATCACTTGGACCTCA 186
QY 41 AlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
Db 187 GCGCAGACGACTGAAGTCTTAGTTCGTGTAAGCTCTGACCATCCAAAGTAAGAAATTT 246
QY 61 GlyAspAlaGlyGlnTyrThrCysHisLysGlyLysValLeuSerArgSerLeuLeu 80
Db 247 GGAGATGCTGGCCAGTATACCTGCCATAAAGCAGCAAGTTTCGAGCCCTCACTCTG 306
QY 81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGlu 100
Db 307 TTGATTCACAAAAGAAAGATGAGAAATTGGTCCACTGATATCTTAAAGCAACAGAAAGAA 366
QY 101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
Db 367 TCCAAAATATAGATCTTCTGAAATGTGAGCAAGAAATATCTTGACGTTTCAACATGC 426
QY 121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
Db 427 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGCACAAAGAGCAGAGCCCTC 486
QY 141 SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgVal 160
Db 487 TCTGACCCCAAGGGGTGACATGTGAGACACTTTCAGCAGAGCGTCAGAGTG 546
QY 161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGlnLysSerAlaCysProSer 180
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Db 547 GACACAGGAGGATTATTAAGAAATACACAGTGGAGTGTGAGGAGGCGCATGCTGCCCTCT
Qy 181 AlaGluGluSerLeuProIleGluValValAlaSpAlaIleHisLysLeuTyrGlu 200
Db 607 GCCGAGGAGAGCCCTACCCATCGAGTGTGCTGCTGATCTTATTCACAAAGCTCAAGTATGAA 666
Qy 201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeu 220
Db 667 AACATACACAGCAGCCTTCTTCATCAGACATCATCAACACAGCCACCCACCAACCTG 726
Qy 221 GluLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
Db 727 CAGCTGAAGCCATTGGAATAATCTCGGACGTGAGGTGACGTGGGAATACCCCGACACC 786
Qy 241 TrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGluAlaGlnGlyLysAsn 260
Db 787 TGGAGCACCCACACTTCTACTTCTCTCTCCATCTTTCATACAGGCCACAGGCGCAAGAAC 846
Qy 261 AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValAlaCysHis 280
Db 847 AATAGAGAAAGAAAGATAGACTCTGCTGAGACAAGACCTCAGCCAAAGTGTGTCAC 906
Qy 281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsp 300
Db 907 AAGGATGCCAAGATCCCGCTGCACACCCGAGACCGGCTACTATAGTTTCATCTGAGCGAC 966
Qy 301 TrpAlaSerValSerCysSer 307
Db 967 TGGGCATCTGTGCCCTGCTGACT 987

RESULT 6
AAK35615
ID AAK35615 standard; cDNA to mRNA; 990 BP.
AC AAK35615;
XX
XX 09-JUL-1999 (first entry)
DT
XX
XX Nucleic acid encoding canine Interleukin-12 (IL-12).
DE
XX Interleukin-12; IL-12; dog; cat; immune disease; CatIL12; heterodimer;
KW tumour; skin disease; infectious disease; allergic disease; ds.
XX
XX Canis sp.
FH Key Location/Qualifiers
FT 1..990
FT CDS /*tag= a
XX
XX JP11106350-A.
XX
XX 20-APR-1999.
XX
XX 15-MAY-1998; 98BP-0133345.
XX
XX 07-AUG-1997; 97JP-0213755.
XX 16-MAY-1997; 97JP-0127690.
XX
XX (TORA ) TORAY IND INC.
XX
XX WPI; 1999-308068/26.
XX P-PSDB; AAY02339.
XX
XX A prevention and treating agent containing interleukin 12 (CatIL12) -
XX for prevention and treatment of dog and cat immune diseases
XX
XX Claim 1; Page 12; 16pp; Japanese.
XX
XX The present sequence encodes canine interleukin-12 (IL-12). The
XX specification describes a method for the prevention and treatment
XX of dog and cat immune diseases. The treatment used an agent comprising
XX dog IL-12 (CatIL12) proteins to form a heterodimer. The agent is

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CC useful for preventing and treating dog and cat immune diseases.
CC including tumours, skin diseases, infectious diseases and allergic
CC diseases.
XX
XX Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 1,6e-160 Length: 990
XX Score: 1644.00 Matches: 305
XX Percent Similarity: 99.67% Conservative: 1
XX Best Local Similarity: 99.35% Mismatches: 1
XX Query Match: 99.46% Indels: 0
XX DB: Gaps: 0
XX
XX US-09-917-265-53 (1-307) x AAK35615 (1-990)
Qy 1 IleTrpGluLeuGluLysAspValTyrValValGluLeuAspTrpHisProAspAlaPro 20
Db 67 ATATGGGAACCTGGAGAAAGATGTTATCTGTAGAGTGTGACTGGCACCCTGATGCCCC 126
Qy 21 GluLeuMetValValLeuThrCysHisThrProGluGluAspAspIleThrTrpHisr 40
Db 127 GGAGAAATGGTGTCTCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 186
Qy 41 AlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGlyPhe 60
Db 187 GCCACAGCAGCAGTGAAGTCTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 246
Qy 61 GlyAspAlaGlyGlnTyrThrCysHisLysGlyLysValLeuSerArgSerLeuLeu 80
Db 247 GGAGATGCTGGCAGATATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 306
Qy 81 LeuIleHisLysLysGluLysAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGlu 100
Db 307 TTGATTCACAAAAAGAAAGATGATGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 366
Qy 101 SerLysAsnLysIlePheLeuLysCysGlnAlaLysAsnTyrSerGlyArgPheThrCys 120
Db 367 TCCAAAAATTAAGATCTTCTGAAATGTGAGCAAAAGATTAATTCGTGACGTTTCACATGC 426
Qy 121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
Db 427 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTAAAGATGACAGAGCTTC 486
Qy 141 SerAspProGlnGlyValIleThrCysGlyAlaValIleThrLeuSerAlaGlyArgVal 160
Db 487 TCTGACCCCCCAAGGGGTGACATGTGAGCAGTACACTTTCAGCAGAAAGGTTCAGACTG 546
Qy 161 AsnAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProSer 180
Db 547 GACAAACAGGATTTAAGAAAGATACACAGTGTGCTGAGGAGGCGAGTGCCTGCCCTCT 606
Qy 181 AlaGluGluSerLeuProIleGluValValAlaSpAlaIleHisLysLeuTyrGlu 200
Db 607 GCCGAGGAGAGCCCTACCCATCGAGTGTGCTGCTGATCTTATTCACAAAGCTCAAGTATGAA 666
Qy 201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeu 220
Db 667 AACATACACAGCAGCCTTCTTCATCAGACATCATCAACACAGCCACCCACCAACCTG 726
Qy 221 GluLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
Db 727 CAGCTGAAGCCATTGGAATAATCTCGGACGTGAGGTGACGTGGGAATACCCCGACACC 786
Qy 241 TrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGluAlaGlnGlyLysAsn 260
Db 787 TGGAGCACCCACACTTCTACTTCTCTCTCCATCTTTCATACAGGCCACAGGCGCAAGAAC 846
Qy 261 AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValAlaCysHis 280
Db 847 AATAGAGAAAGAAAGATAGACTCTGCTGAGACAAGACCTCAGCCAAAGTGTGTCAC 906
Qy 281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsp 300

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Db      907 AACGATGCCAAGATCCCGCAAGCCGACCGCTACTATGATTCATCTCGAGCGAC 966
Oy      301 TTPAlaserValserCysSer 307
Db      967 TGGGCATCTGTGCGCTGCAGT 987

RESULT 7
AA03152
ID      AAX03152 standard: cDNA to mRNA: 990 BP.
XX
AC      AAX03152:
XX
DT      30-MAR-1999 (first entry)
XX
DE      Nucleic acid encoding canine interleukin 12.
XX
KW      Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW      skin disease; viral infection; allergic disease; breast tumour;
KW      eosinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW      othematoma; pneumoedema; skin soft pedicled soft tumour; anal tumour;
KW      otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW      allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW      dog parvovirus infection; distemper virus; cat plaque virus infection;
KW      feline leukaemia; allergy; pollinosis; ds.
XX
OS      Canis sp.
XX
FH      Key
FT      Location/Qualifiers
FT      CDS
FT      1..990
FT      /tag= a
FT      /product= Interleukin_12
PN      WO951327-A1.
XX
PD      19-NOV-1998.
XX
PF      07-MAY-1998: 98WO-JP02031.
XX
PR      16-MAY-1997: 97JP-0127690.
XX
PA      (TORA ) TORAY IND INC.
PI      Okano F, Satoh M, Yamada K:
XX
DR      WPI: 1999-070100/06.
DR      P-PSDB: AAM84371.
XX
PT      New therapeutic and prophylactic agents - comprise
PT      genetically-engineered canine interleukin 12, used to treat, e.g.
PT      canine and feline immunological diseases
XX
PS      Claim 1: Page 23-25: 45pp: Japanese.
XX
CC      The present sequence encodes a canine interleukin 12 (IL-12) protein.
CC      The IL-12 protein can be used in therapeutic or prophylactic agents.
CC      The agents can be used to prevent and treat canine and feline
CC      immunological diseases including dog and cat tumours, skin diseases,
CC      viral infections and allergic diseases, especially tumours, breast
CC      tumour, eosinophilic granuloma, epidermoid tumour, skin tumour, lipoma,
CC      othematoma, pneumoedema, skin soft pedicled soft tumour and anal
CC      tumour; skin diseases, otitis externa, dermatitis, eczema, fungal
CC      diseases of the skin, pyoderma, allergic dermatitis, nettle rash,
CC      traumatic dermatitis and hair loss; infections; dog parvovirus infection
CC      and distemper virus, cat plaque virus infection and feline leukaemia, and
CC      allergic diseases, e.g. pollinosis.
XX
SQ      Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 other;
XX

Alignment Scores:
Pred. No.: 166-160 Length: 990
Score: 1644.00 Matches: 305
Percent Similarity: 99.67% Conservative: 1

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Best Local Similarity: 99.35% Mismatches: 1
Query Match: 99.46% Indels: 0
DB: 20 Gaps: 0
US-09-917-265-53 (1-307) x AAX03152 (1-990)

Oy      1 ILETPGLUeugluLysAspValTyrValValGluLeuAspTrpHisProAspAlaPro 20
Db      67 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGAGCTGGACCTGATGCCCCC 126
Oy      21 GlycLueValValLeuThrCysHisThrProGluLysAspSpleThrTrpThrSer 40
Db      127 GGAGAAATGSGTGCTCCTCACCCTGCATACCCCTGAAGAGATGACATCTGGACCTCA 186
Oy      41 AlaGlnSerSerGluValIleuGlySerGlyLysThrIleuThrIleGlnValLysGluPhe 60
Db      187 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTGAACCTGTGACCAATCCAAAGATTTT 246
Oy      61 GlyAspAlaGlnTyrThrCysHisLysGlyGlyLysValLeuSerArgSerLeuLeu 80
Db      247 GGAGATGCTGGCCAGTATACCTGCGCATAAAGAGCGCAAGTTCTGAGCCGCTCCTCTG 306
Oy      81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGlu 100
Db      307 TTGATTCACAAAGAAAGATGAATTTGGTCCACGTATCTTAAGGAAGAAAGAA 366
Oy      101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
Db      367 TCCAAAATTAAGATCTTCTGAAATGAGGCAAGAAATTAATCTGGACGTTTCACATGC 426
Oy      121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
Db      427 TCGTGCGCTGACGGCAATCACTACTGATTTGAAATTCAGTGTCCAAAGATACAGAGCTTC 486
Oy      141 SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgVal 160
Db      487 TCTGACCCCAAGAGGGGTGACATGTGGAGCAGTACACTTCACAGCAGAGGTCAGAGTG 546
Oy      161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGlnLysSerAlaCysProSer 180
Db      547 GACAAACAGGATTAATAAGATGACACAGTGCAGTGCAGGACGCAATGCTGCCCTCT 606
Oy      181 AlaGlnLysSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
Db      607 GCGGAGAGAGCCTACCACATCGAGGTGTGTGTGATCTATTCCAAAGCTCAAGTATGAA 666
Oy      201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPheAsnLeu 220
Db      667 AACTACACCGCAGAGCTTCTTCATCAGACATCATCAAAACCCAGCCCAAAACCTG 726
Oy      221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
Db      727 CAGCTGAAGCCATTGGAATAATTCGCGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 786
Oy      241 TrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 260
Db      787 TGGAGACACCCCAATTCTCTACTTCTCCCTACATTTTGCTACAGGCCCGCCAGCAGAAC 846
Oy      261 AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValLysHis 280
Db      847 AATGAGAAAGAAAGAAATATACACTCTCGTGCAGCAAGCCCTCACCAGGTCGTGTGCAC 906
Oy      281 LysAspAlaLysIleLeuArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsp 300
Db      907 AACGATGCCAAGATCCGCGTGAAGCCCGAGACCGCTACTATAGTTCATCTGGAAGCAG 966
Oy      301 TTPAlaserValserCysSer 307
Db      967 TGGGCATCTGTGCGCTGCAGT 987

RESULT 8
AA164378
ID      AA164378 standard: DNA: 990 BP.

```

```

XX AC AA164378;
XX XX 23-NOV-2001 (first entry)
XX DE Canine coding sequence #1.
XX XX Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
XX OS Canis familiaris.
XX FH Key
XX FT CDS 1..990 Location/Qualifiers
XX FT sig_peptide 1..66 /product= "Canine protein #1"
XX FT mat_peptide 67..387 /tag= b
XX FT /tag= c
XX PN JP2001161378-A.
XX PD 19-JUN-2001.
XX PF 26-SEP-2000; 2000JP-0292946.
XX PR 01-OCT-1999; 99JP-0281234.
XX PA (TORA ) TORAY IND INC.
XX DR WPI; 2001-592466/67.
XX DR P-PSDB; AAG66480.
XX PT Preparation of a highly pure protein, interleukin 12, a protein
XX PT inhibiting the activity of interleukin 12, and a treating agent and a
XX PT treating method for immunopathy of mammalian
XX PS Claim 6; Page 14; 21pp; Japanese.
XX CC The present invention relates to a method for the preparation of a highly
XX CC pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
XX CC the activity of IL12 is contacted to an ion exchanging carrier and/or a
XX CC pigment carrier to get IL12 and/or a protein inhibiting the activity of
XX CC IL12. The protein is used as a preventive agent for dog immunopathy. The
XX CC present sequence was used in the method of the present invention.
XX SQ Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 other;

Alignment Scores:
Pred. No.: 1,6e-160 Length: 990
Score: 1644.00 Matches: 305
Percent Similarity: 99.67% Conservative: 1
Best Local Similarity: 99.35% Mismatches: 1
Query Match: 99,46% Indels: 0
DB: 22 Gaps: 0

US-09-917-265-53 (1-307) x AA164378 (1-990)
OY 1 IietrpgluLeugluLysAspValTyrValValGluLeuAspTrpHisProAspAlaPro 20
DB 67 AATGGCACTGGAGAAAGATGTTATGTTGTAAGATTGGACTGGACCCCTGATGGCCCC 126
OY 21 GlyIuMetValValLeuThrCysHisThrProGluGluAspAspIleThrTrpTrpSer 40
DB 127 GGAGAAATGCTGCTCACTGACCTACCTGCAAGAAAGATGACATCACTTGACCTCA 186
OY 41 AlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
DB 187 GCGCAGACGACGTAAGATCTAGCTCTGCTGTAAGAACTGACCATCCAAAGCAATTT 246
OY 61 GlyAspAlaGlyGlyThrCysHisLysGlyGlyValLeuSerArgSerLeuLeu 80
DB 247 GCGATGCTGGCCAGTATACCTGCTCAATTAAGAGGCGAAGTTCTGAGCGCTACTCTG 306

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OY 81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluIleLysGlu 100
DB 307 TTGATTTCAACAAAAGAGATGCAATTGGCTCCACTGATATCTTAAGGAACAGAAAGA 366
OY 101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
DB 367 TCCAAAATAATAGATCTTCTGAAATGTGAGGCAAGAAATATTTGGACGTTTCATGTC 426
OY 121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerArgGlyPhe 140
DB 427 TGGTGGCTGACGGCAATCAGTACTGATTGAAATTCAGTGTCAAAAGTAGCAGAGCTTC 486
OY 141 SerAspProGluGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgVal 160
DB 487 TCTGACCCCCCAAGGGGTGACATGTGTGAGACAGACACTTTCAGCAGAGGGGTGAGAGTG 546
OY 161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluLysSerAlaCysProSer 180
DB 547 GACAACAGGATTTATAGAAATACACAGTGAAGTGTCAAGAGGCGAGGCGCCCTCTT 606
OY 181 AlaGluGluSerLeuProIleGluValValAlaAspAlaIleHisLysLeuLysTyrGlu 200
DB 607 GCCGAGAGAGAGCTTACCCATCGAGGTCGTGGTGATCTATTACAAAGCTCAAGTATGAA 666
OY 201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeu 220
DB 667 AACTACACACGAGCTTCTTCATCAGACATCATCAAAACAGACCACCCCAAAACCTG 726
OY 221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
DB 727 CAGCTGAAACCAATTTGAAAATTTCTCGGACGCTGAGGCTCAGTGGGAATATCCCAACC 786
OY 241 TrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnLysAsn 260
DB 787 TGGAGCACCCCATTTCTTCTTCTCCGACATTTTGGCATACAGGCCAGGGCAAGAAG 846
OY 261 AsnArgGluLysLysAspArgLeuCysValaLysLysThrSerAlaLysValaLysHis 280
DB 847 AATGAGAAAGAAAGATAGACTGTGGCGAGCAAGACTCAGCCAAAGCTGTCGCGAC 906
OY 281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsp 300
DB 907 AAGGATGCCAAGATCCGCTGCAAGCCGAGACCCCTACTATATGTTCAATCTGAGAGCAG 966
OY 301 TrpAlaSerValSerCysSer 307
DB 967 TGGCATCTGTGCTGCTGCACT 987

RESULT 9
AA18177
ID AAX18177 standard; cDNA; 924 BP.
XX AC AAX18177;
XX DT 07-MAY-1999 (first entry)
XX DE Canine mature CLAF p40 subunit coding sequence.
XX KW CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
XX KW viral disease; canine distemper; canine parvovirus; autoimmune disease;
XX KW canine infectious hepatitis; ds.
XX OS Canis sp.
XX PN WO985511-A1.
XX PD 10-DEC-1998.
XX PF 26-MAY-1998; 98WO-JP02295.
XX PR 03-JUN-1997; 97JP-0161936.
XX XX

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PA (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.
 XX
 PI Eda Y, Imamura T, Maeda H, Tokiyoshi S:
 XX WPI: 1999-070260/06.
 DR P-PSDB; AAW74323.
 XX
 PT Canine cytokine protein which activates canine cytotoxic T
 PT lymphocytes - is useful for treatment of viral and autoimmune
 PT diseases in dogs
 XX
 PS Claim 8; Page 32; 51pp; Japanese.
 XX
 CC This sequence encodes the canine lymphocyte activation factor (CLAF) of
 CC the invention. CLAF activates lymphocytes, especially canine cytotoxic
 CC T cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
 CC recognising it may be used in the treatment of viral diseases in dogs
 CC (such as canine distemper, canine parvovirus and canine infectious
 CC hepatitis). The antibodies may also be used in isolation of CLAF from
 CC culture of the transformant host cells by affinity chromatography. The
 CC p40 homodimer can be used for the treatment of autoimmune diseases in
 CC dogs.

XX
 SO Sequence 924 BP; 273 A; 222 C; 234 G; 195 T; 0 other:

Alignment Scores:

| Pred. No.: | 6,35e-158 | Length: | 924 |
|------------------------|-----------|---------------|-----|
| Score: | 1618.50 | Matches: | 303 |
| Percent Similarity: | 98.70% | Conservative: | 1 |
| Best Local Similarity: | 98.38% | Mismatches: | 3 |
| Query Match: | 97.91% | Indels: | 1 |
| DB: | 20 | Gaps: | 1 |

US-09-917-265-53 (1-307) x AAX18177 (1-924)

```

QY      1  TTTTGTGluLeuGluLysAspValTyrValValGluLeuAspTrpHisProAspAlaPro 20
DB      1  ATATGGAACTCGAAGAAAGATGTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCC 60
QY      21  GtGluMetValValLeuThrCysHisThrProGluGluAspLysIleThrTrpHisSer 40
DB      61  CGAGAAATGCTGGTCTCCTCACCCTGCACTCCCTGAAGAAGATGACATCACTTGAGACTTCA 120
QY      41  AlaGlnSerSerGluValLeuGluLysSerGlyLysTrpLeuThrIleGluValLysGluPhe 60
DB      121  CGCGAGACAGTGAAGTCTCTAGCTTCTGTTAAACTCTGACCATTCACCAATTT 180
QY      61  GtLysAlaGluGlnTyrThrCysHisLysGlyLysValLysSerArgSerLeuLeu 80
DB      181  GCAGATGCTGGCAGTATACCTGCCATTAAGGAGCAAGGTTCTGAGCCGCTCAGCTCTG 240
QY      81  Leu---IleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluLys 99
DB      241  TTTGATTCACAAAAAGAAAGATGAAATTTGCTCCACTGATATTTTAAAGGAGACAGAA 300
QY      100  GluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThr 119
DB      301  GAATGCCAAATAAATTAAGATCTTTCTGAAATGTCGAGCAAGAAATTAATTTCTGACGTTTCA 360
QY      120  CysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGly 139
DB      361  TCTCTGCTGCTGACCGCAATCAGTACGATTGAAATTCAGTCAAAAGTAGCAGAGGC 420
QY      140  PheSerAspProGlnGlyValTyrCysGlyAlaValThrLeuSerAlaGluArgValArg 159
DB      421  TTCTTGACCCCAAGGGGTGACATGTGAGCAGTGCACCTTTCAGCAGAGGGGTTCACA 480
QY      160  ValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerLacysPro 179
DB      481  CTGGACACACGAGGATTAAGACAGTACACAGTGCAGAGGAGGAGGAGTCCCTGCCCC 540
QY      180  SerAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyr 199

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DB      541  TCTGCCGAGAGAGACCTACCCATCGAGGTCTGTGTGATGCTATTTCACAAGCTCAAGTAT 600
QY      200  GluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProThrAsn 219
DB      601  GAAACTACACAGAGAGCTTCTTCATCAGAGACATCATCAAAACAGAGCCACCAAAAC 660
QY      220  LeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAsp 239
DB      661  CTGCAGCTGAACCATTTGAAAATTTCTCGCACACGTGAGAGTACCTGGAAATACCCCGAC 720
QY      240  ThrTrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLys 259
DB      721  ACCTGAGACACCCACATCTCTTCTCTCCCTGACATTTTGCATACAGGCCAGGGCAAG 780
QY      260  AsnAsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValCys 279
DB      781  AACCAATAGGAAAGAAAGATGACTCTGCTGGACAAAGCCTCAGCCCAAGGTCGTGTC 840
QY      280  HisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerTrpSer 299
DB      841  CACAAGATGCCAAGATCCGCGCTGCAGAGCCGACAGCCGCTACTATAGTTCATCCTGGAGC 900
QY      300  AspTrpAlaSerValSerCysSer 307
DB      901  GACTGGCATCTGTGTCTCTGAGT 924

```

RESULT 10

AAX18176
 ID AAX18176 standard; cDNA; 2154 BP.

AC AAX18176;

DT 07-MAY-1999 (first entry)

DE Canine full length CLAF p40 subunit coding sequence.

XX CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;

KW viral disease; canine distemper; canine parvovirus; autoimmune disease;

KW canine infectious hepatitis; ds.

OS Canis sp.

PN WO9855511-A1.

PD 10-DEC-1998.

PF 26-MAY-1998; 98WO-JP02295.

PR 03-JUN-1997; 97JP-0161936.

PA (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.

XX Eda Y, Imamura T, Maeda H, Tokiyoshi S;

DR WPI: 1999-070260/06.

XX P-PSDB; AAW74322.

PT Canine cytokine protein which activates canine cytotoxic T

XX lymphocytes - is useful for treatment of viral and autoimmune

XX diseases in dogs

XX Claim 8; Page 30-31; 51pp; Japanese.

CC This sequence encodes the canine lymphocyte activation factor (CLAF) of
 CC the invention. CLAF activates lymphocytes, especially canine cytotoxic
 CC T cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
 CC recognising it may be used in the treatment of viral diseases in dogs
 CC (such as canine distemper, canine parvovirus and canine infectious
 CC hepatitis). The antibodies may also be used in isolation of CLAF from
 CC culture of the transformant host cells by affinity chromatography. The
 CC p40 homodimer can be used for the treatment of autoimmune diseases in
 CC dogs.

Sequence 2154 BP; 663 A; 448 C; 477 G; 566 T; 0 other;

Alignment Scores:

Pred. No.: 2,04e-157 Length: 2154
Score: 1618.50 Matches: 303
Percent Similarity: 98.70% Conservative: 1
Best Local Similarity: 98.38% Mismatches: 3
Query Match: 97.91% Indels: 1
DB: 20 Caps: 1

US-09-917-265-53 (1-307) x AAX18176 (1-2154)

```

QY 1 ILETRGLUENGLULYSASPVALLTYRVAIValGLUENASPTPHISPROASPALAPro 20
   |||||
Db 118 ATATGGGAACCTGGAGAAAGATGTTATGTTGTAAGTTGACTGGACCTGATGCCCC 177
QY 21 GLYGLUETValValLeuThrCysHisThrProGluGluAspAlIeThrThrSer 40
   |||||
Db 178 GGAGAAATGGTGGCTCACCCTGACCTGACCTGAAGAGATGACATCTGGACCTCA 237
QY 41 AlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
   |||||
Db 238 GCGGAGAGCAGTGAAGCTCCTAGTTCGTGTAATAAATCTGACCATCCAAAGCAATTT 297
QY 61 GLYASPAIAGlyInTyThrCysHisLysGlyGlyLysValLeuSerArgSerLeu 80
   |||||
Db 298 GGAGATGCTGGCCAGTATACCTGCTGCAATAAGAGAGGATTTGAGACCCCTCCTCTG 357
QY 81 Leu---IleHisLysLysGluAspGlyIleThrSerThrAspIleLeuLysGluGlnLys 99
   |||||
Db 358 TTTCATTTCCACAAAAAGAAAGATGAGAAATTTGCTCCACTGATATCTTAAAGGAACAGAAA 417
QY 100 GlnSerLysAsnLysIlePheLeuLysCysGlnValLysAsnTySerGlyArgPheThr 119
   |||||
Db 418 GAATCCAAAAATAGATCTTCTGCAATGTGAGCAAAAGATTTCTGGACCTTACACA 477
QY 120 CysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerArgGly 139
   |||||
Db 478 TGCTGTGGCTGAGCGCAATCAGTACGATTTGAAATTCAGTCCAAAGAGACAGAGGC 537
QY 140 PheSerAspProGlnGlyValIleThrCysGlyValAlaValIleLeuSerAlaGluArgValArg 159
   |||||
Db 538 TTCTCTACCCCCCAAGGGGTGACATGTGGAGCAGTGCACCTTGTAGAGAGGGGTAGA 597
QY 160 ValAspAsnArgAspTyThrLysTyThrValGluLysGlnGlnGlySerAlaCysPro 179
   |||||
Db 598 GTGGACAACAGAGGATTTAAGAAATACACAGTGAAGTGTGAGAGGGGACAGTGCCTGCC 657
QY 180 SerIleAlaGluSerLeuProIleGluValValAlaLysPalaIleHisLysLeuLysTy 199
   |||||
Db 658 TCTGCCGAGGAGACCTTACCATCGAGTGGTGGTGTGATCTATTCACAAAGCTCAAGTAT 717
QY 200 GlnAsnTyThrSerSerPhePheIleArgAspIleIleLysProAspPropProThrAsn 219
   |||||
Db 718 GAAAACTACACACAGACCTTCTCATCAGACATCTCAAAACCAAGCCACCCACAAAC 777
QY 220 LeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyProAsp 239
   |||||
Db 778 CTGCAGCTGAAGCCATGAAAAATTTCTGGCAGCTGAGAGTGCACCTGGAAATACCCGAC 837
QY 240 ThrTrpSerThrProHisSerTyThrPheSerLeuThrPheCysIleGlnAlaGlnGlyLys 259
   |||||
Db 838 ACCGAGAGCACCACCATCTTCTTCTCCCTGCAATTTTGCAATACAGGCCCGAGGCAAG 897
QY 260 AsnAsnArgGlnLysLysAspArgLeuCysValAspLysThrSerAlaLysValValCys 279
   |||||
Db 898 AACATATGAGAAAGAAAGATAGACTGCTGGTGGAGCAAGACCTGAGCCAAAGGTGCTGC 957
QY 280 HisLysAspAlaLysIleArgValGlnAlaArgAspArgTyThrTySerSerSerTrpSer 299
   |||||
Db 958 CACAAAGATGCCAAAGATCCGGGTGCAAGCCGAGAGCCGACTACTATTCATCTCTGAGC 1017
QY 300 AspTrpAlaSerValSerCysSer 307

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Db 1018 GACTGGGCAATCTGTCTGCTGCACT 1041
RESULT 11
AAV56626
ID AAV56626 standard; cDNA; 921 BP.
AC AAV56626;
XX
XX 23-NOV-1998 (first entry)
DE Feline FLAfp40 cDNA mature transcript #1.
XX
XX Cytokine; feline; FLAfp40; FLAfp35; heterodimer; cytotoxic; treatment;
KW T lymphocyte cell; autoimmune disease; ds.
XX
XX Felis catus.
XX
XX W09746583-A1.
XX
XX 11-DEC-1997.
XX
XX 29-MAY-1997; 97MO-JP01824.
XX
XX 04-JUN-1996; 96JP-0165249.
XX
XX (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
XX Fujiyasu T, Imagawa Y, Imamura T, Maeda H, Tokiyoshi S;
XX WPI; 1998-042118/04.
XX DR P-PSDB; AAW76174.
XX
XX Novel feline cytokine protein - useful for treating feline
PT auto-immune diseases, e.g. those caused by feline herpes virus or
PT feline calicivirus
XX
XX Claim 20; Page 55; 94pp; Japanese.
XX
XX This sequence encodes a novel feline cytokine mature protein, FLAfp40.
CC CC This protein can be used in the production of a FLAfp35/FLAfp40
CC heterodimer which can potentiate the cytotoxic activity of feline
CC cytotoxic T lymphocyte cells. Such proteins are used for treatment
CC of feline autoimmune diseases e.g. as caused by feline herpes virus
CC or feline calicivirus.
XX
XX
SQ Sequence 921 BP; 276 A; 227 C; 231 G; 187 T; 0 other;

Alignment Scores:
Pred. No.: 3e-151 Length: 921
Score: 1554.00 Matches: 288
Percent Similarity: 96.74% Conservative: 9
Best Local Similarity: 93.81% Mismatches: 10
Query Match: 94.01% Indels: 0
DB: 19 Gaps: 0

US-09-917-265-53 (1-307) x AAV56626 (1-921)
QY 1 ILETRGLUENGLULYSASPVALLTYRVAIValGLUENASPTPHISPROASPALAPro 20
   |||||
Db 1 ATATGGGAACCTGGAGAAAGATGTTATGTTGTAAGATTTGACTGGACCTGATGCCCC 60
QY 21 GLYGLUETValValLeuThrCysHisThrProGluGluAspAlIeThrThrSer 40
   |||||
Db 61 GGAGAAATGGTGGCTCACCCTGACCTGACCTGAAGAGATGACATCTGGACCTCA 120
QY 41 AlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
   |||||
Db 121 GACCAAGAGAGTGAATCTCTAGGCTGTGTAATAAATCTGACCATCCAAAGCAATTT 180
QY 61 GLYASPAIAGlyInTyThrCysHisLysGlyGlyLysValLeuSerArgSerLeu 80
   |||||
Db 181 GGAGATGCTGGCCAGTATACCTGCTGCAATAAGAGAGGATTTGAGACCTTCTCTC 240

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OY      81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGlu
DB      241 CTGATACGACAAAGAGATGCAATTGGTCCACTGATATCTTAAGCGAAGACAGAAAGAA
OY      101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyRSerGlyArgPheThrCys
DB      301 TCCAAAATAAGATCTTTCTTAAATGTGAGCCAAAGAAATTATTCGACGTTTCACCTGC
OY      121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe
DB      361 TCGTGCGCTGACGGAATCAGTACGATTTGAATTCACTGTCAAAAGCAGACAGAGCTCC
OY      141 SerAspProGlnGlyValThrCysGlyValAlaValThrLeuSerAlaGluArgValArgVal
DB      421 TCTACCCCCCAAGGGGTGACTGTGTGACACGACGACACTCTCAGCAGAGAAGCTCAGAGTG
OY      161 AspAsnArgAspTyRLeuLysLysTyRThrValGluCysGlnGlySerAlaCysProSer
DB      481 GACAACAGCGATTTAAGAACTACACAGTGAAGTCTCAGAGGCGAGTCCCTGCCCGCT
OY      181 AlaGluGluSerLeuProLeuGluValValAlaAspAlaIleHisLysLeuLysTyRGl
DB      541 GCCGAGAGAGCCCTACCCATTGAAGTCGTGGTGAAGCTATTCACAACTCAAGTACGAA
OY      201 AsnTyRThrSerSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeu
DB      601 AACTACACGACGACCTTCTTCATCAGGACATCATCAAAACCGGACCCCAACAGAACCTG
OY      221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyRProAspThr
DB      661 CAATGGAAGCCATTAAAAATTTCTGGCATGTGGAAGTGAAGTGGAGTATACCTGCACACC
OY      241 TrpSerThrProHisSerTyRPheserLeuThrPheCysIleGlnAlaGlnGlyLysAsn
DB      721 TGGGACACCCCACTTCCTACTCTCTTAACATTGGCGGTACAGGTCCAGGCGCAAGAAC
OY      261 AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValValCysHis
DB      781 AACGAGACAAAGAAAGACAGACTCTCGTGGACAAAGACTCAGCCAGGTCTGTGCCAC
OY      281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyRTrpSerSerSerTrpSerAsp
DB      841 AAGGATCCCAAGATCCCGTCCAGCAGAGACCGCTACTATAGCTCATCTCGAGACAAAC
OY      301 TrpAlaSerValSerCysSer 307
DB      901 TGGCATCCGTGTCTCTGCACT 921

RESULT 12
AAV5627
ID      AAV5627 standard; cDNA; 921 BP.
XX      AC      AAV5627;
XX      DT      23-NOV-1998 (first entry)
XX      DE      Feline FLAfp40 cDNA mature transcript #2.
XX      KW      Cytokine; feline; FLAfp40; FLAfp35; heterodimer; cytotoxic; treatment;
XX      KW      T lymphocyte cell; autoimmune disease; ds.
XX      OS      Felis catus.
XX      PN      M09746583-A1.
XX      PD      11-DEC-1997.
XX      PF      29-MAY-1997; 97WO-JP01824.
XX      PR      04-JUN-1996; 96JP-0165249.
XX      PA      (KAGA ) CHEMO-SERO-THERAPEUTIC RES. INST.
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```
XX      FUjiyasu T, Imagawa Y, Imamura T, Maeda H, Tokiyoshi S:
PI      WPI: 1998-042118/04.
DR      P-PSDB: AAW76174.
XX      Novel feline cytokine protein - useful for treating feline
PT      auto-immune diseases, e.g. those caused by feline herpes virus or
PT      feline calicivirus
XX      Claim 21: Page 56-57; 94pp; Japanese.
PS      This sequence encodes a novel feline cytokine mature protein, FLAfp40.
CC      This protein can be used in the production of a FLAfp35/FLAfp40
CC      heterodimer which can potentiate the cytotoxic activity of feline
CC      cytotoxic T lymphocyte cells. Such proteins are used for treatment
CC      of feline autoimmune diseases e.g. as caused by feline herpes virus
CC      or feline calicivirus.
SQ      Sequence 921 BP; 276 A; 228 C; 230 G; 187 T; 0 other:
```

Alignment Scores:

| | | | |
|------------------------|---------|---------------|-----|
| Pred. No.: | 3e-151 | Length: | 921 |
| Score: | 1554.00 | Matches: | 288 |
| Percent Similarity: | 96.74% | Conservative: | 9 |
| Best Local Similarity: | 93.81% | Mismatches: | 10 |
| Query Match: | 94.01% | Indels: | 0 |
| DB: | 19 | Gaps: | 0 |

US-09-917-265-53 (1-307) x AAV5627 (1-921)

```
OY      1 IleTrpGluLeuGluLysAspValTyRValAlaGluLeuAspTrpHisProAspAlaPro
DB      1 ATATGGACACTGGAGAAAGAAAGCTTATGTCTTACAGTTGGACTGGACCTGATGCCCC
OY      21 GlyIleValValLeuThrCysHisThrProGlnGluAspAspIleThrTrpThrSer
DB      61 GCAGAAATGCGTGCCTCACCCTCAATATCTCTGAAGAAATGATCATCCTGACCTGACCTCT
OY      41 AlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe
DB      121 GACCAGACAGCTGAAGTCTTAGGCTGTGTAAACTGTGACCATTCAGTCAAGAAATTT
OY      61 GlyAspAlaGlyGlnTyRThrCysHisLysGlyLysValLeuSerArgSerLeuLeu
DB      181 GCAGATGCTGGCCAGTATACCTGTATTAAGAGAGCGAGGTTCTGAGCCATTCTCTCTC
OY      81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGlu
DB      241 CTGATACGACAAAGAAAGATGGAATTGGTCCACTGATATCTTAAGGAAACAGAAAGAA
OY      101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyRSerGlyArgPheThrCys
DB      301 TCCAAAATAAGATCTTTCTTAAATGTGAGCCAAAGAAATTATTCGACGTTTCACCTGC
OY      121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe
DB      361 TCGTGCGCTGACGGAATCAGTACGATTTGAATTCACTGTCAAAAGCAGACAGAGCTCC
OY      141 SerAspProGlnGlyValThrCysGlyValAlaValThrLeuSerAlaGluArgValArgVal
DB      421 TCTGACCCCCCAAGGGGTGACTGTGTGACACGACGACACTCTCAGCAGAGAAGCTCAGAGTG
OY      161 AspAsnArgAspTyRLeuLysLysTyRThrValGluCysGlnGlySerAlaCysProSer
DB      481 GACAACAGCGATTTAAGAACTACACAGTGAAGTCTCAGAGGCGAGTCCCTGCCCGCT
OY      181 AlaGluGluSerLeuProLeuGluValValAlaAspAlaIleHisLysLeuLysTyRGl
DB      541 GCCGAGAGAGCCCTACCCATTGAAGTCTGTGGAGCTTATTCACAACTCAAGTACGAA
OY      201 AsnTyRThrSerSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeu
```

Db 601 AACTACACGACGACCTTCTTCATCAGGACATCATCAACCGGACCCCAAGAACCTG 660
QY 221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTrpProAspThr 240
Db 661 CAACTGAGCATTAAATAATTTCTCGCATGTGGAAGTGAGCGGGAATTCCTGACACC 720
QY 241 TrpSerThrProHisSerTrpPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 260
Db 721 TGGAGACCCCATCTCTCTCTCTTAAACATTTGGCTACAGGTCCAGGCAAGAAC 780
QY 261 AsnArgGluLysLysAspArgLeuGlyValAspLysSerIleAlaValLysHis 280
Db 781 AACAGAGAAAGAAAGACAGACTCTCCGTGACAAAGACCTCAGCCAAAGGTCGTGCGCAC 840
QY 281 LysAspAlaLysIleArgValGlnAlaArgAspArgTrpTrpSerSerSerTrpSerAsp 300
Db 841 AAGGATGCCAAGATCCGCGTGCAGACGACGACCGCTACTATAGCTCATCTCTGAGCAAC 900
QY 301 TrpAlaSerValSerCysSer 307
Db 901 TGGGCAATCCGTCCTGCACT 921
RESULT 13
AAF26082
ID AAF26082 standard; DNA: 990 BP.
XX
AC AAF26082;
XX
DT 24-APR-2001 (first entry)
XX
DE Feline IL-12p40 encoding DNA SEQ ID 8.
XX
KW Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KM Interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
OS
XX Felis sp.
XX MO200104280-A2.
XX 18-JAN-2001.
PD 08-JUL-2000; 2000MO-DE02262.
PF 08-JUL-1999; 99CH-0001258.
PR 08-JUL-1999; 99CH-0001258.
XX
PA (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA (UYZU-) UNIV ZUERICH.
XX
PI Leutenegger C, Schrott M, Wittig B, Lutz H;
XX WPI; 2001-147190/15.
DR
XX
XX Vaccine for treating or preventing lentivirus infection in cats,
PT contains nucleic acid sequence encoding viral protein under control of
PT eukaryotic promoter -
XX
PS Claim 14; Page 36; 37pp; German.
XX
XX This invention describes a novel vaccine (A) for prevention or treatment
CC of lentivirus infection in felines which comprises an immunizing nucleic
CC acid sequence (I) that contains, or comprises, at least part of a gene
CC encoding a protein (II) of the virus, under control of a eukaryotic
CC promoter functional in the relevant animal. (II) is especially the
CC envelope (env) protein. The invention also describes (1) vaccine (A)
CC containing an immunizing protein, or fragment, from a lentivirus plus at
CC least one of interleukin (Il)-12 and/or -16; and (2) preparation of a
CC lentivirus protein, or fragment, especially derived from feline immune
CC deficiency virus (FIV), by expressing the corresponding nucleic acid
CC sequence in a host cell. The products of the invention have antiviral
CC activity. The vaccine (A) and related protein-based vaccines, are
CC particularly used to treat or prevent lentivirus infections in domestic
CC cats, especially feline immune deficiency virus (FIV). Vaccination with
CC (A) allows differentiation between vaccinated and infected animals, from

CC the antibody status. The vaccines may be formulated with an adjuvant
CC (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC immune response, particularly a Th1 response.
XX
SQ Sequence 990 BP; 283 A; 249 C; 248 G; 210 T; 0 other;
Alignment Scores:
Pred. No.: 3,32e-151 Length: 990
Score: 1594.00 Matches: 288
Percent Similarity: 96.74% Conservative: 9
Best Local Similarity: 93.81% Mismatches: 10
Query Match: 94.01% Indels: 0
DB: 22 Gaps: 0
US-09-917-265-53 (1-307) x AAF26082 (1-990)
QY 1 IietrGluLeuGluLysAspValIyValIValGluLeuAspTrpHisProAspAlaPro 20
Db 67 ATATGGGAACGTGAGAAACGTTATGTTGTAAGAGTTGAGCTGCACCCGTATGCCCCC 126
QY 21 GlyGluMetValIValLeuThrCysHisThrProGluGluAspAlaIleThrTrpHiser 40
Db 127 GGAGAAATGTGTGTCTCTTACCTGCATTAATCTCTGGAAGAAGATGACATCCTGACACT 186
QY 41 AlaGlnSerSerGluValLeuGlySerGlyLysTrpLeuThrIleGlnValLysGluPhe 60
Db 187 GACCAAGACGAGTAAGACTCTAGGCTCTGTAACCTGACCATCCAACTCAAGAAATTT 245
QY 61 GlyAspAlaGlyGlyTrpThrCysHisLysGlyGlyValLeuSerArgSerLeu 80
Db 247 GCAGATGCTGGCCAGTATACCTGTCTTAAGAGAGGAGGAGCTGTGAGCCATTCTTC 306
QY 81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluLysGlu 100
Db 307 CTGATACACAAAAGAGATGAAATTTGTCACATGATATCTTAAGGACACAAAGAA 366
QY 101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTrpSerGlyArgPheThrCys 120
Db 367 TCCAAAATTAAGATCTTTCTAAATGTGAGCAAAATTAATTCGTGAGCTTTCACCTGC 426
QY 121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgLysPhe 140
Db 427 TGTGTGCTACGCGCAATCAGTACCGATTGGAATTCACGTCAAAAAGCAGCAGAGCTCC 486
QY 141 SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgVal 160
Db 487 TCTGACCCCAAGAGGGGTACTGTGAGCAGCAGACACTCTCAGCAAGAGAGTCAAGAG 546
QY 161 AspAsnArgAspTrpLysLysTrpThrValGluCysGlnGluGlySerAlaCysProSer 180
Db 547 GACAAACAGGATTATTAAGATACAGAGTGAAGTCAAGAGGAGGAGTCCCGCGCT 606
QY 181 AlaGluGlnSerLeuProIleGluValValAlaValAlaIleHisLysLeuLysTrpGlu 200
Db 607 GCGAGAGAAAGCTTACCTTCAAGTCGTGGAGCGCATTCACAAAGTCAAGTCAAGCA 666
QY 201 AsnTrpThrSerSerPhePheIleArgAspIleLeuLysProAspProThrAsnLeu 220
Db 667 AACTACACGACGAGCTTCTTCATCAGGACATCATCAAAACCGACCCCAAGAACTCG 726
QY 221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTrpProAspThr 240
Db 727 CAACTGAACCCATTAAATAATTTCTCGCATGTGGAAGTGAGCGGGAATTCCTGACACC 786
QY 241 TrpSerThrProHisSerTrpPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 260
Db 787 TGGAGACCCCATCTCTCTCTCTTAAACATTTGGCTACAGGTCCAGGCAAGAAC 846
QY 261 AsnArgGluLysLysAspArgLeuGlyValAspLysSerIleAlaValLysHis 280
Db 847 AACAGAGAAAGAAAGACAGACTCTCCGTGACAAAGACCTCAGCCAAAGGTCGTGCGCAC 906
QY 281 LysAspAlaLysIleArgValGlnAlaArgAspArgTrpTrpSerSerSerTrpSerAsp 300


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Db      907  AAGGATGCCAAGATCCCGTCAAGCAGGACCCCTACTATACCTCATCTCGAGCAAC 966
QY      301  TTPAlaSerValSerCysSer 307
Db      967  TGGGCATCCGTCGTCTGCACT 987

RESULT 14
AAF26085
ID  AAF26085 standard; DNA: 990 BP.
XX
AC  AAF26085;
XX
DT  24-APR-2001 (first entry)
XX
DE  Feline IL-12p40 encoding DNA.
XX
KW  Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KM  immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW  Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS  Felis sp.
XX
PN  WO200104155-A2.
XX
PD  18-JAN-2001.
XX
PF  08-JUL-2000; 2000MO-DE02263.
XX
PR  08-JUL-1999; 99CH-0001259.
XX
PA  (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIERS.
PA  (UYZU-) UNIV ZUERICH.
PA  (REGC) UNIV CALIFORNIA.
XX
PI  Lutz H, Leutenegger C, Pedersen N, Schroff M, Wiltig B;
DR  WPI: 2001-147178/15.
XX
PT  Recombinant feline interleukin-12, useful as immunostimulant and for
PT  treating e.g. viral infections in cats, and related nucleic acid
PT  constructs.
XX
PS  Claim 3; Page 30; 35pp; German.
XX
XX  This invention describes a novel feline interleukin-12 (fIL-12)
CC  polypeptide (I) that is expressed, by recombinant gene expression in
CC  eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC  of subunits p35 and p40. These proteins are formed so that, in equimolar
CC  concentrations and in presence of an immunizing antigen, they can be
CC  administered to carnivores, particularly domestic cats. The invention
CC  also describes a nucleic acid construct (II) encoding fIL-12 containing
CC  sequences at least 95% identical with the p40- and p35-encoding sequences
CC  (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC  as immunostimulants for immunization against infectious diseases and/or
CC  for treating infections of tumors in felines, especially domestic cats.
CC  The products of the invention have immunostimulatory, antiviral and
CC  antitumor activity. Nucleic acid constructs that encode (II) are useful
CC  as adjuvants for prophylactic immunization against viral diseases and for
CC  treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC  of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC  is useful for carnivores, and particularly domestic cats in the
CC  following: (i) as immunostimulant, for preventative or therapeutic use;
CC  and (ii) treating tumors and autoimmune diseases, or diseases associated
CC  with a Th1 defect, especially pre-existing infections by feline immune
CC  deficiency virus (FIV), feline leukemia virus and corona virus.
XX
SQ  Sequence 990 BP; 283 A; 249 C; 248 G; 210 T; 0 other:

Alignment Scores:
Pred. No.:      3 32e-151      Length:      990
Score:          1554.00      Matches:      288
Percent Similarity: 96.74%      Conservative: 9

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Best local Similarity: 93.81%      Mismatches: 10
Query Match:          94.01%      Indels:      0
DB:                  22          Gaps:      0

US-09-917-265-53 (1-307) x AAF26085 (1-990)

QY      1  ILETPGLueugluLysAspValTYrValValGluLeuAspTRpHisProAspAlaPro 20
Db      67  ATATGGGAAGTGGGAAAAAGCATTATCTGTGTAGAGTTGGAGCTGGACCTGATGCCCCC 126
QY      21  GlyLmeValValLeuThrCysHisThrProGluLysAspIleThrTPThSer 40
Db      127  GGAGAAATGGTGCTCTTACCTGCATATCTCTGAGAGATGACATCAGCTGGACCTCT 186
QY      41  AlagInSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
Db      187  GACCAGAGCAGTGAAGCTGAGCTGAGTGAAGAACTCTGACATCCAAATCAAGAAATTT 246
QY      61  GLYAspAlaGlyGlnTYrThrCysHisLysGlyGlyLysValLeuSerArgSerLeuLeu 80
Db      247  GCAGATCTGGCCAGTATACCTGTGATAAAGAGAGCCAGGTTCTGAGCCATTCCTTCCTC 306
QY      81  LeuIleHisLysLysGluAspGlyIleTRPserThrAspIleLeuLysGluGlnLysGlu 100
Db      307  CTGATACACAAAAAGAAAGATGGAATTTGGTCCACGTATGCTTAAGGAAACAGAAAGAA 366
QY      101  SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTYrSerGlyArgPheThrCys 120
Db      367  TCCAAAAATTAAGATCTTTCTAATAATGAGGCAAAAGAAATTAATCTGACCTTCACCTGC 426
QY      121  TRPTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
Db      427  TGGTGCTGACGGCAATCACTAGCCGATTTAAATTCCTGCAAAACAGCAGAGGCTCC 486
QY      141  SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgVal 160
Db      487  TCTGACCCCAAGAGGGTGACTTGGAGCAGCGACACTTCACAGAGAAAGTCCAGAGTG 546
QY      161  AspAsnArgAspTYrLysLysTYrThrValGluCysGlnGluGlySerAlaCysProSer 180
Db      547  GACAAACGAGGATTAATAAGAGTACACAGTGAGGTGAGGAGGCACTGCTGCCGCT 606
QY      181  AlagLueLysSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTYrGlu 200
Db      607  GCCGAGAGAGACCTACCATCTTGAAGTGTGTGGACCTTATTCACAAAGCTCAAGTACGAA 666
QY      201  AsnTYrThrSerSerPhePheIleArgAspIleIleLysProAspProPothrAsnLeu 220
Db      667  AACTACACGACGAGCTCTTCATCAGGAGCATCATCAACCGGACCCAGAACCTG 726
QY      221  GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTYrProAspThr 240
Db      727  CAACGTGAAGCCATTAAAAAATTCGCGCATGTGAACTGAGTGGGAAATCCCTGACACC 786
QY      241  TRPserThrProHisSerTYrPheSerLeuThrPheCysLysIleGlnIleGlnLysAsn 260
Db      787  TGGAGACACCCCATCTCTCTCTCTTAACTTTGGCTACAGCTCCAGGCGCAAGAAC 846
QY      261  AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValCysHis 280
Db      847  AACAGAGAAAGAAAGACACAGACTCTCCGTGCAACAGACCTCCAGGTCGTGTCAC 906
QY      281  LysAspAlaLysIleArgValIleArgAlaArgAspArgTYrTYrSerSerSerTPSerAsp 300
Db      907  AAGGATGCCAAGATCCCGTCAAGCAGGACCGCTACTATAGCTCATCTGAGCAAC 966
QY      301  TTPAlaSerValSerCysSer 307
Db      967  TGGGCATCCGTCGTCTGCACT 987

RESULT 15
AAV56625
ID  AAV56625 standard; cDNA: 2193 BP.

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XX AC AAV56625:
XX 23-NOV-1998 (first entry)
XX DE Feline FLAPp40 cDNA.
XX KW Cytokine; feline; FLAPp40; FLAPp35; heterodimer; cytotoxic; treatment;
XX T lymphocyte cell; autoimmune disease; ds.
XX OS Felis catus.
XX FH Key Location/Qualifiers
XX FT CDS 64..1053
XX FT /tag- a
XX FT sig-peptide 64..129
XX FT /tag- b
XX FT mat-peptide 130..1050
XX FT /tag- c
XX FT /product- "FLAPp40"
XX FT /note- "feline cytokine"
XX PN M09746583-A1.
XX PD 11-DEC-1997.
XX PF 29-MAY-1997: 97MO-JP01824.
XX PR 04-JUN-1996: 96JP-0165249.
XX PA (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX PI Fujiyasu T, Imagawa Y, Imamura T, Maeda H, Tokiyoshi S;
XX DR WPI: 1998-042118/04.
XX DR P-PSDB: AAW76173.
XX PT Novel feline cytokine protein - useful for treating feline
XX PT autoimmune diseases, e.g. those caused by feline herpes virus or
XX PT feline calicivirus
XX PS Claim 19: Page 52-54; 94pp; Japanese.
XX CC This sequence encodes a novel feline cytokine protein, FLAPp40. This
XX CC protein can be used in the production of a FLAPp35/FLAPp40 heterodimer
XX CC which can potentiate the cytotoxic activity of feline cytotoxic T
XX CC lymphocyte cells. Such proteins are used for treatment of feline
XX CC autoimmune diseases e.g. as caused by feline herpes virus or feline
XX CC calicivirus.
XX SQ Sequence 2193 BP; 680 A; 451 C; 493 G; 569 T; 0 other;

Alignment Scores:
Pred. No.: 9,95e-151 Length: 2193
Score: 1554.00 Matches: 288
Percent Similarity: 96.74% Conservative: 9
Best Local Similarity: 93.81% Mismatches: 10
Query Match: 94.01% Indels: 0
DB: 19 Gaps: 0

US-09-917-265-53 (1-307) x AAV56625 (1-2193)
OY 1 ILETTPGLULENGULYASPAVALTYRVAIVAGLULENAsPTPHISProAsPALAPro 20
DB 130 ATATGGGAAGTGGAGAAAAGCTTATGTTAGTAGAGTTGGACCGACCCCTGATGCCCCC 189
OY 21 G|G|L|U|E|T|A|V|A|L|L|E|U|T|H|C|Y|S|H|S|T|H|P|R|O|G|L|U|G|L|U|A|S|P|I|E|H|T|T|P|H|S|E|R 40
DB 190 GGAGAAATGCTGCTCCACCTCACTACCTGGAAGAGATGACATCACTGACCTGACCTCT 249
OY 41 AlagIserSerGIuValLeuGIysSerGIySThrLeuThrIleGIuValIysGIuPhe 60
DB 250 GACCAAGACGAGTAACTCTAGGCTCTGTGTAAGACTGTGACCATCCACAGTCAAGAAATTT 309

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OY 61 GLYAsPALaG|yG|In|T|Y|T|H|C|Y|S|H|S|L|yS|G|L|yS|V|A|L|L|E|U|S|E|R|A|R|G|S|E|R|L|E|U| 80
DB 310 GCAGATGCTGGCCAGTATACCTGTCATTAAGAGAGCGAGGTTCTGAGCATTCGTTCTCTC 369
OY 81 L|E|U|I|E|H|S|L|yS|L|yS|G|L|U|A|S|P|I|E|T|P|S|E|R|T|H|A|S|P|I|E|L|E|U|L|yS|G|L|U|N|L|yS|L|U 100
DB 370 CGATATACACAAAAGAGAGATGGAATTTGGTCCACTGATATCTTAAGGAGACAGAAAGA 429
OY 101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTySerGIyArPheThrCys 120
DB 430 TCCAAAATTAAGATCTTTCTTAATATGTGAGCAAGAAATTTATTCGAGAGTTTACCTGC 489
OY 121 T|P|T|P|L|E|U|T|H|A|L|L|S|E|R|T|H|A|S|P|L|E|U|L|yS|P|H|E|S|E|R|V|A|L|L|yS|S|E|R|A|R|G|L|yP|H|E 140
DB 490 TGGTGCTGACGCGCATACATGACCATTTGAAATTCACCTGTCACAAAGCAGAGAGCTCC 549
OY 141 SerAspProGInGlyValIThrCysGlyAlaIThrLeuSerAlaGluAlaGlyAla 160
DB 550 TGTGACCCCAAGGGGGTGCTGTGTGAGCAGCGACACCTCAGCAGAAAGAGTCGAGCTG 609
OY 161 AspAsnArgAspTyTrLysIyS|T|Y|T|H|V|A|G|L|U|C|Y|S|G|I|N|G|L|yS|E|R|A|L|A|C|Y|S|P|R|O|S|E|R 180
DB 610 GACAAACAGGATTTATAGACATACAGTGCAGAGAGGAGTGCCTGCCGGCT 669
OY 181 AlagIuGIuSerLeuProIleGIuValIValIAsPALaIleHISLysLeuLysTyGIu 200
DB 670 GCCGAGAGAGGCTGACCATTCGAGTGAAGTGGTGGAGCTATTCACAAACCTCAAGTACGAA 729
OY 201 AsnTyTrH|S|E|R|S|E|R|P|H|E|L|L|E|A|R|G|A|S|P|I|E|L|E|U|S|P|R|O|A|S|P|R|O|T|H|S|E|R|L|E|U 220
DB 730 AACTACACCGACGAGCTTCTTCATCAGGAGCATCATCAACCGGACCCCAAGAACTG 789
OY 221 G|N|L|E|U|L|yS|P|R|O|L|E|U|L|yS|A|S|E|R|A|R|G|H|I|S|V|A|G|I|U|A|S|E|R|T|P|G|L|U|T|Y|P|R|O|A|S|P|H| 240
DB 790 CAAC|T|G|A|A|C|C|A|T|T|A|A|A|A|T|T|C|T|G|C|G|C|A|T|G|G|A|A|G|A|G|T|G|G|A|A|P|A|C|C|T|G|A|C|A|C|C 849
OY 241 T|P|S|E|R|T|H|P|R|O|H|I|S|S|E|R|T|Y|R|H|E|S|E|R|L|E|U|T|H|P|R|H|E|C|Y|S|I|L|E|G|I|N|A|L|G|I|N|L|yS|A|S|N 260
DB 850 TGGAGCACC|C|C|C|A|C|A|T|T|C|T|C|T|C|T|T|C|T|T|A|C|A|T|T|T|G|C|G|T|A|C|A|G|G|T|C|C|A|G|G|C|A|A|G|A|A|C 909
OY 261 AsnArgGIuLysLysAspArgLeuCysValAspLysThrSerAlaLysValAlCysHIS 280
DB 910 AACAGAGAAAAGAAAGACAGACTTCCTGGACAAAGACTCAGCCAAAGCTGTGTCAC 969
OY 281 LysAsPALaLysIleArgValGlnAlaArgAspArgTyTrSerSerSerTrpSerAsp 300
DB 970 AAGATGCCAAGATCCGCGCTGCAGAGCAGAGACGCCCTACTATAGCTCATCTGAGACAAC 1029
OY 301 T|P|A|L|S|E|R|V|A|L|S|E|R|C|Y|S|S|E|R 307
DB 1030 TGGCATCCGCTGCTCCGAGT 1050

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Search completed: July 16, 2003, 20:24:02
 Job time : 221.05 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: July 16, 2003, 19:41:51 ; Search time 1460.26 Seconds

(without alignments)
3404.860 Million cell updates/sec

Title: US-09-917-265-53

Perfect score: 1653

Sequence: 1 IWELEKDYVVEFLDWHPPAP.....QARDRYSSSWSDMASVSCS 307

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-o=/cgn2_1/USPTO/spool/US09917265/runat_15072003_092107_1610/app_query.fasta_1.3114
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-LOCALIGN=200 -THR.SCORE=pcr -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pcr -NOM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09917265.acgn_1_1.6304.etunal_15072003_092107_1610 -NCPU=6 -ICPU=3
-NO_MMAR -LARGEOBUSER -NEG.SCORES=0 -WAIT -DSPBLOCK=100 -LONCLOG
-FCAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: em_estba:*
2: em_estchum:*
3: em_estcin:*
4: em_estlm:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estc1:*
10: gb_estc2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estlm:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrl:*
22: em_gss_fun:*
23: em_gss_nam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------------|---------------------|
| 1 | 497.5 | 30.1 | 475 | 12 BF704417 | BF704417 M1-P-E6-a |
| 2 | 354 | 21.4 | 535 | 17 AZ441303 | AZ441303 IM0232M24 |
| 3 | 324 | 19.6 | 569 | 17 AZ853726 | AZ853726 2M0157M01 |
| 4 | 170 | 10.3 | 668 | 17 AG079702 | AG079702 Pan trogl |
| 5 | 156 | 9.4 | 509 | 12 BG554242 | BG554242 dab70907. |
| 6 | 153.5 | 9.3 | 875 | 9 AL537375 | AL537375 AL537375 |
| 7 | 152.5 | 9.2 | 882 | 14 BQ223533 | BQ223533 ACENECOURT |
| 8 | 150.5 | 9.1 | 997 | 9 AL528607 | AL528607 AL528607 |
| 9 | 144.5 | 8.7 | 873 | 9 AL518132 | AL518132 AL518132 |
| 10 | 138.5 | 8.4 | 511 | 12 BG359887 | BG359887 dab88605. |
| 11 | 134.5 | 8.1 | 591 | 14 BM685621 | BM685621 UT-E-C10- |
| 12 | 134 | 8.1 | 324 | 17 AQ981401 | AQ981401 RPCI-23-3 |
| 13 | 133.5 | 8.1 | 481 | 14 BM710190 | BM710190 UT-E-CQ1- |
| 14 | 133.5 | 8.1 | 769 | 14 BM719097 | BM719097 UT-E-EQ1- |
| 15 | 129.5 | 7.8 | 683 | 10 AW950312 | AW950312 EST362382 |
| 16 | 129.5 | 7.8 | 938 | 12 BE901933 | BE901933 601676878 |
| 17 | 127.5 | 7.7 | 912 | 13 B1760931 | B1760931 603043131 |
| 18 | 127 | 7.7 | 1082 | 14 BM919605 | BM919605 ACENECOURT |
| 19 | 126 | 7.6 | 700 | 14 BQ749057 | BQ749057 UT-M-FB0- |
| 20 | 123.5 | 7.5 | 502 | 10 BE650170 | BE650170 UT-M-BH3- |
| 21 | 123.5 | 7.5 | 624 | 12 BG713383 | BG713383 p411n.pk0 |
| 22 | 123 | 7.4 | 846 | 9 AL525319 | AL525319 AL525319 |
| 23 | 122.5 | 7.4 | 412 | 9 AL629081 | AL629081 fco96d01.y |
| 24 | 120.5 | 7.3 | 361 | 14 T28073 | T28073 EST26562.Hu |
| 25 | 119.5 | 7.2 | 666 | 14 BM935910 | BM935910 UT-M-CGDP |
| 26 | 119.5 | 7.2 | 859 | 12 BG434397 | BG434397 602506409 |
| 27 | 119 | 7.2 | 675 | 12 BG621100 | BG621100 602616982 |
| 28 | 118 | 7.1 | 742 | 9 AL549396 | AL549396 AL549396 |
| 29 | 118 | 7.1 | 906 | 12 BG754874 | BG754874 602714263 |
| 30 | 118 | 7.1 | 918 | 9 AL550798 | AL550798 AL550798 |
| 31 | 118 | 7.1 | 927 | 9 AL553060 | AL553060 AL553060 |
| 32 | 118 | 7.1 | 948 | 9 AL545121 | AL545121 AL545121 |
| 33 | 118 | 7.1 | 950 | 9 AL551603 | AL551603 AL551603 |
| 34 | 118 | 7.1 | 973 | 34 AL548148 | AL548148 AL548148 |
| 35 | 117 | 7.1 | 707 | 14 BM718865 | BM718865 UT-E-BQ1- |
| 36 | 117 | 7.1 | 793 | 13 B1834803 | B1834803 603090245 |
| 37 | 116.5 | 7.0 | 916 | 9 AL576559 | AL576559 AL576559 |
| 38 | 115.5 | 7.0 | 488 | 12 BF997791 | BF997791 MR2-GN012 |
| 39 | 115 | 7.0 | 877 | 14 BQ230610 | BQ230610 ACENECOURT |
| 40 | 114.5 | 6.9 | 890 | 12 BG620398 | BG620398 602617523 |
| 41 | 114.5 | 6.9 | 1642 | 14 BM919170 | BM919170 ACENECOURT |
| 42 | 114 | 6.9 | 856 | 9 AL546165 | AL546165 AL546165 |
| 43 | 114 | 6.9 | 1022 | 9 AL554313 | AL554313 AL554313 |
| 44 | 113.5 | 6.9 | 779 | 13 B1333959 | B1333959 602997231 |
| 45 | 113.5 | 6.9 | 866 | 13 B1520198 | B1520198 603071446 |

ALIGNMENTS

RESULT 1
LOCUS BF704417 475 bp mRNA linear EST 22-DEC-2000
DEFINITION M1-P-E6-acc-g-09-1-UM.s1 M1-P-E6 Sus scrofa CDNA clone
ACCESSION BF704417
VERSION BF704417.1 GI:11989825
KEYWORDS EST.
SOURCE Sus scrofa
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
REFERENCE 1 (bases 1 to 475)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene

Sequencing: M13rev

LIBRARY
Vector : PKS145
R.Site 1 : SacI
R.Site 2 : SacI

FEATURES
source
1. 668
Location/Qualifiers

/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-075107.R"
/sex="male"
/cell_type="lymphoblast"

BASE COUNT 180 a 138 c 137 g 213 t
ORIGIN

Alignment Scores:

Pred. No.: 5.46e-09 Length: 668
Score: 170.00 Matches: 30
Percent Similarity: 82.50% Conservative: 3
Best Local Similarity: 75.00% Mismatches: 7
Query Match: 10.28% Indels: 0
DB: 17 Gaps: 0

US-09-917-265-53 (1-307) x AG079702 (1-668)

OY 100 GluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThr 119
Db 542 GAACCCAGACTTACACCTTTGTAGATCGAGACCAAGATTATTCAGACGTTTACC 483
OY 120 CysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerArgGly 139
Db 482 TGCTGGTGGCTGACCAATCAGTACTGATTTGACATTGAGTCTCAAAAAGCAGCAGG 423

RESULT 5
LOCUS BG554242 509 bp mRNA linear EST 09-APR-2001
DEFINITION dab70a07.y2 NICHD XGC Emb4 Xenopus laevis cDNA clone IMAGE:4202388
sequence.

ACCESSION BG554242
VERSION BG554242.1 GI:13566022
KEYWORDS EST
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
Xenopus; Xenopus.

REFERENCE 1 (bases 1 to 509)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT other ESTs: dab70a07.x1
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Washington University Genome Sequencing Center
through the I.M.A.G.E. Consortium/ILNL at: InfoImage.lnl.nih.gov
Seq primer: -40RP from Gibco
High quality sequence stop: 385.
Location/Qualifiers

FEATURES
source
1. 509
Location/Qualifiers

/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="IMAGE:4202388"
/clone_lib="NICHD XGC Emb4"
/dev_stage="embryo, stage 31-32"
/lab_host="DH10B (phage-resistant)"
/note="Organ: whole embryo; Vector: PCMV-SPORE6; Site_1:"

NotI, Site.2: SalI; Cloned unidirectionally. Primer: Oligo
dT. Average insert size 2.1 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection (XGC
Library.)

BASE COUNT 111 a 146 c 124 g 128 t
ORIGIN

Alignment Scores:

Pred. No.: 1.5e-07 Length: 509
Score: 156.00 Matches: 52
Percent Similarity: 41.03% Conservative: 28
Best Local Similarity: 26.67% Mismatches: 75
Query Match: 9.44% Indels: 40
DB: 12 Gaps: 8

US-09-917-265-53 (1-307) x BG554242 (1-509)

OY 64 GlyIleuTyrThrCysHisLysGlyGlyValLeuSerArgSerLeuLeuHis 83
Db 6 GGCACTACACGCTGCTACAGTCACTCGGGATCTGCTGCTTCCAGAAAG 65
OY 84 LysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluLysLysAsn 103
Db 66 GGATACCCCCAGGAGCCCGTCA-----
OY 104 LysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpLeu 123
Db 90 ---GTTTTC-----TGTAGCTTCAGACTATGAG---ACCTTTCCTGCTTCGGA 137
OY 124 ThrAlaIleSerThrAspLeuLysPheSerValLysSerArgGlyLysSerArg 143
Db 138 TCCAGTGTGACAGCGCTTCTCCCTTCAGATTACTGCTCTTATCGGACGATATC 197
OY 144 GlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgValAsp 163
Db 198 ATCGTGGGCTGTGCTGCGAGGACCGCGCCCATATGCTGCTCGTAGAAGTCT 257
OY 164 AspTyr---LysLysTyrThrValGluLysGlnGluLysSerAlaCysProSerAla 182
Db 258 GAGTCTGAGGCTCCTCAGACATCAATCAAGGAAACCCGCTGGGATCCAGTTTC 317
OY 183 GluSerLeuProIleGluValValAspAlaIleHisLysLeuLysTyrGluAsnTyr 202
Db 318 CGGCTGCTGGAGTGCACGCTG-----
OY 203 ThrSerSerPhePheIleArgAspIleLysProAspProThrAsnLeuGlnLeu 222
Db 339 -----CACTTATTGTAAACCGGACCCCTCAGAGACTTGTGGTG 380
OY 223 LysProLeuLysAsnSer---ArgHisValGluValSerTrpGluTrpAspTrp 241
Db 381 GAACCAATCCCGTTCGCTCCAGAGAGGCTTCAGTCACTGATTCATTCATCCACT 440
OY 242 ---SerThrProHisSerTyrPheSerLeuThrPheCysIleGln 255
Db 441 CCCAAGAGCCTCAT-----TTCCAGCTCAAGTTCGTTTCAG 479

RESULT 6
LOCUS AL537375 875 bp mRNA linear EST 13-FEB-2001
DEFINITION AL537375 LTL FL013 Fbri1 Homo sapiens cDNA clone CS0P025YJ10 5
prime, mRNA sequence.
ACCESSION AL537375
VERSION AL537375.1 GI:12800868
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 875)
AUTHORS Li W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)

[illegible]

| Accession | Organism | Source | Reference | Title | Journal | Comment |
|------------|--|--------|-----------|---|---------|---------|
| Db 679 | AAGTACAAAGTCTCCATAGTGCAGCAATGCCCTGGGCCACCAATGCCACAGCTATACCC | | 679 | AAGTACAAAGTCTCCATAGTGCAGCAATGCCCTGGGCCACCAATGCCACAGCTATACCC | | |
| Qy 207 | Phel1earyt---Asp1le1le1y1Proa5p1r0thrA5n1eug1n1eUy5Pro1eu | | 207 | Phel1earyt---Asp1le1le1y1Proa5p1r0thrA5n1eug1n1eUy5Pro1eu | | |
| Db 739 | TTTGACGACGTTCCACCAATTTGTGAACCTGATCTCTCCAGAAATGTGTGAACCCGGCCAGTG | | 739 | TTTGACGACGTTCCACCAATTTGTGAACCTGATCTCTCCAGAAATGTGTGAACCCGGCCAGTG | | |
| Qy 226 | --Lysan5eArGh15val1Gluval1e1r1p1u1r1Proa5p1r1r1p1e1r1Pro | | 226 | --Lysan5eArGh15val1Gluval1e1r1p1u1r1Proa5p1r1r1p1e1r1Pro | | |
| Db 799 | CCCAAGCAACCCCTGCCCGCTGGAGCTGACGTGACGTCAGACCCCTGACCTGACCT | | 799 | CCCAAGCAACCCCTGCCCGCTGGAGCTGACGTGACGTCAGACCCCTGACCTGACCT | | |
| Qy 245 | His1e1r1r1p1e1s1e1r | | 245 | His1e1r1r1p1e1s1e1r | | |
| Db 859 | GAGTCTTCCCTCA | | 859 | GAGTCTTCCCTCA | | |
| RESULT 7 | | | | | | |
| LOCUS | | | | | | |
| DEFINITION | BO223533 882 bp mRNA linear EST 02-MAY-2002 | | | | | |
| ACCESSION | AGNCOCURT.7551196 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6066162 | | | | | |
| VERSION | 5', mRNA sequence. | | | | | |
| KEYWORDS | BO223533 GI:20404933 | | | | | |
| SOURCE | EST. | | | | | |
| ORGANISM | human. | | | | | |
| REFERENCE | Homo sapiens | | | | | |
| AUTHORS | Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi; | | | | | |
| TITLE | Mammalia: Eutheria: Primates: Catarrhini: Homiidae: Homo. | | | | | |
| JOURNAL | NIH-MGC http://mgs.nci.nih.gov/. | | | | | |
| COMMENT | 1 (bases 1 to 882) National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs@mail.nih.gov Tissue Procurement: ATCC/DCTP/DTP cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: LAM1343 row: j column: 19 High quality sequence stop: 659. Location/Qualifiers 1..882 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:6066162" /clone_id="NIH_MGC_72" /tissue_type="melanotic melanoma" /lab_host="DH10B (phage-resistance)" /note="Organ: skin; Vector: pCMV-SPORT6; Site:1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2 kb. Library constructed by Life Technologies.." BASE COUNT 194 a 261 c 246 g 181 t ORIGIN Alignment Scores: Pred. No.: 8.57e-07 Length: 882 Score: 152.50 Matches: 56 Percent Similarity: 41.18% Conservative: 56 Best local Similarity: 20.59% Mismatches: 97 Query Match: 9.23% Indels: 63 DB: 14 Gaps: 11 US-09-917-265-53 (1-307) x BO223533 (1-882) Qy 51 Lys1r1h1e1u1r1l1e1g1n1a1l1y5g1u1p1h1e1g1y1a5p1l1a1g1n1y1r1h1e1r1y5s1h1s1y5 Db 3 AGGAGGCTGCTGCTGAGAGTGGGTGACAGCTCAGCAGCTGCGAAGCTATTTATGCTACCG 62 Qy 71 G1y1c1y1l1y5v1a1l1e1u5e1r1a1r1g5e1r1e1u1e1u1e1h1s1l1y5l1y5g1u1a5p1c1y1l1e1r1p 90 | | | | | |

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Db      63 CCGCGCCCGCCAGCTGGAGCTGTCAGTCTGCTGTC-----leu 98
Qy      91 SerThrAspIleuLysGluGlnLysSerLysAsnLysIlePheLeuLysGlu 110
Db      99 -----GATGTTCCCGCGAGAGACCCAG-----CTCTCTGCTTC 134
Qy      111 AlalysAnTyTyrSerGlyArgPheThrCysTrpTyr-----leu 123
Db      135 CGGAGAGAGCCCTCAGCAATGTTGTTGAGATGGGCTCTCGGAGACCCCATCCCTG 194
Qy      124 Thr-----AlalSerThrAspLeuLysPheSerValLysSerSerArgLysPheSer 141
Db      195 ACAGCAAAAGCCTGCTGCTTGGGAGAAAGTTTCAGAACAGTCCGCGAGACTTTCAG 254
Qy      142 AspProGlnGlyAlaThrCysGlyAlaValThrLeuSerAlaGluArgValArgAla 161
Db      255 GAGCCG-----TGC-----263
Qy      162 AsnArgAspTyrLysLysTyrThrValGluCysGlnGlySer-----AlaCys 178
Db      264 -----CAGTATTCAGAGAGTCCAGAGATTCCTCTGCGCAGTTAGCAGTC 308
Qy      179 ProSerAlaGluGlnLysLeuProIleGluValAlaValAlaAspAlaIleHisLysLeuLys 198
Db      309 CCGGAGGAGAGACGCTTCTTACATAGTGTCCATGTGCGCCGACAGTACGTGCGGAGC 368
Qy      199 TyrGluAnTyTyrThrSerSerPhePheIleArgAspIleLysProAspProThr 218
Db      369 AAGTTCAGCAAAAGCTCAAACTTCAGAGGTTTGGAATCTTGACGCGTGAATCCGCGCC 428
Qy      219 AsnLeuGlnLysProLeu-----LysAsnSerArgHisValGluValSerTrpGluTyr 237
Db      429 AACATCAGAGTACTGCGCGTGGCCAGAAACCCCGCTGCTCAGTGTACCTGCGCAAGAC 488
Qy      238 ProAspThrTrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGln 257
Db      489 CCCACACTCGGAGACTCA-----TCTTTTACAGACTGAGGTTTACAGTCAAGATATCGG 542
Qy      258 GlyLysAsnAsnArg-----GluLysLysAspArgLysCysVal 270
Db      543 GCTGACAGCTCAAAAGACATTACACACATGATGATGTCAGAGACCTCCAGCATCTATGTC 602
Qy      271 AspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValAlaAlaArg 290
Db      603 ATCCAGCAGCGCTGGAGCGGCTGAGGAC-----GTGGTCAAGCTTGTGCTCCAG 653
Qy      291 AspArgTyrTyrSerSerSerTrpSerAspTrpAla 302
Db      654 GAGGAGTTCGGCAAGCGGAGTGGAGCGAGTGGAGC 689

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RESULT 8
AL528607
LOCUS
DEFINITION
AL528607 LTI_NFL001_NBC4 997 bp mRNA linear EST 13-FEB-2001
prime, mRNA sequence.
AL528607
AL528607.1 GI:12792100
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS
TITLE
L1, W.B., Gruber, C., Jessee, J. and Polayes, D.
JOURNAL
Full-length cDNA libraries and normalization
Unpublished (2001).
COMMENT
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr.
FEATURES
SOURCE
1. 997
/organism="Homo sapiens"

```

BASE COUNT      180 a      331 c      290 g      184 t      12 others
ORIGIN
Alignment Scores:
Pred. No.:      1.75e-06      Length:      997
Score:      150.50      Matches:      67
Percent Similarity:      36.13%      Conservative:      32
Best Local Similarity:      24.45%      Mismatches:      94
Query Match:      9.10%      Indels:      83
DB:      Gaps:      12

US-09-917-265-53 (1-307) x AL528607 (1-997)
Qy      19 AlaProGlyGluMetValIleLeuThrCysHisThrProGluLys----- 33
Db      192 CCGCGCGCGGAGTGTCTACGCGCCAGARACAGATGCACAGAGAGCCACCATGTGCGAG 251
Qy      34 -----AspAspIleThr-----TrpThrSerAla 41
Db      252 TACGAGCGCTGGGCTGCTGACGTGACACTCCATGTGGACAGMAAACTGGAGTGTGG 311
Qy      42 GlnSerSerGluValLeuGly-----SerGlyLysThrLeu 53
Db      312 GTGACGTTGGGGGTAAATGAGACAGACCTGCGCCCTGACCTGCTCAAGCTCTGAGCTG 371
Qy      54 ThrIleGlnValLysGluPheGlyAspAlaGlyGlnTyrThrCysHisLysGlyLys 73
Db      372 GTGCTCCATGCGCTGAGACTGGGACAGCTGCGCTCAAGCTGCTTCCACCGTACTCC 431
Qy      74 ValLeuSerArgSerLeuLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAsp 93
Db      432 TGGCACCCTGGCCACCAAGTCTGCTGCAATG-----GGCTTG----- 470
Qy      94 IleLeuLysGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsn 113
Db      471 -----CCGCGCGGAGGCTGTGCTGCTACCTGCTCCACACTCCACACT 509
Qy      114 TyrSerGlyArgPheThrCysTrpTrpPheThrAlaIleSerThrAspLeuLysPheSer 133
Db      510 TACCCCAAGGCTTACTGACGCTGGCATCTGCCACCCCACTTACATT----- 560
Qy      134 ValLysSerSerArgGlyPheSerAspProGlnGlyAlaThrCysGlyAlaValThrLeu 153
Db      561 -----CCCAAC-----ACCTTCAATGTGACTGTGCTG 587
Qy      154 SerAlaGluArgValArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGln 173
Db      588 CATGCTCCAAATTAATTATGTC-----TGTGA- 613
Qy      174 GluLysSerAlaCysProSerAlaGluGlnLysLeuProIleGluValAlaValAlaAspAla 193
Db      614 GAAAGG-----CCACGCTCAAGAAACGCTCCCACTTGGTACATGACACCTGTT 664
Qy      194 IleHisLysLeuLysTyrGlu-----AsnTyr 202
Db      665 CTCGACC-ATCAAGTACAGAGTCTTCATAGTGCAGCAATGCTTGGCCACAAATGCC 722

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| Qy | Db | Qy | Db | RESULT 9 | LOCUS | DEFINITION | ACCESSION | VERSION | KEYWORDS | SOURCE | ORGANISM | REFERENCE | AUTHORS | TITLE | JOURNAL | COMMENT | FEATURES | | | | | | | | |
|-----|-----|-----|-----|----------|----------|--------------------------|-----------|----------|------------|-------------|----------|-----------|--------------|---|---|--------------------|--|--|--------------------|--------------------|---|----------------------------------|---|---------------------|--------|
| 203 | 723 | 222 | 783 | AL518132 | AL518132 | AL518132 LTI_NFL011_NBC1 | AL518132 | AL518132 | AL518132.1 | GI:12781625 | EST. | Human. | Homo sapiens | Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | Mammalia: Euthera; Primates; Catarrhini; Hominiade; Homo. | 1 (bases 1 to 873) | Li, W. B., Gruber, C., Jesssee, J. and Polayes, D. | Full-length cDNA libraries and normalization | Unpublished (2001) | Contact: Genoscope | Genoscope - Centre National de Sequencage | BP 101 91006 Evry cedex - France | Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr. | Location/Qualifiers | 1..873 |

| | | | | | |
|---|----------|---|-------|-------|-----------|
| BASE COUNT | 148 a | 298 c | 251 g | 165 t | 11 others |
| ORIGIN | | | | | |
| Alignment Scores: | | | | | |
| Pred. NO.: | 7.05e-06 | Length: | 873 | | |
| Score: | 144.50 | Matches: | 62 | | |
| Percent Similarity: | 36.63% | Conservative: | 27 | | |
| Best local Similarity: | 25.51% | Mismatches: | 96 | | |
| Query Match: | 8.74% | Indels: | 60 | | |
| DB: | 9 | Gaps: | 11 | | |
| US-09-917-265-53 (1-307) x AL518132 (1-873) | | | | | |
| QY | 21 | G YGLuMeTValIaLleuThrCYsHisTrPProGluGluASP---AspIleThrTrP--- | 38 | | |
| | | | | | |
| Db | 264 | GGCTCTGACGTGACACTKCCATGTGGGACACGAAACTGGAGTGGCTGGCTGACGTGGCG | 323 | | |
| QY | 39 | ---ThrSerAlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnVal | 57 | | |
| | | | | | |
| Db | 324 | GTAATATKGACAGACCTGGCCCTGGACCTGTGCTCAACGGCTCTTACCTGTGGTCTGCATGGC | 383 | | |

| | | | |
|------------|--|--|-----------------------------|
| Qy | 58 | ysysgluphegiyaspaplaiglylphyrthrcyshtslsglyglylsvalleuserarg | 77 |
| | | | |
| | | | |
| Db | 384 | ctggaactggggccacagtgkcccttgcaccccttccacccgtgactctcgacactctggc | 443 |
| Qy | 78 | serleuleuleuilehtslsglysgluspcllylterpserthraspileuleucysgu | 97 |
| | | | |
| Db | 444 | caccagatgctgcgcgatgtr-----ggcttg----- | 470 |
| Qy | 98 | glnylsgluserlysasnllysilepheleulcysguialalysasntryserglyarg | 117 |
| | | | |
| Db | 471 | -----ccggccgggagcccttcttcagctgcgcctcccaacacattaccccaagggc | 521 |
| Qy | 118 | phethrcystptptpleuthralaleserthraspleulyspheserVallyserser | 137 |
| | | | |
| Db | 522 | tttctactccatcgcatctgccaccccccacttaccatt----- | 560 |
| Qy | 138 | argclypheseraspptroglnglyvalthrcysglyalavalthleuseralaglary | 157 |
| | | | |
| Db | 561 | -----cccaac-----accttccatgttactgtcctcgcacgtccaaa | 599 |
| Qy | 158 | valargyalaspasnaargsptrylslsyttrythralvalglucysglnglucylserala | 177 |
| | | | |
| Db | 600 | attatgtrc-----tgca-caagca----- | 619 |
| Qy | 178 | cysproseralaglgluserleuproilegluvalvalaspallehtslsleu | 197 |
| | | | |
| Db | 620 | ---ccgacccctcaagAACCCCTGCACATTGCGTACATGCACCCGTTCCTCCACS-ATC | 674 |
| Qy | 198 | lystrfgrlu-----asntrythserperphe | 206 |
| | | | |
| Db | 675 | aagTACAAGGCTCCATAGTGTACAGCAATGCCCTGGGCCAACATGCCACAGCTATCAC | 734 |
| Qy | 207 | phelleary--aspillellelysproaspropothraasleuGlnleulysproleu | 225 |
| | | | |
| Db | 735 | TTTGACAGAGTTCACCATGTGAGACGTCATGCTCCACAAATGTGTGATGCCGGCAGTG | 794 |
| Qy | 226 | ---lysansseraighisvalgluvalsertrpglutryrproaspthtrpserthpro | 244 |
| | | | |
| Db | 795 | CCGACGACCCCTCCGGCTGGAGCTGACGTGCAGACCCCTCGACCTGGCCTGAMCCT | 854 |
| Qy | 245 | HisserTryr 247 | |
| | | | |
| Db | 855 | GAGTCITTT 863 | |
| RESULT 10 | | | |
| LOCUS | BG359887 | 511 bp | mRNA linear EST 06-MAR-2001 |
| DEFINITION | dab88905.y1 NICHD XGC Emb2 Xenopus laevis cDNA clone IMAGE:4404680 | | |
| | 5' similar to TR:Q16342 Q16342 INTERLEUKIN-11 RECEPTOR. ; mRNA | | |
| | sequence. | | |
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| VERSION | BG359887.1 | GI:13240578 | |
| KEYWORDS | EST. | | |
| SOURCE | African clawed frog. | | |
| ORGANISM | Xenopus laevis | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| AUTHORS | Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; | | |
| | Xenopodidae; Xenopus. | | |
| | 1 (bases 1 to 511) | | |
| | Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D., | | |
| | Martin,J., Wille,T., Underwood,K., Theising,B., Bowers,Y., Person, | | |
| | B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R., | | |
| | Waterston,R. and Wilson,R. | | |
| | Washu Xenopus EST project, 1999 | | |
| | Unpublished (1999) | | |
| TITLE | Other-ESTs: dab88905.x1 | | |
| JOURNAL | Contact: Sandy Clifton, Ph.D. | | |
| COMMENT | Washu Xenopus EST project, 1999 | | |
| | Washington University School of Medicine | | |
| | 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA | | |
| | Tel: 314 286 1800 | | |
| | Fax: 314 286 1810 | | |
| | Email:est@watson.wustl.edu | | |

| | | | |
|-------------------|--|--|----------|
| OY | 246 | SerTyrPheSerLeuThrPheCysIleGlnIacInglLysAsnAsnArgGlutLysLys | 265 |
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| DB | 276 | TCT---TTTCCTGTCAACTTCTTCTTGCGCATCCA----- | 308 |
| OY | 266 | AspArgLeuCysValAlaLys----- | -Thr 273 |
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| DB | 309 | --CCCTCATCTCGACAGCAGTGCAGCATGTGGAGCTGTCCGACGCCACAGCACACACC | 365 |
| OY | 274 | SerAlaLysValAlaCysHisLysAspAlaLysIleArgValAlaAlaArgAspArgTyr | 293 |
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| OY | 294 | TyrSerSerSerTyrPserAspTrpAla | 302 |
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| RESULT_12 | A0981401 | 324 bp DNA linear GSS 29-JAN-2000 | |
| A0981401/C | RPCI-23-304012.TV RPCI-23 Mus musculus genomic clone RPCI-23-304012 | | |
| LOCUS | | | |
| DEFINITION | | | |
| ACCESSION | A0981401 | | |
| VERSION | A0981401.1 GI:6813702 | | |
| KEYWORDS | GSS. | | |
| SOURCE | house mouse. | | |
| ORGANISM | Mus musculus | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| AUTHORS | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | |
| | 1 (bases 1 to 324) | | |
| | Zhao,S., Nieman,W., Feldblum,T., Malek,J., Shatsman,S., Akinret | | |
| | ,B., Levitus,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P. | | |
| | and Fraser,C.M. | | |
| | Mouse BAC End Sequences from Library RPCI-23 | | |
| | Unpublished (1999) | | |
| TITLE | Other GSSs: RPCI-23-304012.TV | | |
| JOURNAL | Contact: Shaying Zhao | | |
| COMMENT | Department of Eukaryotic Genomics | | |
| | The Institute for Genomic Research | | |
| | 9712 Medical Center Dr., Rockville, MD 20850, USA | | |
| | Tel: 301 838 0200 | | |
| | Fax: 301 838 0208 | | |
| | Email: szhaoy@tigr.org | | |
| | Clones are derived from the mouse BAC library RPCI-23. For BAC | | |
| | library availability, please contact Pieter de Jong | | |
| | (pietere@jong.med.buffalo.edu). Clones may be purchased from | | |
| | BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) | | |
| | or from Reseach Genetics (info@resgen.com). BAC end page: | | |
| | http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html | | |
| | Plate: 304 row: O column: 12 | | |
| | Seq primer: SP6 | | |
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| | /strain="C57BL/6J" | | |
| | /db_xref="taxon:10090" | | |
| | /clone="RPCI-23-304012" | | |
| | /clone_id="RPCI-23" | | |
| | /sex="Female" | | |
| | /lab_host="DH10B" | | |
| | /note="Organ: Kidney/Brain; Vector: pBAC3.6; Site: 1: | | |
| | EcoRI; Site: 2: EcoRI; Female C57BL/6J mouse kidney dna/or | | |
| | brain genomic DNA was isolated and partially digested | | |
| | with a combination of EcoRI and EcoRI MethyIase. Size | | |
| | selected DNA was cloned into the pBAC3.6 vector at the | | |
| | EcoRI sites. The ligation products were transformed into | | |
| | DH10B electrocompetent cells (BRL Life Technologies). | | |
| | " | | |
| BASE COUNT | 100 a 56 c 60 g 104 t 4 others | | |
| ORIGIN | | | |
| Alignment Scores: | 2.64e-05 Length: 324 | | |
| Pred. No.: | | | |

| Score: | 134.00 | Matches: | 25 |
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| Best Local Similarity: | 69.44% | Mismatches: | 9 |
| Query Match: | 8.11% | Indels: | 0 |
| | 17 | Gaps: | 0 |
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| OY | 122 | TrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSer | 137 |
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| LOCUS | BM710190 | 481 bp | mRNA linear EST 28-FEB-2007 |
| DEFINITION | UI-E-COI-agg-j-18-0-UI-r1 UI-E-COI Homo sapiens cDNA clone | | |
| ACCESSION | UI-E-COI-agg-j-18-0-UI 5', mRNA sequence. | | |
| VERSION | BM710190 | | |
| KEYWORDS | EST. | | |
| SOURCE | human. | | |
| ORGANISM | Homo sapiens | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. | | |
| AUTHORS | 1 (bases 1 to 481) | | |
| TITLE | Bonaldo,M.F., Lennon,G. and Soares,M.B. | | |
| JOURNAL | Normalization and subtraction: two approaches to facilitate gene discovery | | |
| MEDLINE | Genome Res. 6 (9), 791-806 (1996) | | |
| COMMENT | 9704447 Contact: Soares, MB Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565 Email: msoares@blue.weeg.uiowa.edu Tissue Procurement: Dr. Gregg Hageman cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com). Seq primer: M13 Reverse. Location/Qualifiers 1..481 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="UI-E-COI-agg-j-18-0-UI" /clone_lib="UI-E-COI" /tissue_type="optic nerve" /dev_stage="adult" /lab_host="DH10B (Life Technologies) (T1 phage resistan)" /note="Ostern: eye; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-E-COI is a normalized cDNA library containing the following tissue(s): optic nerve. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (d)18 tail. The sequence tag for this library is CCAATTAGCTG. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)." | | |

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Comphen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: July 16, 2003, 19:43:49 ; Search time 43.293 Seconds
(without alignments)
2174.711 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 441362 seqs, 15338381 residues
Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 10 | 1418.5 | 85.8 | 1018 | 4 | US-08-458-356-194 Sequence 194, App |
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| 13 | 1418.5 | 85.8 | 1623 | 2 | US-08-751-767A-9 | Sequence 9, Appl |
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| 14 | 1418.5 | 85.8 | 2362 | 1 | US-08-265-087-1 | Sequence 1, Appl |
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| 24 | 193 | 11.7 | 1404 | 6 | 5480796-8 | Patent No. 5480796 |
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| 29 | 193 | 11.7 | 3319 | 4 | US-08-795-473B-2 | Sequence 2, Appl |
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| 37 | 170 | 10.3 | 1591 | 4 | US-09-211-590-1 | Sequence 1, Appl |
| 38 | 170 | 10.3 | 1591 | 5 | PCT-US91-03896-1 | Sequence 1, Appl |
| 39 | 149.5 | 9.0 | 2456 | 4 | US-09-151-102-1 | Sequence 1, Appl |
| 40 | 149.5 | 9.0 | 2456 | 4 | US-08-929-846-1 | Sequence 1, Appl |
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| 42 | 146.5 | 8.9 | 1714 | 4 | US-09-151-102-3 | Sequence 3, Appl |
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| 44 | 145 | 8.8 | 1800 | 4 | US-08-702-665A-4 | Sequence 4, Appl |
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ALIGNMENTS

RESULT 1
US-09-079-984A-11
Sequence 11, Application US/09079984A
Patent No. 6231850
GENERAL INFORMATION:
APPLICANT: Okano, Fumiyoshi, Satoh, Masahiro,
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: Canine interleukin 12, a production method
TITLE OF INVENTION: thereof, an immune disease treatment method and preventive
TITLE OF INVENTION: method using it
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Miller & Christenbury Intellectual Property
ADDRESS: Department of Schnader, Harrison, Segal and Lewis, LLP
STREET: 1600 Market Street, 39th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,984A
FILING DATE: 15-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Austin R. Miller
REGISTRATION NUMBER: 16,602
REFERENCE/DOCKET NUMBER: 1051-98
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-1810
TELEFAX: (215) 568-6946
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:

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? LENGTH: 990 base pairs
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? STRANDEDNESS: double
? TOPOLOGY: linear
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? ORIGINAL SOURCE:
? ORGANISM: Canis familiaris
? FEATURE:
? NAME/KEY: Canine IL12
? LOCATION: 1 to 987
? IDENTIFICATION METHOD: Similarity
US-09-079-984A-11

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Query Match: 100.00% Indels: 0
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QY 101 SerLysAsnLys1lePheLeuLysCysGluAlaLysAsnTrpSerGlyArgPheThrcys 120
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QY 181 AlaGluGlnSerLeuPro1leGlnValValAlaAla1leHisLysLeuLysTrpGlu 200
DB 607 GCCGAGAGAGCCTTACCATCGAGTGTGGTGGATGCTATTCTCAAGCTCAAGTATGAA 666
QY 201 AsnTrpThrSerSerPhePhe1leArgAsp1le1leLysProAspProProThrAsnLeu 220
DB 667 AACTACACACAGCGCTTCTTCATCAGACATCATCAAAACCAACCCCAAAACCTG 726
QY 221 GlnLeuLysProLeuLysAsnSerArgHisValGlnValSerTrpGluTrpProAspThr 240
DB 727 CAGCTGAACCATTTGAAAAATTTCTCGGACAGTGGAGTCAAGCTGGGAATACCCGACACC 786
QY 241 TrpSerThrProHisSerTrpPheSerLeuThrPheCys1leGlnAlaGlnGlyLysAsn 260

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DB 967 TGGGATCTGTGTCTCTGCACT 987

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RESULT 2
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? Patent No. 6231850
? GENERAL INFORMATION:
? APPLICANT: Okano, Fumiyoshi, Satoh, Masahiro,
? APPLICANT: Yamada, Katsushige
? TITLE OF INVENTION: Canine interleukin 12, a production method
? TITLE OF INVENTION: thereof, an immune disease treatment method and preventive
? TITLE OF INVENTION: method using it
? NUMBER OF SEQUENCES: 16
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Miller & Christenbury Intellectual Property
? ADDRESSEE: Department of Schneider, Harrison, Segal and Lewis, LLP
? STREET: 1600 Market Street, 39th Floor
? CITY: Philadelphia
? STATE: PA
? COUNTRY: USA
? ZIP: 19103
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy Disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: WordPerfect 5.1
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/079,984A
? FILING DATE: 15-MAY-1998
? ATTORNEY/AGENT INFORMATION:
? NAME: Austin R. Miller
? REGISTRATION NUMBER: 16,602
? REFERENCE/DOCKET NUMBER: 1051-98
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (215) 563-1810
? TELEFAX: (215) 568-6946
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 990 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA to mRNA
? ORIGINAL SOURCE:
? ORGANISM: Canis familiaris
? FEATURE:
? NAME/KEY: Canine IL12
? LOCATION: 1 to 987
? IDENTIFICATION METHOD: Similarity
US-09-079-984A-1

Alignment Scores:
Pred. No.: 1.8e-184 Length: 990
Score: 1640.00 Matches: 304
Percent Similarity: 99.67% Conservative: 2
Best Local Similarity: 99.02% Mismatches: 1
Query Match: 99.21% Indels: 0
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US-09-917-265-53 (1-307) x US-09-079-984A-1 (1-990)

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 QY 81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGlu 100
 Db TTGATTCACAAAAAAGATGGAATTTGTCACATGATATCTTAAAGCAACAGAAAGAA 366
 QY 101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
 Db TCCAAAAATAGACTTCTTGAATGTGAGGCAAAAGATTTATCTGACGTTTCACATGC 426
 QY 121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
 Db TGTGTGCTGAGCGCATCACTGATGATTTGAATTCAGTGTCAAGTACCAAGAGCTTC 486
 QY 141 SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgVal 160
 Db TCTGACCCCAAGGCGTGCATCTGCAGCAGTGCACCTTTCACACAGAGAGGCTCAGAGTGC 546
 QY 161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluLysSerAlaCysProSer 180
 Db GACACACAGGATTTATAGAGTACACAGTGCAGTGCAGAGGAGGAGTGCCTCCCTCT 606
 QY 181 AlaGluGluSerLeuProIleGluValValAspAlaIleHisLysLeuLysTyrGlu 200
 Db GCCGAGAGAGGCTACCATCGAGTGTGCTGATGATTCACACAGTCAAGTCAAGTGA 666
 QY 201 AsnTyrThrSerSerPheIleArgAspIleIleLysProAspProProThrAsnLeu 220
 Db AACTACACACGACCTTCTTCATCAGACATCATCAACCAACACCCACCAACCAACTG 726
 QY 221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpLeuLysProAspThr 240
 Db CAGCTGAGCCATGGAATTTCTCGCACGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 786
 QY 241 TrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 260
 Db TGGAGACACCCCATCTCTCTCTCCCTGACATTTTGCATACAGGCCCAAGGCAAGAAC 846
 QY 261 AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValValCysHis 280
 Db AATAAGAAAGAAAGATAGACTCTCGTGCACAAACCTCAACCCCAAGCTCGTGCAC 906
 QY 281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsp 300
 Db AAGCATGCCAGATCCGCTGCAGGCCGAGACCGCTACTATGATTCATCTGAGAGCAG 966
 QY 301 TrpAlaSerValSerCysSer 307
 Db TCGGCATCTGTGCCCTGCAGT 987

RESULT 3

US-08-848-760B-24
 : Sequence 24, Application US/08848760B
 : Patent No. 6248721
 : GENERAL INFORMATION:
 : APPLICANT: Chang, Lung-Ji
 : TITLE OF INVENTION: Animal Model For Evaluation Of Vaccines
 : NUMBER OF SEQUENCES: 33
 : CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
 STREET: 2421 N.W. 41st Street, Suite A-1
 CITY: Gainesville
 STATE: Florida
 COUNTRY: United States of America
 ZIP: 32606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentln Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/848,760B
 FILING DATE: 25-Jan-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/838,702
 FILING DATE: 09-Apr-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: PACE, DORAN R.
 REGISTRATION NUMBER: 38,261
 REFERENCE/DOCKET NUMBER: CNG-100C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (352) 375-8100
 TELEFAX: (352) 372-5800
 INFORMATION FOR SEQ. ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 987 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "DNA"
 SEQUENCE DESCRIPTION: SEQ ID NO: 24:
 US-08-848-760B-24
 Alignment Scores:
 Pred. No.: 2,13e-158 length: 987
 Score: 1419.50 matches: 261
 Percent Similarity: 91.86% conservative: 21
 Best Local Similarity: 85.02% mismatches: 24
 Query Match: 85.87% indels: 1
 DB: Gaps: 1
 US-09-917-265-53 (1-307) x US-08-848-760B-24 (1-987)
 QY 1 IletRPGluLeuGlulysAspValTyrValValGluLeuAspTrpHisProAspAlapro 20
 Db ATATGGGAAGTGGAGAAAGATGTTTATGTTGAGAGTGGACCTGGACCTGATGCCCC 126
 QY 21 GlyGluMetValValLeuThrCysHisThrProGluGluAspIleThrTrpThrSer 40
 Db GGAGAAATGATGCTCTCCACTCCCTCCATACCCTCGAAGAGATGACATCACTTGACCTCA 186
 QY 41 AlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
 Db GGCGAGAGAGTCAATCACTCAGTCTGCTGTAAGAACTGACCATCCAAAGTCAAGAAATTT 246
 QY 61 GlyAspAlaGlyGlnTyrThrCysHisLysGlyGlyLysValLeuSerArgSerLeuLeu 80
 Db GGAGATGCTGGCCAGATACCTCCATTAAGAGGAGAGGAGTCTTGAGCCCTCAGCTCTG 306
 QY 81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGlu 100
 Db TTGATTCACAAAAAAGATGGAATTTGTCACATGATATCTTAAAGCAACAGAAAGAA 366
 QY 101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
 Db TCCAAAAATAGACTTCTTGAATGTGAGGCAAAAGATTTATCTGACGTTTCACATGC 426
 QY 121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
 Db TGTGTGCTGAGCGCATCACTGATGATTTGAATTCAGTGTCAAGTACCAAGAGCTTC 486

QY 141 SeraspProGlnGlyValThrCysGluValAlaThrLeuSerAlaGluArgValAla 160
DB 487 TCTGACCCCAAGGGGTGACGTCGAGAGCTGCTACACTCTGCGAGAGAGATGACAGG 546
QY 161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProSer 180
DB 547 GACAAACAGAGATAT---GAGTACTCACTGAGAGTCCGAGAGACATGCTGCGAGCT 603
QY 181 AlaGluGluSerLeuProGlnGluValValAlaAlaAlaLeuHisLysLeuLysTyrGlu 200
DB 604 GCTGAGAGAGCTCTCCCATTCAGTCACTGATGATGATGATGATGATGATGATGATGAT 663
QY 201 AsnTyrThrSerSerPhePheLeuArgAspPheLeuLysProAspProPheAsnLeu 220
DB 664 AACTACACACACACCTCTTCATCAGGACATCATCAACCTGACCCCAACCAACTTG 723
QY 221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTyrGluTyrProAspThr 240
DB 724 CAGCTGAAGCCATTAAAGAAATTCCTGCGAGAGTGAAGTCAAGTGAAGTCAAGTGAAG 783
QY 241 TrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 260
DB 784 TGGAGTACTCCACTTCT 843
QY 261 AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValAlaCysHis 280
DB 844 AAGAGGAAAGAAAGATGAGTCTTCACCGACGACCAACCTCAGCAGCAGCTCATCTGCGC 903
QY 281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTyrSerAsp 300
DB 904 AAAAATGCCAGCATTTAGCTGGGCGCCGAGGACCGCTACTACTACTACTACTACTACT 963
QY 301 TrpAlaSerValSerCysSer 307
DB 964 TGGGATCTGCTGCTGCTGCTGCT 984
RESULT 4
US-09-310-842-4
Sequence 4, Application US/09310842A
Patent No. 6451593
GENERAL INFORMATION:
APPLICANT: Wiltig, Prof. Burghardt
APPLICANT: Jungmans, Claas
TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene
FILE REFERENCE: XI 597/99
CURRENT APPLICATION NUMBER: US/09/310,842A
EARLIER FILING DATE: 1995-05-12
EARLIER APPLICATION NUMBER: DE 196 48 625.4
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 1870
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: gene
LOCATION: (1)..(1870)
OTHER INFORMATION: Interleukin-12 (IL-12, p40-subunit); Oligo DNA Dumbbell
FEATURE:
NAME/KEY: misc_binding
LOCATION: (1)..(2)
OTHER INFORMATION: Intramolecular binding site; the T-nucleotides at position 1 to
FEATURE:
NAME/KEY: misc_binding
LOCATION: (1869)..(1870)
OTHER INFORMATION: Intramolecular binding site; the T-nucleotides at position 1869
FEATURE:
OTHER INFORMATION: to 1870 can be modified with amino or caroxy features
OTHER INFORMATION: Description of Artificial Sequence: Strandness: both; nucleic

OTHER INFORMATION: acid (linear), hypothetical: No. 6451593 anti-sense: No
US-09-310-842-4
Alignment Scores:
Pred. No.: 5,71e-158
Score: 1419.50
Percent Similarity: 91.86%
Best Local Similarity: 85.02%
Query Match: 85.87%
DB: 4
Gaps: 1
US-09-917-265-53 (1-307) x US-09-310-842-4 (1-1870)
QY 1 IleTPrpGluLeuGluLysAspValTyrValValGluLeuAspTyrPheProAspAlaPro 20
DB 699 ATATGGAACTGAAGAAAGATGTTATGCTGTAATAATGATGATGATGATGATGATGATGAT 758
QY 21 GlyIleuValValLeuThrCysHisThrProGluLysAspPheThrTyrPheSer 40
DB 759 GGAGAAATGGTGTCTCACCCTGACACCCCTGAGAAAGATGTTACCTGACCTTG 818
QY 41 AlaGlnSerSerGluValLeuGluGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
DB 819 GACCAGAGAGTGAAGTCTTAGGCTGCGAAACCCTGACCATCAAGTCAAGAGTTT 878
QY 61 GlyAspAlaGlyGlnTyrThrCysHisLysGlyLysValLeuSerArgSerLeuLeu 80
DB 879 GGAGATGCTGGCCAGTACACCTGTCAACAAAGAGAGGAGGAGTCTTAAGCATTCGCTCTG 938
QY 81 LeuIleHisLysLysGluAspGlyIleTyrPheThrAspIleLeuLysGluGlnLysGlu 100
DB 939 CTGCTTACCAAAAGAGAGATGAAATTTGTCACAGATATATTTAAAGGACCAAGAAAGAA 998
QY 101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
DB 999 CCCAAATATAGACCTTTTAAAGATCCGAGGCCAAGAAATTTCTGAGAGTTTCACCTGC 1058
QY 121 TrpTPrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgIlePhe 140
DB 1059 TGGTGGCTGACGACATCATGACTGATTTGACATTCAGTCAAAAGAGCAGAGCGCTCT 1118
QY 141 SeraspProGlnGlyValThrCysGluValAlaThrLeuSerAlaGluArgValAla 160
DB 1119 TCTGACCCCAAGGGGTGACGTCGAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1178
QY 161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProSer 180
DB 1179 GACAAACAGAGATAT---GAGTACTCACTGAGAGTCCGAGAGACATGCTGCGAGCT 1235
QY 181 AlaGluGluSerLeuProGlnGluValValAlaAlaAlaLeuHisLysLeuLysTyrGlu 200
DB 1236 GCTGAGAGAGCTCTCCCATTCAGTCACTGATGATGATGATGATGATGATGATGATGAT 1295
QY 201 AsnTyrThrSerSerPhePheLeuArgAspPheLeuLysProAspProPheAsnLeu 220
DB 1296 AACTACACACACACCTCTTCATCAGGACATCATCAACCTGACCCCAACCAACTTG 1355
QY 221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTyrGluTyrProAspThr 240
DB 1356 CAGCTGAAGCCATTAAAGAAATTCCTGCGAGAGTGAAGTCAAGTGAAGTCAAGTGAAG 1415
QY 241 TrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 260
DB 1416 TGGAGTACTCCACTTCT 1475
QY 261 AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValAlaCysHis 280
DB 1476 AAGAGGAAAGAAAGATGAGTCTTCACCGACGACCAAGCTCAAGCTCAAGCTCAAG 1535
QY 281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTyrSerAsp 300
DB 1536 AAAAATGCCAGCATTTAGCTGGGCGCCGAGGACCGCTACTACTACTACTACTACTTTGAG 1595

US-08-186-529-1

Alignment Scores:

| | | | |
|------------------------|-----------|---------------|-----|
| Pred. No.: | 2,79e-158 | Length: | 987 |
| Score: | 1418.50 | Matches: | 261 |
| Percent Similarity: | 91.86% | Conservative: | 21 |
| Best Local Similarity: | 85.02% | Mismatches: | 24 |
| Query Match: | 85.81% | Indels: | 1 |
| DB: | 1 | Gaps: | 1 |

US-09-917-265-53 (1-307) x US-08-186-529-1 (1-987)

```

OY 1 IletpGluLeuGluLysAspValTyrValAlaGluLeuAspTrpHisProAspAlaPro 20
Db ATATGGGAAGCTGAAGAAGATGTTATGCTAGCAATTTGATGATCGGATGCCCT 126
OY 21 GlyIuMetValValLeuThrCysHisThrProGluGluAspAspIleThrTrpHisSer 40
Db GGAGAAATGGTGGCTCCTACCTGTGACACCCCTGAAGAAGATGGTATCCTGACCTTG 186
OY 41 AlaGlnSerSerGluValIleGluGlySerGlyLysThrIleGlnValLysGluPhe 60
Db GACCAGAGCAGTGGAGCTTAAAGCTGTGCAAAACCTGACATCCAAAGTCAAGAGTTT 246
OY 61 GlyAspAlaGlyGlnTyrThrCysHisLysGlyGlyLysValLeuSerArgSerLeu 80
Db GAGATGCTGGCAGTACACCTGTCAAAAGAGGCGAGGTTCTTAAGCCATTGCTCTG 306
OY 81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGlu 100
Db CTGCTTCTCAAAAAGAGATGGAATTTGCTCAGATTTTAAAGACCAAGAAAGAA 366
OY 101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerLysArgPheThrCys 120
Db CCAAAAATAGACCTTTCTTAAGATCGAGGCAAAATATTTCTGAGCTTCACTGC 426
OY 121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerArgGlyPhe 140
Db TGTGTGCTGACGACATCAGTACTGATTTGACATTCAGTCAAAAGCAGAGAGCTCT 486
OY 141 SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgVal 160
Db TCTGACCCCAAGGGGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 546
OY 161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluLysSerAlaCysProSer 180
Db GACAAACAAGAGTAT---GAGTACTCAGTGGAGTCCAGAGAGAGAGTCCCTGCCACT 603
OY 181 AlaGluGlnSerLeuProIleGluValValAlaAspAlaIleHisLysLeuLysTyrGlu 200
Db GCTGAGAGAGTCTGCCATTTAGGTGATGTTGATGCTGCTGCTGCTGCTGCTGCTG 663
OY 201 AsnTyrThrSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeu 220
Db AACTACACAGAGCTTCTTCATCGAGACATCATCAACTGACCCCAAGAGAACTTG 723
OY 221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
Db CAGCTGAAGCATTAAAGAAATTCCTGGCAGGTGAGGTCAGCTGGAGTACCTCGACACC 783
OY 241 TrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 260
Db TGGAGTACTCCACATTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 843
OY 261 AsnArgGluLysLysAspArgLeuLysValAspLysThrSerAlaLysValAlaCysHis 280
Db AAGAGAGAAAGAAAGATAGAGTCTTCACGAGACAAGACCTGACGACGGTCACTGCCC 903
OY 281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsp 300
Db AAAATGCTCCAGCATTTAGCTGGGGGCCAGACGCTACTACTATGCTATCTTGAGAGCAA 963
OY 301 TrpAlaSerValSerCysSer 307

```

Db 964 TGGGCACTGTGCTGCCCTGCAGT 984

RESULT 7

US-08-640-386A-1

Sequence 1, Application US/08640386A

Patent No. 5756085

GENERAL INFORMATION:

APPLICANT: Sykes, Megan

TITLE OF INVENTION: USE OF INTERLEUKIN-12 TO PREVENT

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

STREET: Genetics Institute, Inc., Legal Affairs

CITY: Cambridge

STATE: MA

COUNTRY: USA

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/640,386A

FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

REFERENCE/DOCKET NUMBER: GI 5225A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-498-8224

TELEFAX: 617-876-5851

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 987 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

CELL TYPE: Lymphoblast

CELL LINE: RPMI 8866

FEATURE:

NAME/KEY: CDS

LOCATION: 1..987

US-08-640-386A-1

Alignment Scores:

| | | | |
|------------------------|-----------|---------------|-----|
| Pred. No.: | 2,79e-158 | Length: | 987 |
| Score: | 1418.50 | Matches: | 261 |
| Percent Similarity: | 91.86% | Conservative: | 21 |
| Best Local Similarity: | 85.02% | Mismatches: | 24 |
| Query Match: | 85.81% | Indels: | 1 |
| DB: | 1 | Gaps: | 1 |

US-09-917-265-53 (1-307) x US-08-640-386A-1 (1-987)

```

OY 1 IletpGluLeuGluLysAspValTyrValAlaGluLeuAspTrpHisProAspAlaPro 20
Db ATATGGGAAGCTGAAGAAGATGTTATGCTAGCAATTTGATGATCGGATGCCCT 126
OY 21 GlyIuMetValValLeuThrCysHisThrProGluGluAspAspIleThrTrpHisSer 40
Db GGAGAAATGGTGGCTCCTACCTGTGACACCCCTGAAGAAGATGGTATCCTGACCTTG 186
OY 41 AlaGlnSerSerGluValIleGluGlySerGlyLysThrIleGlnValLysGluPhe 60
Db GACCAGAGCAGTGGAGCTTAAAGCTGTGCAAAACCTGACATCCAAAGTCAAGAGTTT 246

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OY 61 GLYASPALAGLYINTYRTHRCYSHISLYSGLYLYSVALLEUSERARGSERLEU 80
DB 247 GGAGATGCTGGCCAGACACTGTCTCAAAAGAGGCGAGGTCTTAAGCCATTGCTCTG 306
OY 81 LEUILEHISLYSGLYNASPGLYLETTPSERTHASPILEULEULYSGLYINLYSGLU 100
DB 307 CTGCTTCACAAAAGACATGCAATTTGGTCCAGTCATATTTAAAGCAGCAAGAA 366
OY 101 SERLYSASNLISLEPHEULEULYSGLYLALALYASNTYSERGLYARGPHETHRYS 120
DB 367 CCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGATTAATCTGACCTTTCACCTGC 426
OY 121 TPTTPLEUTHRALALESERTHRASPLEULYSPHESERVALLYSSERSEARGGLYPHE 140
DB 427 TGTGCTGCTACGACATCATCTACTGATTTTGACATTGACTGTCAAAAGCAGCAGCTCT 486
OY 141 SERASPPROGLINGLYVALTHRCYSGLYAVALTHLEUSERALAGLUARGVAL 160
DB 487 TCTGACCCCAAGGCGTGACGTGCGGAGCTGCTACACTCTCTCAGAGAGAGTCAAGGC 546
OY 161 ASPASNARGASPTYRILYSYTYRTHRVALGLUCYSGLYINGLYSERALACYPROSER 180
DB 547 GACAACAAGAGATAT--GAGTACTAGTGGAGCTGCCAGAGACAGTGCCTGCCAGCT 603
OY 181 ALAGLUGLUSERLEUPROTLLEGUVALVALASPALALEHISLYSLEULYTYRGLU 200
DB 604 GCTGAGAGAGACTGCTGCCATTGAGGTCAAGTGTGATGCCGTTTCAACAGCTCAAGTATGAA 663
OY 201 ASNTYRTHRSERSEPHEHEILEARGASPILEILELYSPROASPPROPTHASNL 220
DB 664 AACTACACGACGAGCTTTTCAAGCATCAGGACATCATCAAACTGACCCCAAGAACTTG 723
OY 221 GINLEULYSPROLEULYSASNSERATGHSVALGLUVALSERTPGLUTYRPROASPTH 240
DB 724 CAGCTGAACCCATTAAAGAAATTCCTCGGAGGTGAGTCAAGTCAAGTCAAGTCAAGTCAAG 783
OY 241 TTPSERTHPROHISSEYRTHPHESELEUTHRPHCYSLLEGINLAGINGLYLSAS 260
DB 784 TGGACTACTCCACATTCTTCTACTTCTCTGACATTTGGCGTTTCAGGTCCAGGCGAAGAGC 843
OY 261 ASNARGLULYSLYSASPARGLUCYVALASPLYSTHSERALALYVALCYSHIS 280
DB 844 AAGAGAGAAAAGAGATAGAGTCTTCACGACCAACACTCAGCCAGCTCATCTGCCG 903
OY 281 LYSASPALALYSLIARGVALGLINLALAGSPARGTYRTHRSERSEYRTHSPSERASP 300
DB 904 AAAAATGCCAGCATTAAGCTCGGCGCCAGACCCGCTACTATAGCTCATCTTGACAGCAA 963
OY 301 TRPALASERVALSERCYSSER 307
DB 964 TGGCATCTGTGCTGCTGCACT 984

```

```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/184,009
FILING DATE: 19-JAN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEX: 425066CURTMS
INFORMATION FOR SPO ID NO: 194:
SEQUENCE CHARACTERISTICS:
LENGTH: 1018 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-184-009-194

Alignment Scores:
Pred. No.: 2,93e-158 Length: 1018
Score: 1418.50 Matches: 261
Percent Similarity: 91.86% Conservative: 21
Best Local Similarity: 85.02% Mismatches: 24
Query Match: 85.81% Gaps: 1
DB: 2

US-09-917-265-53 (1-307) x US-08-184-009-194 (1-1018)
OY 1 ILETTPGLULEUGLULYSASPVALTYYRVALGLULEUNASPTPHISPROASPALAPRO 20
DB 98 ATATGGGAATCGAAGAAAGATGTTTATGTCGTGAATTTGATGATGATGATGATGATGATGATG 157
OY 21 GLYGLMERVALVLEUTHRCYSHISHTHPRGGLUGLUNASPSPILETTPPTTHSER 40
DB 158 GGAGAAATGGTGTCTCTCACCTGTGACACCCCTGAAGAAAGATGTATCACCTGACCTTG 217
OY 41 ALAGLISERSEGLUVALLEUGLYSERGLYLYSTHRLEUTHRILEGINLALYSGLU 60
DB 218 GACACAGACGAGTACAGCTTAAAGCTTCGCAAAACCTGACCATTCAGTCAAGCAAGACTTT 277
OY 61 GLYASPALAGLYINTYRTHRCYSHISLYSGLYLYSVALLEUSERARGSERLEU 80
DB 278 GGAGATGCTGGCCAGTACACTGTCAACAAAGGAGCGAGGTCTAAGCCATTGCTCTG 337
OY 81 LEUILEHISLYSGLYNASPGLYLETTPSERTHASPILEULEULYSGLYINLYSGLU 100
DB 338 CTGCTTCACAAAAGAGATGGAATTTGGTCCAGTCAATTTTAAAGACCAAGAAAGAA 397
OY 101 SERLYSASNLISLEPHEULEULYSGLYLALALYASNTYSERGLYARGPHETHRYS 120
DB 398 CCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGATTAATCTGAGCTTTCACCTGC 457
OY 121 TPTTPLEUTHRALALESERTHRASPLEULYSPHESERVALLYSSERSEARGGLYPHE 140
DB 458 TGTGCTGCTACGACATCATCTACTGATTTTGACATTGACAGTGTCAAAAGCAGCAGAGCTCT 517
OY 141 SERASPPROGLINGLYVALTHRCYSGLYAVALTHLEUSERALAGLUARGVAL 160
DB 518 TCTGACCCCAAGGCGTGACGTGCGGAGCTGCTACACTCTCTCAGAGAGAGTCAAGGC 577
OY 161 ASPASNARGASPTYRILYSYTYRTHRVALGLUCYSGLYINGLYSERALACYPROSER 180
DB 578 GACAACAAGAGATAT--GAGTACTAGTGGAGTGGCAGGAGAGAGTGCCTGCCAGCT 634
OY 181 ALAGLUGLUSERLEUPROTLLEGUVALVALASPALALEHISLYSLEULYTYRGLU 200
DB 635 GCTGAGAGAGACTGCTGCCATTGAGTCAAGTGTGATGCCGTTTCAACAGCTCAAGTATGAA 694

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RESULT 8
US-08-184-009-194
: Sequence 194, Application US/08184009
: Patent No. 5833975
:
: GENERAL INFORMATION:
: APPLICANT: Paolelli, Enzo
: APPLICANT: Taraglia, James
: APPLICANT: Cox, William L.
: TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
: NUMBER OF SEQUENCES: 217
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Curtis, Morris & Safford
: STREET: 530 Fifth Avenue
: CITY: New York
: STATE: NY
: COUNTRY: USA
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible

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QY 201 AsnTYrThrSerSerPhePheIleArgAspIleIleLysProAspProProthrasLeu 220
 Db 695 AACTACACCGACGAGCTTCTTCATCAGGACATCATCAACCTGACCACCAAGACTTG 754
 QY 221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTrpProAspThr 240
 Db 755 CAGCTGAAGCATTAAAGAAATTCCTCGCAGGTGAGGTGACGCGGAGTACCTGACACC 814
 QY 241 TrpSerThrProHisSerTrpPheSerLeuThrPheCysIleGlnAlaGlnLysAsn 260
 Db 815 TGGAGTACTCCACATTCTCTACTCTCCCTGACATTCCTGCGTTGAGGTCCAGGCAAGAC 874
 QY 261 AsnArgGlnLysLysAspArgLeuCysValAspLysThrSerAlaLysValValCysHis 280
 Db 875 AAGAGAGAAAGAAAGATAGAGTCTTCACGGACAAACCTCAGCCAGCTCATCTGCCGC 934
 QY 281 LysAspAlaLysIleLeuArgValGlnAlaArgAspArgTrpTrpSerSerTrpSerAsp 300
 Db 935 AAAAATGCCAGCATTTAGCCTGCGGCGCCAGGACCGCTACTATAGTCTCATCTTGAGCCGA 994
 QY 301 TrpAlaSerValSerCysSer 307
 Db 995 TGGCATCTGTGCTGCAGT 1015

RESULT 9

US-08-458-356-194
 : Sequence 194, Application US/08458356
 : Patent No. 5942235
 : GENERAL INFORMATION:
 : APPLICANT: Paoletti, Enzo
 : APPLICANT: Tartaglia, James
 : APPLICANT: Cox, William I.
 : TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
 : NUMBER OF SEQUENCES: 217
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Curtis, Morris & Safford
 : STREET: 530 Fifth Avenue
 : CITY: New York
 : STATE: NY
 : COUNTRY: USA
 : ZIP: 10036
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/458,356
 : FILING DATE: 02-JUN-1995
 : CLASSIFICATION: 424
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 08/184,009
 : FILING DATE: 19-JAN-1994
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Frommer, William S.
 : REGISTRATION NUMBER: 25,506
 : REFERENCE/DOCKET NUMBER: 454310-2530
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (212) 840-3333
 : TELEFAX: (212) 840-0712
 : TELEX: 425066CURTMS
 : INFORMATION FOR SEQ ID NO: 194:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 1018 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: cDNA
 : US-08-458-356-194

Alignment Scores:

Pred. No.: 2,93e-158 Length: 1018
 Score: 1418.50 Matches: 261

Percent Similarity: 91.86% Conservative: 21
 Best Local Similarity: 85.02% Mismatches: 24
 Query Match: 85.81% Indels: 1
 DB: 2 Gaps: 1

US-09-917-265-53 (1-307) x US-08-458-356-194 (1-1018)

QY 1 IletPGLuLeuGluLysAspValIleValValGluLeuAspTrpHisProAspAlaPro 20
 Db 98 ATATGGAACTGAGAAAGATGTTATGTCGAGAAATTGGATTGGATCCGATCCCTCC 157
 QY 21 GlyGluMetValValLeuThrCysHisTrpProGluGluAspIleIleThrTrpSer 40
 Db 158 GGAGAAATGTGTGCTCCTCAGCTGTGACACCCCTGAAAGAGATGATGACCTGAGACCTTG 217
 QY 41 AlaGlnSerSerGlnValLeuGlnSerGlnLysThrLeuThrIleGlnValLysGluPhe 60
 Db 218 GACGACAGCAGTACGAGTCTTACGCTCTGCAAAACCTGACCATCCAAAGTAAAGATT 277
 QY 61 GlyAspAlaGlnIleTrpThrCysHisLysGlnIleValLysValLeuSerArgSerLeuLeu 80
 Db 278 GGAGATGCTGGCCAGTACACCTGTCAAAAGAGCGAGGCTTAAAGCATTCCTCCTG 337
 QY 81 LeuIleHisLysLysGluAspGlyIleTrpSerTrpAspIleLeuLysGlnIleGlu 100
 Db 338 CTGCTTCACAAAAGAGATGAAATTCGTCTCCTGCTCACTGATTTTAAAGACCAAGAAAGA 397
 QY 101 SerLysAsnLysIlePheLeuLysCysGlnAlaLysAsnTrpSerGlyArgPheThrCys 120
 Db 398 CCCAAAATTAACACCTTCTTAAGATCGCAGGCGCAAGATTAATTCGAGCTTCACCTGC 457
 QY 121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
 Db 458 TGGTGGCTGACCAACATAGTACTGATTTGACATTCAGTGTCAAAAGACGAGAGCTCT 517
 QY 141 SerAspProGlnGlyValIleThrCysGlnIleValIleThrLeuSerAlaGluArgVal 160
 Db 518 TCTGACCCCAAGGGGTGACGTGCGGAGCTGCTACACTTCTGCAGAGAGATCGAGAGG 577
 QY 518 TCTGACCCCAAGGGGTGACGTGCGGAGCTGCTACACTTCTGCAGAGAGATCGAGAGG 577
 Db 578 GACAAACAAAGAGTAT---GAGTACTCAGAGGAGTCGACAGAGACGAGTCCGCCAGCT 634
 QY 181 AlaGluGluSerLeuProIleGluValValValAlaIleHisLysLeuLysTrpGlu 200
 Db 635 GCTGAGAGAGTCTGCCCTTACGATGATGATGATGATGATGATGATGATGATGATGAT 694
 QY 201 AsnTYrThrSerSerPhePheIleArgAspIleIleLysProAspProProthrasLeu 220
 Db 695 AACTACACCGACGAGCTTCTTCATCAGGACATCATCAACCTGACCACCAAGACTTG 754
 QY 221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTrpProAspThr 240
 Db 755 CAGCTGAAGCATTAAAGAAATTCCTCGCAGGTGAGGTGACGCGGAGTACCTGACACC 814
 QY 241 TrpSerThrProHisSerTrpPheSerLeuThrPheCysIleGlnAlaGlnLysAsn 260
 Db 815 TGGAGTACTCCACATTCTCTACTCTCCCTGACATTCCTGCGTTGAGGTCCAGGCAAGAC 874
 QY 261 AsnArgGlnLysLysAspArgLeuCysValAspLysThrSerAlaLysValValCysHis 280
 Db 875 AAGAGAGAAAGAAAGATAGAGTCTTCACGGACAAACCTCAGCCAGCTCATCTGCCGC 934
 QY 281 LysAspAlaLysIleLeuArgValGlnAlaArgAspArgTrpTrpSerSerTrpSerAsp 300
 Db 935 AAAAATGCCAGCATTTAGCCTGCGGCGCCAGGACCGCTACTATAGTCTCATCTTGAGCCGA 994
 QY 301 TrpAlaSerValSerCysSer 307
 Db 995 TGGCATCTGTGCTGCAGT 1015

RESULT 10
 US-08-460-736-194

Sequence 194, Application US/08460736
Patent No. 6265189
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: Tartaglia, James
APPLICANT: Cox, William I.
TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
NUMBER OF SEQUENCES: 217
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,736
FILING DATE: 02-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/184,009
FILING DATE: 19-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEX: 425066CURTMS
INFORMATION FOR SEQ ID NO: 194:
SEQUENCE CHARACTERISTICS:
LENGTH: 1018 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-460-736-194

Alignment Scores:
Pred. No.: 2 93e-158 Length: 1018
Score: 1418.50 Matches: 261
Percent Similarity: 91.86% Conservative: 21
Best Local Similarity: 85.02% Mismatches: 24
Query Match: 85.81% Indels: 1
DB: 4 Gaps: 1

US-09-917-265-53 (1-307) x US-08-460-736-194 (1-1018)

QY 11etfpgluehluysaspaValtyrValglueusprtrpHisProaspalaPro 20
Db 98 ATATGGGAAGTGAAGAAAGATGTTATGTGTGAAGATGATTCGGAGCCCT 157
QY 21 GYGLImetValValleuthrCysSHStHrPProgluLuaspaspiethrtrpHrSer 40
Db 158 GGAGAAATGGTCTCTCACCTGTGACCCCTGACACCATGATACCTGACCTTG 217
QY 41 AlaglnSerSerIuValleuGlySerGlyLysThrleuthrIleGlnValLysGluPhe 60
Db 218 GACCAAGCAGTGTAGCTTACGCTCTGGCAAAACCTGACCATCCCAAGTCAAGAGCTTT 277
QY 61 GYAspAlaGlyLysIleThrCysSHStHrPProgluLuaspaspiethrtrpHrSer 80
Db 278 GGAGATGCTGGCCAGTACACCTGTCACAAGAGGAGGAGGTCTTAACCATTCGCTCTG 337
QY 81 LeuIleHisLysLysGluSpGlyIletrpSerThrAspIleLeuLysGluGlnLysGlu 100
Db 338 CTGCTTCACAAAAGAGATGGAATTTGGTCCACTCATATTTAAAGGACAGAAAGAA 397

QY 101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTrpSerGlyArgPheThrCys 120
Db 398 CCAAAAATTAAGACTTTCTTAAGATGCGAGGCCAAGAAATTTCTTGACGCTTACCTGC 457
QY 121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
Db 458 TGTGTGGCTGACGACATCAGTACATGATTTGACATTCAGTGTCAAAAGCAGGAGCGCT 517
QY 141 SerAspProGlnGlyValThrCysGlyAlaValIleLeuSerAlaGluArgValArgVal 160
Db 518 TGTGACCCCAAGGCGTGCCTGCGAGCTTCACCTCTCTGACAGAGAGTCAAGAGG 577
QY 161 AspAsnArgAspTrpLysLysTrpThrValGluCysGlnGlnGlySerAlaCysProSer 180
Db 578 GACACACAGAGATAT--GAGTACTCATGGAGTGCCAGAGACAGTGCCTGCCAGCT 634
QY 181 AlaGluGluSerLeuProIleGluValValAlaAlaValIleHisLysLysLysTrpGlu 200
Db 635 GCTAGAGGAGACTTCCCATTTGAGGTGATGCTGATGCGCTTCAACAGCTCAAGATATA 694
QY 201 AsnTrpThrSerSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeu 220
Db 695 AACTACACACACACTTCTTCATCAGGACATCATCAAACTGACCCCAAGAACCTTG 754
QY 221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTrpProAspThr 240
Db 755 CAGCTGAAGCCATTAAAGAAATTCGCGAGGTGAGGTCAGCTGGAGTACCTGACACC 814
QY 241 TrpSerThrProHisSerTrpPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 260
Db 815 TGGAGTACTCCACATTCCTACTTCTCCCTGACATTTGCGTTACAGGTCCAGGCAAGAGC 874
QY 261 AsnArgGluLysLysAspArgLeuCysValAlaLysLysThrSerAlaLysValAlaCysHis 280
Db 875 AAGAGAGAAAGAAAGATAGAGCTTCACGACCAAGACCTCAGCAGCTATCTGCCGC 934
QY 281 LysAspAlaLysIleGluValGlnAlaArgAspArgTrpTrpSerSerSerTrpSerAsp 300
Db 935 AAAATGTCACACATTAGCTGCGGGCCCGAGGACCGCTACTTACTTCTTGGAGCGAA 994
QY 301 TrpAlaSerValSerCysSer 307
Db 995 TGGCATCTGTGCTCCGAGT 1015

RESULT 11
US-08-751-767A-3
Sequence 3, Application US/08751767A
Patent No. 5994104
GENERAL INFORMATION:
APPLICANT: ANDERSON, ROBERT J.
APPLICANT: GRANT, HUGH
APPLICANT: MACDONALD, IAN D.
TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,767A
FILING DATE: 08-NOV-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.

REGISTRATION NUMBER: 36,663
 REFERENCE/DOCKET NUMBER: 117-221
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 7038164100
 TELEFAX: 7038164100
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1399 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 43..1026
 US-08-751-767A-3

Alignment Scores:
 Pred. No.: 4,79e-158
 Score: 1418.50
 Percent Similarity: 91.86%
 Best Local Similarity: 85.02%
 Query Match: 85.81%
 Gaps: 1

US-09-917-265-53 (1-307) x US-08-751-767A-3 (1-1399)

1 IletpGluLeuGluLysAspValTyrValAlaGluLeuAspTyrPheHisProAspAlaPro 20
 109 ATATGGAACTGAAAGAAAGATGTTATGCTGTAAGATTGATGATTCGGATGCCCT 168
 21 GlyIuMetValValLeuThrCysHisThrProGluGluAspSerLeuThrPheHis 40
 169 GGAGAAATGGTGGTCTCCTGACCTGACACCCCTGAAAGATGATGATCCTGACCTG 228
 41 AlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
 229 GACCAAGACAGTGGTGGTCTGAGCTGGCAAAACCTGACATCCAAAGTCAAGAGTTT 288
 61 GlyAspAlaGlyGlnTyrThrCysHisLysGlyGlyLysValLeuSerArgSerLeu 80
 289 GGAGATCTGGCAGTACCTCTCAACAAAGAGGCGAGGATCTTAAGCATTGCTGCTCG 348
 81 LeuIleHisLysLysGluAspGlyIleTyrSerThrAspIleLeuLysGluGlnLysGlu 100
 349 CTGCTTCACAAAAGAGAGATGGAATTGCTCAGATGATTTTAAAGCAGCAAGAA 408
 101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAspTyrSerGlyArgPheThrCys 120
 409 CCCAAAATAAGACCTTTCTAAGATCCGAGGCCAAGAAATATTCTGGACGTTTCACTGC 468
 121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
 469 TGTGTGCTCAGCAACATCAGTACTGATTTGACATTCAGTCAAAAGCAGCAGAGGCTCT 528
 141 SerAspProGlnGlyValThrCysGlyAlaValIleThrLeuSerAlaGluArgValArgVal 160
 529 TCTGACCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTTGCAAGAGAGTCAAGAGG 588
 161 AspAsnAlaGlyAspTyrLysLysTyrThrValGluCysGlnGlnGlySerAlaCysProSer 180
 589 GACAACAAGAGACTAT---GAGTACTCAGTGGAGTGGCAGAGAGACAGTGCCTGCCAGCT 645
 181 AlaGluGluSerLeuProIleGluValValAlaLysAlaIleHisLysLeuLysTyrGlu 200
 646 GCTGAGGAGAGCTGCCATTTGAGTGCATGTTGATGATCCCTGTCACAGCTCAAGATGAA 705
 201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPheThrAsnLeu 220
 706 AACTACACACAGCAGCTTCTTCATCAGGACATCATCAAACTGACCCAGCAAGAACTTG 765
 221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240

Db 766 CAGTGAAGCCATTAAAGAAATTCGCGAGCTGAGCTCAGCTGGGAGATACCTGACACC 825
 Oy 241 TrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 260
 Db 826 TGGAGTACTCCACATTCCTTCTCCTGACATTCCTGCGTTCAGGTCCAGGGCAAGAC 885
 Oy 261 AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValAlaCysHis 280
 Db 886 AAGAGAGAAAGAAAGATAGAGCTTCACGAGACAGACCTCAGCCAGCTCATCTGCCGC 945
 Oy 281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsp 300
 Db 946 AAAAATGCCAGATTAGCTGCGCGGCCAGACCGCTACTATAGCTCATCTTGAGACCAA 1005
 Oy 301 TrpAlaSerValSerCysSer 307
 Db 1006 TGGGCAATCTGTGCTGCACT 1026

RESULT 12

US-08-751-767A-11
 ? Sequence 11, Application US/08751767A
 ? Patent No. 5994104
 ? GENERAL INFORMATION:
 ? APPLICANT: ANDERSON, ROBERT J.
 ? APPLICANT: GRANT, HUGH
 ? APPLICANT: MACDONALD, IAN D.
 ? TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN
 ? NUMBER OF SEQUENCES: 80
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: NIXON & VANDERHVE P.C.
 ? STREET: 1100 NORTH GLEBE ROAD
 ? CITY: ARLINGTON
 ? STATE: VA
 ? COUNTRY: USA
 ? ZIP: 22201
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Floppy disk
 ? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: PatentIn Release #1.0, Version #1.30
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/08/751,767A
 ? FILING DATE: 08-NOV-1996
 ? CLASSIFICATION: 536
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: SADOFF, B.J.
 ? REGISTRATION NUMBER: 36,663
 ? REFERENCE/DOCKET NUMBER: 117-221
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: 7038164100
 ? TELEFAX: 7038164100
 ? INFORMATION FOR SEQ ID NO: 11:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 1560 base pairs
 ? TYPE: nucleic acid
 ? STRANDEDNESS: double
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: cDNA
 ? FEATURE:
 ? NAME/KEY: CDS
 ? LOCATION: 1..1557
 ? US-08-751-767A-11

Alignment Scores:
 Pred. No.: 5.67e-158
 Score: 1418.50
 Percent Similarity: 91.86%
 Best Local Similarity: 85.02%
 Query Match: 85.81%
 Gaps: 1

US-09-917-265-53 (1-307) x US-08-751-767A-11 (1-1560)

QY 1 IletRpLuleuGluLysAspValTyrValValGluLeuAspTrpHisProAspAlaPro 20
Db 4 ATATGGAGACTGAAAGAAAGATGTTATGTCTGATACATTGGATTGGATCCGATGCCCT 63
QY 21 GlyGluMetValValLeuThrCysHisThrProGluLysAspIleThrTrpThrSer 40
Db 64 GGAGAAATGGTGGTCTCAGCTGTGACACCCCTGAAGAGATGATATCAGCTGAGACCTTG 123
QY 41 AlagInserSerGluValLeuGlySerGlyLysThrIleuThrIleGlnValLysGluPhe 60
Db 124 GACCAGAGCAGTGAAGGCTTATAGGCTGTGGCAAAACCTGACCATTCAGTAAGAGATT 183
QY 61 GlyAspAlaGlyGlnTyrThrCysHisLysGlyLysValLeuSerArgSerLeuLeu 80
Db 184 GGAGATCGTGGCCAGTACCTGTCCACAAAGAGGAGCGAGCTTCAACCCATTCCTCTCTG 243
QY 81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGlu 100
Db 244 CTGCTTCACAAAAGGAAGATGGAATTTGTCACCTATATTTTAAAGACCAAGAA 303
QY 101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
Db 304 CCAAAAATATAGACCTTTCTAAGATGCGAGGCCAAGATTTATTTGACGTTTACCTGC 363
QY 121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
Db 364 TGTGGCTGACGACATCAGTACGATTGATTCAGCTGCTCAAAACAGACAGAGCTCT 423
QY 141 SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgVal 160
Db 424 TCTGACCCCAAGGGGTGAGCTGGAGCTGCTACACTCTCTGAGAGAGAGTCAAGAG 483
QY 161 AspAsnArgAspTyrLysLysTyrThrValGluLysGlnGluLysSerIleAspProSer 180
Db 484 GACAACAGAGAGAT---GAGTACTCAGTGGAGTGGCAGAGACAGACATGCTGCCAGCT 540
QY 181 AlaGlnGluSerLeuProIleGluValValAlaAspAlaIleHisLysLeuLysTyrGlu 200
Db 541 GCTGAGAGAGTCTGCCCATTTGAGTCAATGGTGGATCCCTGCACAGCTCAAGTATGAA 600
QY 201 AsnTyrThrSerSerPhePheIleArgAspIleLysProAspProThrAsnLeu 220
Db 601 AACTACACCGACGACTTCTTCATCAGGACATCATCAACCTGACCCACCAAGACCTTG 660
QY 221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
Db 661 CACTGAGACCATTAAGAAATTTCTCGCAGCTGAGGTGAGCTGGAGTACCTGGACACC 720
QY 241 TrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 260
Db 721 TGGAGTACTCCACATTCCTACTCTCTCCCTGACATTCGCTTCAGTCCAGGCGCAAGAC 780
QY 261 AsnArgGluLysLysAspArgLeuGlyValAspLysThrSerAlaLysValValCysHis 280
Db 781 AAGAGAGAAAGAAAGATAGAGTTCACGACACAGACCTCAGCAGCATCTGCGCGC 840
QY 281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsp 300
Db 841 AAAAATGCCAGCATTCAGCTGCGCGCGCCAGACCGCTACTACTATCTTGAGCGAA 900
QY 301 TrpAlaSerValSerCysSer 307
Db 901 TCGCATCTGTCCTCCCTGCACT 921

RESULT 13

US-08-751-767A-9
Sequence 9, Application US/08751767A
Patent No. 5994104
GENERAL INFORMATION:
APPLICANT: ANDERSON, ROBERT J.
APPLICANT: GRANT, HUGH
APPLICANT: MACDONALD, IAN D.
TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN

NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,767A
FILING DATE: 08-NOV-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B. J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 117-221
TELEPHONE: 7038164091
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1623 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1620
US-08-751-767A-9
Alignment Scores:
Pred. No.: 6,02e-158 Length: 1623
Score: 1418.50 Matches: 261
Percent Similarity: 91.86% Conservative: 21
Best Local Similarity: 85.02% Mismatches: 24
Query Match: 85.81% Indels: 1
DB: Gaps: 1
US-09-917-265-53 (1-307) x US-08-751-767A-9 (1-1623)
QY 1 IletRpLuleuGluLysAspValTyrValValGluLeuAspTrpHisProAspAlaPro 20
Db 67 ATATGGAGACTGAAAGAAAGATGTTATGTCTGATACATTGGATTGGATCCGATGCCCT 126
QY 21 GlyGluMetValValLeuThrCysHisThrProGluLysAspIleThrTrpThrSer 40
Db 127 GGAGAAATGGTGGTCTCAGCTGTGACACCCCTGAAGAGATGATATCAGCTGAGACCTTG 186
QY 41 AlagInserSerGluValLeuGlySerGlyLysThrIleuThrIleGlnValLysGluPhe 60
Db 187 GACCAGAGCAGTGAAGGCTTATAGGCTGTGGCAAAACCTGACCATTCAGTAAGAGATT 246
QY 61 GlyAspAlaGlyGlnTyrThrCysHisLysGlyLysValLeuSerArgSerLeuLeu 80
Db 247 GGAGATCGTGGCCAGTACCTGTCCACAAAGAGGAGCGAGTTCAAACCCATTCCTCTCTG 306
QY 81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGlu 100
Db 307 CTGCTTCACAAAAGGAAGATGGAATTTGTCACCTATATTTTAAAGACCAAGAA 366
QY 101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
Db 367 CCAAAAATATAGACCTTTCTAAGATGCGAGGCCAAGATTTATTTGACGTTTACCTGC 426
QY 121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
Db 427 TGTGGCTGACGACATCAGTACGATTGATTCAGTGTGTCAAAACAGACAGAGCTCT 486


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OY 261 AsnaAGGIGLULSLYASpArgrLeucYValAspLYSThrSerAlaLYSValCYSHLS 285
DB 876 AAGAGAGAAACAAAGACATAGAGTCTTCCACCGACACMACCTCCACCCAGCGTCCGCC 935
OY 281 LysAspAlaLYSLeIeaYrValGlnAlaArGAspArGTYrTYrSerSerSerTrpSerAsp 300
DB 936 AAAATTCAGCATTAAGCCTGCGGGCCGACGACCGCTACTATTAAGTCATCTTGAGCGAA 995
OY 301 TrpAlaSerValSerCYSer 307
DB 996 TGGGATCTGTCTCCCTGCGAGT 1016

RESULT 15
US-08-621-493-1
: Sequence 1, Application US/08621493
: Patent No. 5723127
: GENERAL INFORMATION:
: APPLICANT: Scott, Phillip
: APPLICANT: Trinchieri, Giorgio
: TITLE OF INVENTION: Compositions and Methods for Use of
: TITLE OF INVENTION: IL-12 as an Adjuvant
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Howson and Howson
: STREET: Spring House Corporate Center, PO Box 457
: CITY: Spring House
: STATE: Pennsylvania
: COUNTRY: USA
: ZIP: 19477
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/621,493
: FILING DATE: 25-MAR-1996
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/265,087
: FILING DATE: 17-JUN-1994
: APPLICATION NUMBER: US 08/229,282
: FILING DATE: 18-APR-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Bak, Mary E.
: REGISTRATION NUMBER: 31,215
: REFERENCE/DOCKET NUMBER: WSP51AUSA
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 215-540-9206
: TELEFAX: 215-540-5818
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2362 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: unknown
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 33..1016
: US-08-621-493-1

Alignment Scores:
Pred. No.: 1,08e-157 Length: 2362
Score: 1418.50 Matches: 261
Percent Similarity: 91.86% Conservative: 21
Best Local Similarity: 85.02% Mismatches: 24
Query Match: 85.81% Indels: 1
DB: 1 Gaps: 1

US-09-917-265-53 (1-307) x US-08-621-493-1 (1-2362)

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| QY | 21GlyGluMetValValLeuThrCysHisThrProGluGluAspIleThrTrpThrSer | 40 |
| Dp | 159GGAGAAATGGTGGTCTCTACCTGTGACACCCCTGAAGAAGATGGTATACCTGGACCTTG | 218 |
| QY | 41AlaGlnSerSerGluValLeuGlySerGlyTyrThrLeuThrIleGlnValLysGluPhe | 60 |
| Dp | 219GACCAAGAGAGTGGAGGCTTTAGGCGCTGGCAAAACCCGACCATTCACAAAGTCAAGAGCTTT | 278 |
| QY | 61GlyAspAlaGlyGlnTrpThrCysHisLysGlyGlyLysValLeuSerArgSerLeuLeu | 80 |
| Dp | 279GGAGATGCTGGCCAGTACCTGTGACAAAGAGGCGGTTCTTAAGCCATTGCTCTCTG | 338 |
| QY | 81LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGlu | 100 |
| Dp | 339CTGCTTCACAAAAGGAAGATGGATTTGGTCCACTGATATTTTAAAGACACAAAGAA | 398 |
| QY | 101SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys | 120 |
| Dp | 399CCCAAAATAAGACCTTTCTTAAGAGTGCAGAGGCCAAAGATTATCTGGACGTTTCACTTC | 458 |
| QY | 121TrpTrpLeuThrValIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe | 140 |
| Dp | 459TGGTGGCTGACGCAATCTAGTACTATATTGGACATTCAATGTGCAAAGAGCAGGGCTCT | 518 |
| QY | 141SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgVal | 160 |
| Dp | 519TCTGACCCCCAAGGGGTGACGTGGGAGCTGTACTCTCTGCAAGAGAGTCAAGCG | 578 |
| QY | 161AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProSer | 180 |
| Dp | 579GACAAACAAGAGATAT--GAGTACACAGTGGAGTCCAGAGACAGACAGTCCCTGCCAGCT | 635 |
| QY | 181AlaGlnGlnSerLeuProIleGlnValValValAspAlaIleHisLysLeuLysTyrGlu | 200 |
| Dp | 636GCTGAGAGAGAGTGGCCCATTTAGGTCATGTGGATGCGCTTCACACAGCTCAAGTATGAA | 695 |
| QY | 201AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeu | 220 |
| Dp | 696AAGTACACAGCAGCTTCTTTCATCAGGACATCATCAAACTGACCCACCAACAAAGACTTG | 755 |
| QY | 221GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr | 240 |
| Dp | 756CAAGCTAAGCCATTAAAGATTCTCGGCAAGGTGGAGGTACCTGGAGTACCTGGACACC | 815 |
| QY | 241TrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnIleGlnGlyLysAsn | 260 |
| Dp | 816TGGAGTACTCCACATTCTCTTCTCCCTGACATTTCTCGTTGACGGTCCAGGCAAGAGC | 875 |
| QY | 261AsnArgGlnLysLysAspArgLeuCysValAspLysThrSerAlaLysValValCysHis | 280 |
| Dp | 876AAGAGAGAAAAGAAAGATAGAGTCTTCAACGGACAAGACCTCAGCCAGGTCATCTGCCGC | 935 |
| QY | 281LysAspAlaLysIleLeuArgValGlnAlaLeuArgAspArgTyrTyrSerSerSerTrpSerAsp | 300 |
| Dp | 936AAAAATGCCAGATTAGCTGCGGGCCAGCAGCCGCTACTTATGCTCATCTTGGAGCGAA | 995 |
| QY | 301TrpAlaSerValSerCysSer | 307 |
| Dp | 996TGGGCATCTGTGCTCCCTGCAGT | 1016 |

Search completed: July 17, 2003, 09:32:10
Job time : 49.293 secs

US-09-917-265-53 (1-307) X US-08-621-493-1 (1-2362)

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: July 16, 2003, 19:59:04 ; Search time 209.737 Seconds
(without alignments)
3019.692 Million cell updates/sec

Title: US-09-917-265-53
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Sequence: 1 IWELEKDYVVELDWHDPAP.....QARDRYSSWSMDASVSCS 307

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1439767 seqs, 1031500376 residues
Total number of hits satisfying chosen parameters: 2879534

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=published_Applications_NA -QFMT=fastap -SUFFIX=p2n.rnpb -MIMATCH=0.1
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-TRANS-human40.csl -LIST=45 -OCALICN=200 -THR_SCORE=pct -THR_MAX=100
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Database :

Published Applications_NA:*
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17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------------------------|
| 1 | 1653 | 100.0 | 921 | 10 | US-09-917-265-52 Sequence 52, Appl |

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| C | 2 | 1653 | 100.0 | 921 | 10 | US-09-917-265-54 | Sequence 54, Appl |
| C | 3 | 1653 | 100.0 | 987 | 10 | US-09-917-265-58 | Sequence 58, Appl |
| C | 4 | 1653 | 100.0 | 987 | 10 | US-09-917-265-60 | Sequence 60, Appl |
| C | 5 | 1653 | 100.0 | 1533 | 10 | US-09-917-265-66 | Sequence 66, Appl |
| C | 6 | 1653 | 100.0 | 1533 | 10 | US-09-917-265-68 | Sequence 68, Appl |
| C | 7 | 1653 | 100.0 | 1599 | 10 | US-09-917-265-61 | Sequence 61, Appl |
| C | 8 | 1653 | 100.0 | 1599 | 10 | US-09-917-265-63 | Sequence 63, Appl |
| C | 9 | 1653 | 100.0 | 2267 | 10 | US-09-917-265-107 | Sequence 107, App |
| C | 10 | 1653 | 100.0 | 2267 | 10 | US-09-917-265-109 | Sequence 109, App |
| C | 11 | 1554 | 94.0 | 921 | 15 | US-10-079-616-6 | Sequence 6, Appl1 |
| C | 12 | 1554 | 94.0 | 921 | 15 | US-10-079-616-7 | Sequence 7, Appl1 |
| C | 13 | 1554 | 94.0 | 987 | 10 | US-09-917-265-29 | Sequence 29, Appl |
| C | 14 | 1554 | 94.0 | 987 | 10 | US-09-917-265-31 | Sequence 31, Appl |
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| C | 16 | 1550 | 93.8 | 985 | 10 | US-09-917-265-55 | Sequence 55, Appl |
| C | 17 | 1550 | 93.8 | 985 | 10 | US-09-917-265-57 | Sequence 57, Appl |
| C | 18 | 1546 | 93.5 | 921 | 10 | US-09-917-265-26 | Sequence 26, Appl |
| C | 19 | 1546 | 93.5 | 921 | 10 | US-09-917-265-28 | Sequence 28, Appl |
| C | 20 | 1546 | 93.5 | 1533 | 10 | US-09-917-265-43 | Sequence 43, Appl |
| C | 21 | 1546 | 93.5 | 1533 | 10 | US-09-917-265-45 | Sequence 45, Appl |
| C | 22 | 1546 | 93.5 | 1599 | 10 | US-09-917-265-38 | Sequence 38, Appl |
| C | 23 | 1546 | 93.5 | 1599 | 10 | US-09-917-265-40 | Sequence 40, Appl |
| C | 24 | 1419.5 | 85.9 | 987 | 11 | US-09-826-825-24 | Sequence 24, Appl |
| C | 25 | 1419.5 | 85.9 | 1870 | 15 | US-10-228-811-4 | Sequence 4, Appl1 |
| C | 26 | 1419.5 | 85.9 | 2318 | 15 | US-10-172-399-7 | Sequence 7, Appl1 |
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| C | 28 | 1419.5 | 85.9 | 8578 | 10 | US-09-828-825-3 | Sequence 3, Appl1 |
| C | 29 | 1419.5 | 85.9 | 8608 | 10 | US-09-828-825-7 | Sequence 7, Appl1 |
| C | 30 | 1419.5 | 85.9 | 8623 | 10 | US-09-828-825-5 | Sequence 5, Appl1 |
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| C | 33 | 1419.5 | 85.9 | 8644 | 10 | US-09-828-825-13 | Sequence 13, Appl |
| C | 34 | 1419.5 | 85.9 | 8659 | 10 | US-09-828-825-11 | Sequence 11, Appl |
| C | 35 | 1418.5 | 85.8 | 987 | 11 | US-09-754-014-2 | Sequence 2, Appl1 |
| C | 36 | 1418.5 | 85.8 | 987 | 11 | US-09-754-014-3 | Sequence 3, Appl1 |
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| C | 39 | 1418.5 | 85.8 | 2362 | 11 | US-09-924-703-3 | Sequence 3, Appl1 |
| C | 40 | 1058.5 | 64.0 | 1840 | 15 | US-10-172-399-3 | Sequence 3, Appl1 |
| C | 41 | 193 | 11.7 | 3477 | 11 | US-09-935-868-25 | Sequence 25, Appl |
| C | 42 | 193 | 11.7 | 3477 | 11 | US-10-287-035-25 | Sequence 25, Appl |
| C | 43 | 193 | 11.7 | 3507 | 15 | US-09-935-868-23 | Sequence 23, Appl |
| C | 44 | 193 | 11.7 | 3507 | 15 | US-10-287-035-23 | Sequence 23, Appl |
| C | 45 | 178 | 10.8 | 1363 | 11 | US-09-359-672-6 | Sequence 6, Appl1 |

ALIGNMENTS

RESULT 1
US-09-917-265-52
Sequence 52, Application US/09917265
Patent No. US2002052030A1
GENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Boroahs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USFS TH
FILE REFERENCE: 1X-5
CURRENT APPLICATION NUMBER: US/09/917,265
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 109
SOFTWARE: PatentIn version 3.1
SEQ ID NO 52
LENGTH: 921
TYPE: DNA
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(921)
OTHER INFORMATION:
US-09-917-265-52

Alignment Scores:

Pred. No.: 3, 21e-194 Length: 921
 Score: 1653.00 Matches: 307
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-09-917-265-53 (1-307) x US-09-917-265-52 (1-921)

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DB 121 GCGCAGACGACGTAGTCTGCTGTAAGCTGACCATCCCAAGTCAAGAAATTT 180
QY 61 GIYASPALAGLYGLNTYTRTHRCYSHISLYSGLYLYSVALLEUSERARGSERLEU 80
DB 181 GGAGATGCTGGCCACTATACCTGCCTAAAGAGGCAAGTTCTAGCCGCTCCTCCTG 240
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DB 241 TTGATTTCACAAAAAAGAAAGATGGAAATTGGTCCACATGATCTTAAAGAACAGAAAGA 300
QY 101 SERLYSASNLYSILEPHELEULYSCYSGUALALYSASNTYRSEGLYARGPHETHRYS 120
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QY 301 TRPALASERVALSERCYSSER 307
DB 901 TGGGCATCTGTCTCTGCAGT 921

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RESULT 2

US-09-917-265-54/c

Sequence 54, Application US/09917265

Patent No. US20020052030A1

GENERAL INFORMATION:

APPLICANT: Wondeling, Ramani S.

TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH

FILE REFERENCE: IM-5

CURRENT FILING DATE: 2001-07-27

PRIOR APPLICATION NUMBER: 60/223, 016

PRIOR FILING DATE: 2000-08-04

NUMBER OF SEQ ID NOS: 109

SOFTWARE: PatentIn version 3.1

SEQ ID NO 54

LENGTH: 921

TYPE: DNA

ORGANISM: Canis familiaris

US-09-917-265-54

Alignment Scores:

Pred. No.: 3, 21e-194 Length: 921
 Score: 1653.00 Matches: 307
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-09-917-265-53 (1-307) x US-09-917-265-54 (1-921)

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DB 441 TCTGACCCCAAGGGGTGACATGTGAGAGAGTACACTTTCAGCAGAGAGGCTCAGAGTG 682
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: Sequence 58, Application US/09917265
: Patent No. US20020052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: APPLICANT: Boroughs, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
: FILE REFERENCE: IM-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: PRIOR FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: PRIOR FILING DATE: 2000-08-04
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 58
: LENGTH: 987
: TYPE: DNA
: ORGANISM: Canis familiaris
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(987)
: OTHER INFORMATION:
US-09-917-265-58
Alignment Scores:
Pred. No.: 3,55e-194 Length: 987
Score: 1653.00 Matches: 307
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
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QY 41 AlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
Db 187 GCGCAGACGACGTAAGATCTCTAGCTTCTGTAAGAACCTCTGACCATCCAGTCAAGAAATTT 246
QY 61 GlyAspAlaGlyGlnTyrrThrCysHisLysGlyGlyLysValLeuSerArgSerLeuLeu 80
Db 247 GGAGATGCTGCCAGTATACCTGCCATTAAGAGAGCAAGGTTCTGAGCCGCTCCTCTG 306

QY 81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGlu 100
Db 307 TTGATTCACAAAAGAAAGATGAGATTTGGTCCACTGATATCTTAAAGAAACAGAAAGAA 366
QY 101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrrSerGlyArgPheThrCys 120
Db 367 TCCAAAATATAGATCTTCTCTGAATATGAGGCAAAAGAAATTTCTGGACGTTTCACATGC 426
QY 121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
Db 427 TGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTCCAAAAGATGACGAGGCTTC 486
QY 141 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluArgValArgVal 160
Db 487 TCTACCCCAAGGGGGTGGACATGGAGCACTGACCTTTCAGCAGAGAGGGTCAGAGTG 546
QY 161 AspAsnArgAspTyrrLysLysTyrrThrValGluCysGlnGluGlySerAlaCysProSer 180
Db 547 GACAAACAGGATTTAAAGAACTACACAGTGAAGTGTAGAGAGGACAGTGCCTGCCCTCT 606
QY 181 AlaGluLysLeuProIleGluValValLysAspAlaIleHisLysLeuLysTyrrGlu 200
Db 607 GCCGAGGAGAGCCCTACCCATCGAGCTGCTGCTGATCTTATTCACAAAGCTCAAGTATGAA 666
QY 201 AsnTyrrThrSerSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeu 220
Db 667 AACTACACACGACCTTCTTATCAGAGACTCATCAAAACCCAGACCCACCAAAACCTG 726
QY 221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrrProAspThr 240
Db 727 CAGCTGAAGCCATTGAAAAATTTCTCGGCACCTGAGAGTGCACCTGGAAATACCCGACACC 786
QY 241 TrpSerThrProHisSerTyrrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 260
Db 787 TGGAGCACCCACCATTCCTACTCTCCCTGACATTTTGCAATACAGGCCCGACGCAAGAAC 846
QY 261 AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValValCysHis 280
Db 847 AATAGAGAAAAGAAAGATAGACTCTGCTGTCGACAAAGCTCAGCAAGTGTGTGTGCCAC 906
QY 281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrrTyrrSerSerSerTrpSerAsp 300
Db 907 AAGGATGCCAAAGATCCCGTGCAAGCCCGAGACCGCTACTATATTCATCTTGACGAGAC 966
QY 301 TrpAlaSerValSerCysSer 307
Db 967 TGGGCATCTGTCTATGATGCACT 987
RESULT 4
US-09-917-265-60/c
: Sequence 60, Application US/09917265
: Patent No. US20020052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: APPLICANT: Boroughs, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
: FILE REFERENCE: IM-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: PRIOR FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: PRIOR FILING DATE: 2000-08-04
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 60
: LENGTH: 987
: TYPE: DNA
: ORGANISM: Canis familiaris
US-09-917-265-60
Alignment Scores:
Pred. No.: 3,55e-194 Length: 987
Score: 1653.00 Matches: 307

Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-09-917-265-53 (1-307) x US-09-917-265-60 (1-987)

QY 1 ILETPGLULEUGLULYSASPYALTYRYVALIGLULEUASPTRPHISPROASPALAPRO 20
 DB ATATGGGAACCTGGAGAAAGATGTTATGTTAGAGTTGAGCTGGACCGCATGCCGCC 862
 QY 21 GYGLUMETVALVALLLEUTHRCYSHISHPROGLUGLULASPAPILEHTRPHRSER 40
 DB GGAGAAATGCTGCTCCTACCTGACCTGACCTGACCTGAGAAAGATGACATCTGGAGCTCA 802
 QY 41 ALAAGINSERSEGLUVALLEUGLISERGLYLSYTHRLUTHRIEGLINALLYSGIUPHE 60
 DB GCGCAGAGCAGTGAAGTCTAGGTTCTGTGTAAGCTCAGCTCACCATCCAAAGATTT 742
 QY 61 GLYASPALAGLYGLNTRYTHRCYSHISLYSGLYGLYVALLEUSERARISERLEUEN 80
 DB GGAGATGCTGGCCAGATACCTGCCATTAAGAGGCAAGGTTCTGAGCGCTCAGCTCC 682
 QY 81 LEULLIEHISLYSGIULASPGLYILETPSERTHRASPILEULYSGIULINLYSGIU 100
 DB TTGATTCACAAAAGAGATGAAATTTGCTCCAGATATCTTAAAGAGACAGAAAGAA 622
 QY 101 SERLYSASNLYSILEPHEULYSCYGLUALALYSASNTYSEGLYARPHETRCYS 120
 DB TCCAAAAATAGATCTTCTGAAATGTGAGGCAAGATTTATTCGACGTTTCACATGC 562
 QY 121 TPTPTPLEUTHRALIIESETHRASPLEULYSPHESERVALLYSERARISERAGLYPHE 140
 DB TGGTGGCTCAGCGCATCATGATCTGATTTGAAATTCAGTCAAAAGTGCAGAGGCTTC 502
 QY 141 SERASPROGLINGLYVALTHRCYSGLYALVALTHLEUSERALAGLUARYVALARGVAL 160
 DB TTTGACCCCAAGGGGTGACATGTGAGCAGTGCCTTCAGCAGAGGGGTGACAGTGC 442
 QY 161 ASPASNARASPTLYLYLSYSTRYTHRVALIGIUCYSGINGLYSERAACYPROSER 180
 DB GACACACAGGATTTATAGAAAGTACACAGTGCAGTGCAGAGGCGTCCGCCCTCT 382
 QY 181 ALIAGIUGLUSERLEUPROILEGLUVALVALASPALAIEHISLYSEULYSTYRGIU 200
 DB GCCGAGAGAGGCTTACCATCGAGGTCGTGGATGCTATTCCAAAGCTCAAGTATGAA 322
 QY 201 ASNTYRTHRSERSEPHHEILEARGASPIELLELYSPROASPROPROTHIRANLEU 220
 DB AACCTACACAGCAGCTTTCTTCATCAGACATCATCAACACACACCCACCAACCTG 262
 QY 221 GINLEULYSPROLEULYSANSEARHISVALIGIUALISERTPGLIUTYRPROASPIH 240
 DB CAGCTGACAGCATTTGAAAAATTCGCGCAGCGTGGAGTGCAGTGGGAATACCCCGAC 202
 QY 241 TRPSETRTHPROHISSEYRPHESERLEUTHRPHIECYSILEGLINALEGLINLYSASN 260
 DB TCGAGACCCCAACATTCCTACTTCCCTGACATTTTTCATACAGGCCCAAGGCAAGAAC 142
 QY 261 ASNATRGILYLSYSPATRYLEUCYSVALASPLYSTHSEALALYSVALIYSHIS 280
 DB AATAGAGAAAAGAAAGATAGACTCTGCGTGACACAGACTCAGCCCAAGGTGCTGCTCCAC 82
 QY 281 LYSASPALALYSEILEARYVALINLAARASPARITYRYSERSESESTYRPSERASP 300
 DB AAGCATGCCAAGATCGCGTGCAGAGCCGACAGACCGCTACTATAGTCACTCGTGAAGCAG 22
 QY 301 TRPALASERVALISERCYSER 307
 DB TGGGATCTGTGTCATGCACT 1

RESULT 5
 US-09-917-265-66

Sequence 66, Application US/09917265
 Patent No. US20020052030A1
 GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT: Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265
 CURRENT FILING DATE: 2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 109
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 66
 LENGTH: 1533
 TYPE: DNA
 ORGANISM: Canis familiaris
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(1533)
 OTHER INFORMATION:
 US-09-917-265-66

Alignment Scores:
 Pred. No.: 6,78e-194 Length: 1533
 Score: 1653.00 Matches: 307
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-09-917-265-53 (1-307) x US-09-917-265-66 (1-1533)

QY 1 ILETPGLULEUGLULYSASPYALTYRYVALIGLULEUASPTRPHISPROASPALAPRO 20
 DB ATATGGGAACCTGGAGAAAGATGTTATGTTAGAGTTGAGCTGGACCGCATGCCGCC 60
 QY 21 GYGLUMETVALVALLLEUTHRCYSHISHPROGLUGLULASPAPILEHTRPHRSER 40
 DB GGAGAAATGCTGCTCCTACCTGACCTGACCTGAGAAAGATGACATCTGGAGCTCA 120
 QY 41 ALIAGINSERSEGLUVALLEUGLISERGLYLSYTHRLUTHRIEGLINALLYSGIUPHE 60
 DB TGGTGGCTCAGCGCATCATGATCTGATTTGAAATTCAGTCAAAAGTGCAGAGGCTTC 180
 QY 61 GLYASPALAGLYGLNTRYTHRCYSHISLYSGLYGLYVALLEUSERARISERLEUEN 80
 DB GGAGATGCTGGCCAGATACCTGCCATTAAGAGGCAAGGTTCTGAGCGCTCAGCTCC 240
 QY 81 LEULLIEHISLYSGIULASPGLYILETPSERTHRASPILEULYSGIULINLYSGIU 100
 DB TTGATTCACAAAAGAGATGAAATTTGCTCCAGATATCTTAAAGGACAGAAAGAA 300
 QY 101 SERLYSASNLYSILEPHEULYSCYGLUALALYSASNTYSEGLYARPHETRCYS 120
 DB TCCAAAAATAGATCTTCTGAAATGTGAGGCAAGATTTATTCGACGTTTCACATGC 360
 QY 121 TPTPTPLEUTHRALIIESETHRASPLEULYSPHESERVALLYSERARISERAGLYPHE 140
 DB TGGTGGCTCAGCGCATCATGATCTGATTTGAAATTCAGTCAAAAGTGCAGAGGCTTC 420
 QY 141 SERASPROGLINGLYVALTHRCYSGLYALVALTHLEUSERALAGLUARYVALARGVAL 160
 DB TCTGACCCCAAGGGGTGACATGTGAGCAGTGCAGACATTTTCAGCAGAGGGGTGAGAG 480
 QY 161 ASPASNARASPTLYLYLSYSTRYTHRVALIGIUCYSGINGLYSERAACYPROSER 180
 DB GACAAACAGGATTTATAGAAAGTACACAGTGCAGAGGTCAGAGAGGAGTGCCTGCTCT 540
 QY 181 ALIAGIUGLUSERLEUPROILEGLUVALVALASPALAIEHISLYSEULYSTYRGIU 200
 DB GCCGAGAGAGGCTTACCATCGAGGTCGTGGATGCTATTCCACAAGCTCAAGTATGAA 600

| | | | |
|----|------|---|------|
| Dd | 1293 | TTGATTCACAAAAAAGAAAGATGGAATTGGCTCCACTGATATCTTAAAGAACACAGAAGA | 1234 |
| Qy | 101 | SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnYrSerGlyArgPheThrCys | 120 |
| Dd | 1233 | TCCAAATAATAGATCTTCTCTGAATGTGAGCCAAAGATTTATCTGCAGCTTTCACATGC | 1174 |
| Qy | 121 | TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe | 140 |
| Dd | 1173 | TGGTGGCTGACGGCCAACTCAGTACGATTTGAAATTCAGTGTCAAAAGTAGCAGAGCTTC | 1112 |
| Qy | 141 | SerAspProGlnGlyValThrCysGlyValaValThrLeuSerAlaGluArgValArgVal | 160 |
| Dd | 1113 | TCTGACCCCCCAAGGGGTGACATGTGGACACGTGACACTTTAGCAGAGAGGGCTCAGAGTG | 1054 |
| Qy | 161 | AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGlnGlySerAlaCysProSer | 180 |
| Dd | 1053 | GACAAACAGGAGTTATTAAGAAAGTACACACATGGAGAGTCCGAGAGGACAGTCCGCCCTCT | 994 |
| Qy | 181 | AlaGlnGlnSerLeuProIleGluValaValaValAspAlaIleHisLysLeuLysTrpIleu | 200 |
| Dd | 993 | GCCGAGGAGAGACCTTACCCATGACAGTCTGCTGTGGATGCTTATTCACAAACCTCAAGTATGAA | 934 |
| Qy | 201 | AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeu | 220 |

| | | | |
|----|-----|--|-----|
| Db | 933 | AACATACACAGCAGCTTCTTATCAGAGACTATCTCAAACGACCCACACAAACTG | 874 |
| Qy | 221 | GLInLeuLysProLeuLysAsnSerArgHisValGluValSerTyrpgLutyrProAspThr | 240 |
| Db | 873 | CAGCTGAAGCATTTGAAAAATTCTCGGCACCTGGAGGTCACACTGGGAATTACCCGACAC | 814 |
| Qy | 241 | TrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn | 260 |
| Db | 813 | TGGAGCACCCACATTCCTACTTCTCCCTGACATTTTGGCATACAGGCCACAGGCACAG | 754 |
| Qy | 261 | AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValCysHis | 280 |
| Db | 753 | AATGAGAGAAAGAAAGATAGACTCTGGCTGGACACAGACCTAGCGAAAGTGTTGGCAC | 694 |
| Qy | 281 | LysAspAlaLysIleLeuValGlnAlaArgAspArgTyrTyrSerSerSerTyrPheSer | 300 |
| Db | 693 | AAGCATCCCAAGATCCCGCTGCAGCCGACCGCTACTATTCATCTCATCTCGAGACGAC | 634 |
| Qy | 301 | TrpAlaSerValSerCysSer | 307 |

RESULT 7
 US-09-917-265-61
 : Sequence 61, Application US/09917265
 : Patent No. US20020052030A1
 : GENERAL INFORMATION:
 : APPLICANT: Wonderling, Ramanl S.
 : APPLICANT: Boroughs, Karen L.
 : TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF

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CURRENT APPLICATION NUMBER: US/09/917,265
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 109
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 61
LENGTH: 1599
TYPE: DNA
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1599)
OTHER INFORMATION:
US-09-917-265-61

Alignment Scores:
    Aligned: 7,21e-194
    Length: 1599

```

Score: 1653.00 Matches: 307
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-09-917-265-53 (1-307) x US-09-917-265-61 (1-1599)

QY 1 ILETTPGLULEUGLULYSASPVALTYRVALVALGULEUASPTPRHISPROASPALAPRO 20
 DB 67 ATATGGGAACGTGAGAAAGATGTTATGTGTAGAGTTGGAGTGGACCCCTGATGCCCC 126
 QY 21 G1YGLUMETVALVALLEUTHRCYSHISTHRPROGLUGLUSPASPILETHTRPTHRSER 40
 DB 127 GGAGAAATGGTGCTCTCATCCCTGACATCCCTGAAGAAAGATGACATCACTTGAGCATCA 186
 QY 41 ALAGINSERSERGLUVALLEUGLYSERGLYSTRHLEUTHRIIEGLINVALYSGLUPHE 60
 DB 187 GCGCAGACGACGTAAGTCTTAGGTTCTGTAAACCTGACCATCCAAAGTCAAAAGATT 246
 QY 61 GLYASPALAGLYGLINTYRTHRCYSHISLYSGLYGLYLSVALLEUSERARGSERLEUEN 80
 DB 247 GGAGATGCTGGCCATATACCTGCGCATAAAGAGGCAAGTTCTAGCCGCTCACTCTG 306
 QY 81 LEULIEHISLYSLYSGLUASPGLYLTETPSETRTHRASPILIEULYSGLUGLUNYSGLU 100
 DB 307 TTGATTTCACAAAAGAAAGATGGATTGGTCCACTGATATCTTAAGAGAACACAAAGAA 366
 QY 101 SERLYSASNLYSILIEPHELEULYSCYGLUALALYSASNTRYSERGLYARGPHEHRCYS 120
 DB 367 TCCAAAAATTAAGATCTTCTGTAAGATGAGGCAAAAGATTATCTGGAGCTTCAACATGC 426
 QY 121 TRPTPRLEUTHRALIESETRTHRASPULYSPHESERVALYSSERSEARGLYPHE 140
 DB 427 TGGTGGCTGAGCGGCATATGCTGATTTGAAATTCAGAGTCAAAAGATGACGAGGCTTC 486
 QY 141 SERASPPROGLINGLYVALTHRCYSGLYALVALTHRLEUSERALAGLUARGVAL 160
 DB 487 TCTGACCCCAAGGGGTGACATGTGAGAGTGCACACTTTCAGCAGAGGGCTCAGAGAG 546
 QY 161 ASPANATGASPTYLYLSYSTYRTHRVALGLUCYSGINGLYSERVALYSPROSER 180
 DB 547 GACAAACAGGAGTTATTAAGAGTACACAGTGGAGTGTGAGAGGAGGAGTCCCTGCTCT 606
 QY 181 ALAGLUGLUSERLEUPROILEGLUVALVALVALASPALALIEHISLYSLEULYSTYRGLU 200
 DB 607 GCCGAGAGAGGCTTACCCATCGAGGTCGTGGATGCTATTCACAAAGCTCAAGATATGA 666
 QY 201 ASNTYRTHRSERSETPHEHLEARGASPIELIELYSPROASPPROPTHRSNLEU 220
 DB 667 AACTACACGACGAGCTTCTTCATCAGAGACATCAACCAAGCCACCCCAAAACCTG 726
 QY 221 GNLULYSPROLEULYSANSEARPHISVALIGLVALSERTRIGLUTYRPROASPTHR 240
 DB 727 CAGCTGAAGCCATTAAAAAATTCTCGCACGTGGAGGTGAGTGGGAATACCCCGACACC 786
 QY 241 TRPSETRTHRPROHISSETRTYRPHESERLEUTHRPHECYSILIEGLNALAGLNGLYLSASN 260
 DB 787 TGGAGACACCCCATTTCTACTTCTCCCGACATTTTGGATATCAGAGCCGACGAGCAAGAAC 846
 QY 261 ASNATRGULYLSYASPARGLUCYSVALASPLYSTRHRSERALYSLYVALYALYSHIS 280
 DB 847 AATAAGAGAAAGAAAGATAGACTTGCCTGGACAGACCTCAGCAAGAGTCTCTGTGCCAC 906
 QY 281 LYSASPALALYSLIARGVALIGLINALARGASPARGYRTRYRSETRSERSETRRPSERASP 300
 DB 907 AAGGATGCCAAGATCCGCTGCAAGCCGAGACCCCTACTATATGTTCACTCGAGCGAC 966
 QY 301 TRPALASERVALSERCYSSER 307
 DB 967 TGGCATCTGTGTCATGCAGT 987

RESULT 8

US-09-917-265-63/c
 ; Sequence 63, Application US/09917265
 ; Patent No. US20020052030A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wonderling, Ramani S.
 ; APPLICANT: Borouhns, Karen L.
 ; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
 ; FILE REFERENCE: IM-5
 ; CURRENT APPLICATION NUMBER: US/09/917,265
 ; CURRENT FILING DATE: 2001-07-27
 ; PRIOR APPLICATION NUMBER: 60/223,016
 ; PRIOR FILING DATE: 2000-08-04
 ; NUMBER OF SEQ ID NOS: 109
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 63
 ; LENGTH: 1599
 ; TYPE: DNA
 ; ORGANISM: Canis familiaris
 ; US-09-917-265-63

Alignment Scores:

Pred. No.: 7 21e-194 Length: 1599
 Score: 1653.00 Matches: 307
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-09-917-265-53 (1-307) x US-09-917-265-63 (1-1599)

QY 1 ILETTPGLULEUGLULYSASPVALTYRVALVALGULEUASPTPRHISPROASPALAPRO 20
 DB 1533 ATATGGGAACGTGAGAAAGATGTTATGTGTAGAGTTGGAGTGGACCCCTGATGCCCC 1474
 QY 21 G1YGLUMETVALVALLEUTHRCYSHISTHRPROGLUGLUSPASPILETHTRPTHRSER 40
 DB 1473 GGAGAAATGGTGCTCTCATCCCTGACATCCCTGAAGAAAGATGACATCACTTGAGCATCA 1414
 QY 41 ALAGINSERSERGLUVALLEUGLYSERGLYSTRHLEUTHRIIEGLINVALYSGLUPHE 60
 DB 1413 GCGCAGACGACGTAAGTCTTAGGTTCTGTAAACCTGACCATCCAAAGTCAAAAGATT 1354
 QY 61 GLYASPALAGLYGLINTYRTHRCYSHISLYSGLYGLYLSVALLEUSERARGSERLEUEN 80
 DB 1353 GGAGATGCTGGCCATATACCTGCGCATAAAGAGGCAAGGTTCTGAGCCGCTCACTCTG 1294
 QY 81 LEULIEHISLYSLYSGLUASPGLYLTETPSETRTHRASPILIEULYSGLUGLUNYSGLU 100
 DB 1293 TTGATTTCACAAAAGAAAGATGGATTGGTCCACTGATATCTTAAGAGAACAGAAAGAA 1234
 QY 101 SERLYSASNLYSILIEPHELEULYSCYGLUALALYSASNTRYSERGLYARGPHEHRCYS 120
 DB 1233 TCCAAAAATTAAGATCTTCTGTAAGATGAGGCAAAAGATTATCTGGACGTTTCACATGC 1174
 QY 121 TRPTPRLEUTHRALIESETRTHRASPULYSPHESERVALYSSERSEARGLYPHE 140
 DB 1173 TGGTGGCTGAGCGGCATATGCTGATTTGAAATTCAGTGCACAAAGATGACGAGGCTTC 1114
 QY 141 SERASPPROGLINGLYVALTHRCYSGLYALVALTHRLEUSERALAGLUARGVAL 160
 DB 1113 TCTGACCCCAAGGGGTGACATGTGAGAGTGAACATTTTCGCGAAGAGGCTGAGAGTG 1054
 QY 161 ASPANATGASPTYLYLSYSTYRTHRVALGLUCYSGINGLYSERALACYSFROSER 180
 DB 1053 GACAAACAGGAGTTATTAAGAGTACACAGTGGAGTGTGAGAGGCGAGTCCGCTCT 994
 QY 181 ALAGLUGLUSERLEUPROILEGLUVALVALVALASPALALIEHISLYSLEULYSTYRGLU 200
 DB 993 GCCGAGAGAGGCTTACCCATCGAGGTCGTGGATGCTATTCACAAAGCTCAAGATATGA 934
 QY 201 ASNTYRTHRSERSETPHEHLEARGASPIELIELYSPROASPPROPTHRSNLEU 220
 DB 933 AACTACACGACGAGCTTCTTCATCAGAGACATCAACCAAGACCCACCCCAAAACCTG 874

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QY 221 GlnLeuTyrProLeuLysAsnSerArgHisValGlnValSerTrpGluTyrProAspThr 240
Db 873 CAGGTGAAGCCATTGAAAAATTTCTGGCACCCTGGAGGCTGACCTGGAAATACCCGACACC 814
QY 241 TrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnIleGlnIlyAsn 260
Db 813 TGGAGCACCCACATTCCTACTTCTCCCTGACATTTTGCAATACAGGCCGACGGAAGAAC 754
QY 261 AsnArgGlnLysLysAspArgLeuGlyCysValAspLysThrSerAlaLysValAlaCysHis 280
Db 753 AATAGAGAAAAGAAAGATAGACTCTGCGTGGCAAGACCTCAGCCAAAGTCTGTGCCAC 694
QY 281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsp 300
Db 693 AAGGATGCCAAGATCCCGCTGTCAGAACCCGAGACCCGACTACTATGTTATCTTGGAGCGAC 634
QY 301 TrpAlaSerValSerCysSer 307
Db 633 TGGCATCTGTGTCTGTCAGT 613

RESULT 9
US-09-917-265-107
: Sequence 107, Application US/09917265
: Patent No. US20020052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
: FILE REFERENCE: IM-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: PRIOR FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: PRIOR FILING DATE: 2000-08-04
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 107
: LENGTH: 2267
: TYPE: DNA
: ORGANISM: Canis familiaris
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (154)..(1140)
: OTHER INFORMATION:
US-09-917-265-107

Alignment Scores:
Pred. No.: 1,2e-193 Length: 2267
Score: 1653.00 Matches: 307
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-917-265-53 (1-307) x US-09-917-265-107 (1-2267)
QY 1 IleTrpGlnLeuGlnLysAspValTyrValValGlnLeuAspTrpHisProAspAlaPro 20
Db 220 AATATGGAACTGGAGAAAGATGTTTATGTTGTAGATTGGACTGGACCCGTGATGCCCCC 279
QY 21 GlyClnMetValValLeuThrCysHisThrProGlnGlnLysAspIleThrTrpThrSer 40
Db 280 GGAGAAATGCTGTGCTCCACCTGCAATACCCCTGAAAGATGATGATCAGCTTGACCTCA 339
QY 41 AlagInSerSerGlnValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
Db 340 GCCCAGAGCAGTGAAGCTCTAGGTTCGTGTAATAACTCTGACCAATCCAAAGCAATTT 399
QY 61 GlyAspAlaGlnTyrTrpThrCysHisLysGlyGlyLysValLeuSerArgSerLeuLeu 80
Db 400 GGAGATGCTGGCAGATATACCTGCATAAAGAGGCAAGGTTCTGAGCCCTCTACTCTG 459
QY 81 LeuIleHisLysLysClnAspGlyIleTrpSerThrAspIleLeuLysGlnGlnLysGlu 100
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Db 460 TTGATTCACAAAAAGAAAGATGCAATTGTGTCACCTGATATCTTAAAGGAACAAAGAA 519
QY 101 SerLysAsnLysIlePheLeuLysCysGlnAlaLysAsnTyrSerGlyArgPheThrCys 120
Db 520 TCCAAAAATAGATCTTCTTGAATGTGAGGCAAAAGAAATTTCTGGACCTTTCACATGTC 579
QY 121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
Db 580 TGTGGCTGAGCGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTACGACAGGCTTC 639
QY 141 SerAspProGlnGlyValIleThrCysGlyAlaValIleThrLeuSerAlaGlnArgValArgVal 160
Db 640 TCTACACCCCAAGGAGGTGACATGTGGAGCACTGACACTTTAGCAGAGAGGCTCAGAGTG 699
QY 161 AspAsnArgAspTyrLysLysTyrThrValGlnCysGlnGlnGlySerAlaCysProSer 180
Db 700 GACAACAGAGGATTTATAGAAAGTACACAGTGAAGTGAAGGAGGAGTCCCTCCCTCT 759
QY 181 AlagInGlnSerLeuProIleGlnValValValAlaSerAlaIleHisLysLeuLysTyrGlu 200
Db 760 GCCAGAGAGCCTTACCCATTCGAGGTGCTGTGGATGCTTATTCACAAGCTTAAGTATGAA 819
QY 201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeu 220
Db 820 AACTACACACACACCTTCTTTCATCAGAGACATCATCAACAGACCCACCAACACTG 879
QY 221 GlnLeuLysProLeuLysAsnSerArgHisValGlnValSerTrpGluTyrProAspThr 240
Db 880 CAGCTGAAGCATGTGAAAAATTCGCGCACCTGGAGGTCACCTGGAAATACCCGACACC 939
QY 241 TrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnIleGlnIlyAsn 260
Db 940 TGGAGCACCCACATTCCTACTTCTCCTGACATTTTGCAATACAGGCCAGGCAAGAAC 999
QY 261 AsnArgGlnLysLysAspArgLeuGlyCysValAspLysThrSerAlaLysValAlaCysHis 280
Db 1000 AATAGAGAAAAGAAAGATAGACTCTGCGTGGCAAGACACTGACCAAGGTGTGTGCCAC 1059
QY 281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsp 300
Db 1060 AAGGATGCCAAGATCCCGCTGCAAGCCCGAGACCCGCTACTACTGATTCCTCGAGCGAC 1119
QY 301 TrpAlaSerValSerCysSer 307
Db 1120 TGGCATCTGTGTCTGTCAGT 1140

RESULT 10
US-09-917-265-109/c
: Sequence 109, Application US/09917265
: Patent No. US20020052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
: FILE REFERENCE: IM-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: PRIOR FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 109
: LENGTH: 2267
: TYPE: DNA
: ORGANISM: Canis familiaris
US-09-917-265-109

Alignment Scores:
Pred. No.: 1,2e-193 Length: 2267
Score: 1653.00 Matches: 307
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0
 US-09-917-265-53 (1-307) x US-09-917-265-109 (1-2267)

QY 1 ILETRPGULEUGLULYSASPVALLTYRVAIValuenuasprrhpsproaspalapro 20
 DB ATATGGGAACTGGGAGAAAGATGTTATGTTGTAGAGTTGGACTGGACCCCGATGCCCCC 1989

QY 21 GLYGLUETVALLEUTHRCYSHSTHPRGUGLULASPAPILETHTRTPHRSer 40
 DB GGAGAAATGGTGCTCCACTGCCATACCCCTTAAGAGATGACATCCTGACCTCA 1929

QY 41 ALAGLISERSEGLUVALLEUGLYSERGLYSTHTRLEUTHRIEGLNALYSLUPHE 60
 DB GCGGAGAGCACTGAAGTCTAGTTCTGTAAACCTGACCATCCCAAGCAAGATTT 1869

QY 61 GLYASPALAGLYGINTYRTHRCYSHSLYSGLYLYSVALLEUSERATGSErleu 80
 DB GGAATGCTGGCCGAGTACTTACCTGCCATTAAGAGGCAAGGTTCGAGCCCTCCTG 1809

QY 81 LEULIHLISLYSGIUAASPGYLIETRPSErTHASPILEULYSGIULINLSGLU 100
 DB TTGATTCACAAAAGAAAGATGGAATTGGTCCACTGATCTTAAGAGCAAGAAAGAA 1749

QY 101 SERLYSASNLYSILPELEULYSCYSGIUALALYASANTYSErGLYARQPHETHRCYS 120
 DB TCCAAAATAGATCTTCTGAATGTGAGGCAAGAAATATCTGAGCTTTCACATGC 1689

QY 121 TRTPRLEUTHRIALLESERTHASPLEULYSPheserValLYSSErATGSLYPHE 140
 DB TGGTGGCTGACGGCAATCACTACTGATTTCAATTCAAGTTCAAAAGATGACGAGCTTC 1629

QY 141 SETASPRGUGLULYVALIHCYSGIYALVALIHLSErALAGLUARQVALA 160
 DB TCTGACCCCAAGGGGTGACATGTGAGCAGTGCACCTTACACAGAGAGGGTCAAGTG 1569

QY 161 ASPASARARQSPYRILYSLYSTRTHRALGLUCYSGIULYSErALACYSPROSEr 180
 DB GAAACAGAGGATTTATAGAAAGTACACAGTGGAGTGTCAAGAGGAGCTGCTGCCCTCT 1509

QY 181 ALAGLULSERLEUProILEGLUVALIValASPALALIEHLISLYSErLYSTYGLU 200
 DB GCGGAGAGAGCCTTACCTCAGCGTGTGGAGTGTATTCACAGAGTCAAGATGAA 1449

QY 201 ASNTYRTHRSERSErHEPHEILEARQAPILEIIELYSPROASPRProTHrASNU 220
 DB AACTACACACAGAGCTTCTTCATCAGACATCATCAACACAGACCCACAAACCTG 1389

QY 221 GINLEULYSPROLEULYSANSErARHISVALIGLULVASErTRPGULNTRPROASPR 240
 DB CAGCTGAAGCCATTGAAAATCTCGGCACGTGGAGGTGAGTGGGAATACCCCGACACC 1329

QY 241 TRPSErTHRPHISSErLYRPHESERLEUTHRPHECYSILEGLNALAGLULYLSAN 260
 DB TGGAGACCCCACTTCTTCTCCCTGACATTTTGGATACAGGCCCAAGGCAAGAAC 1269

QY 261 ASNATRGULYLSASPARGLEUCYSVALASPLYSTHSErVALYVALYCYSHS 280
 DB AATAGAGAAAGAAAGATAGACTGCTGCGGACAGAACCTCAGCCAAAGTGTGGCAC 1209

QY 281 LYSASPALALYSLIEARQVALIGLUALARQASPARQYTYRSErSErTRPSErSP 300
 DB AAGGATGCCAAGATCCGGTGCAGGCCGAGAGCCCTACTATAGTTACTCTGGAGCCAC 1149

QY 301 TRPALASERVALSERCYSEr 307
 DB TGGGCACTGTCTCTGCACT 1128

RESULT 11
 US-10-079-616-6
 : Sequence 6, Application US/10079616
 : Publication No. US20020107366A1

GENERAL INFORMATION:
 APPLICANT: IMAMURA, Takayuki
 MAEDA, Hiroaki
 FUJIYASU, Takeshi
 IMAGAWA, Yoshitaka
 TOKIYOSHI, Sachio
 TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BROWDY AND NEWMARK
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/079, 616
 FILING DATE: 22-Feb-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/011, 143
 FILING DATE: 04-FEB-1998
 APPLICATION NUMBER: PCT/JP97/01824
 FILING DATE: 29-MAY-1997
 APPLICATION NUMBER: JP 165249/1996
 FILING DATE: 04-JUN-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: BROWDY, Roger L.
 REGISTRATION NUMBER: 25, 618
 REFERENCE/DOCKET NUMBER: IMAMURA-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 921 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 US-10-079-616-6

Alignment Scores:
 Pred. No.: 5.39e-182 Length: 921
 Score: 1554.00 Matches: 288
 Percent Similarity: 96.74% Conservative: 9
 Best Local Similarity: 93.81% Mismatches: 10
 Query Match: 94.01% Indels: 0
 DB: 15 Gaps: 0

US-09-917-265-53 (1-307) x US-10-079-616-6 (1-921)

QY 1 ILETRPGULEUGLULYSASPVALLTYRVAIValuenuasprrhpsproaspalapro 20
 DB ATATGGGAACTGGGAGAAAGATGTTATGTTGTAGAGTTGGACTGGACCCCGATGCCCCC 60

QY 21 GLYGLUETVALLEUTHRCYSHSTHPRGUGLULASPAPILETHTRTPHRSer 40
 DB GGAGAAATGGTGCTCCACTGCCATACCCCTTAAGAGATGACATCCTGACCTCA 120

QY 41 ALAGLISERSEGLUVALLEUGLYSERGLYSTHTRLEUTHRIEGLNALYSLUPHE 60
 DB GCGGAGAGCACTGAAGTCTAGTTCTGTAAACCTGACCATCCCAAGCAAGATTT 180

QY 61 GLYASPALAGLYGINTYRTHRCYSHSLYSGLYLYSVALLEUSERATGSErleu 80
 DB GGAATGCTGGCCGAGTACTTACCTGCCATTAAGAGGCAAGGTTCGAGCCCTCCTG 180

QY 81 LEULIHLISLYSGIUAASPGYLIETRPSErTHASPILEULYSGIULINLSGLU 100
 DB TTGATTCACAAAAGAAAGATGGAATTGGTCCACTGATCTTAAGAGCAAGAAAGAA 1749

QY 101 SERLYSASNLYSILPELEULYSCYSGIUALALYASANTYSErGLYARQPHETHRCYS 120
 DB TCCAAAATAGATCTTCTGAATGTGAGGCAAGAAATATCTGAGCTTTCACATGC 1689

QY 121 TRTPRLEUTHRIALLESERTHASPLEULYSPheserValLYSSErATGSLYPHE 140
 DB TGGTGGCTGACGGCAATCACTACTGATTTCAATTCAAGTTCAAAAGATGACGAGCTTC 1629

QY 141 SETASPRGUGLULYVALIHCYSGIYALVALIHLSErALAGLUARQVALA 160
 DB TCTGACCCCAAGGGGTGACATGTGAGCAGTGCACCTTACACAGAGAGGGTCAAGTG 1569

QY 161 ASPASARARQSPYRILYSLYSTRTHRALGLUCYSGIULYSErALACYSPROSEr 180
 DB GAAACAGAGGATTTATAGAAAGTACACAGTGGAGTGTCAAGAGGAGCTGCTGCCCTCT 1509

QY 181 ALAGLULSERLEUProILEGLUVALIValASPALALIEHLISLYSErLYSTYGLU 200
 DB GCGGAGAGAGCCTTACCTCAGCGTGTGGAGTGTATTCACAGAGTCAAGATGAA 1449

QY 201 ASNTYRTHRSERSErHEPHEILEARQAPILEIIELYSPROASPRProTHrASNU 220
 DB AACTACACACAGAGCTTCTTCATCAGACATCATCAACACAGACCCACAAACCTG 1389

QY 221 GINLEULYSPROLEULYSANSErARHISVALIGLULVASErTRPGULNTRPROASPR 240
 DB CAGCTGAAGCCATTGAAAATCTCGGCACGTGGAGGTGAGTGGGAATACCCCGACACC 1329

QY 241 TRPSErTHRPHISSErLYRPHESERLEUTHRPHECYSILEGLNALAGLULYLSAN 260
 DB TGGAGACCCCACTTCTTCTCCCTGACATTTTGGATACAGGCCCAAGGCAAGAAC 1269

QY 261 ASNATRGULYLSASPARGLEUCYSVALASPLYSTHSErVALYVALYCYSHS 280
 DB AATAGAGAAAGAAAGATAGACTGCTGCGGACAGAACCTCAGCCAAAGTGTGGCAC 1209

QY 281 LYSASPALALYSLIEARQVALIGLUALARQASPARQYTYRSErSErTRPSErSP 300
 DB AAGGATGCCAAGATCCGGTGCAGGCCGAGAGCCCTACTATAGTTACTCTGGAGCCAC 1149

QY 301 TRPALASERVALSERCYSEr 307
 DB TGGGCACTGTCTCTGCACT 1128

QY 181 Alaglugluserleuproilegluvalvalaspaalielehislusleustyrslu 200
 |||||||
 DB 541 GCCGAGAGAGCCATCCCATAGTCGTGGAGCGATTACAGCTCAAGTACGAA 600
 QY 201 AsnTYrThrSerSerPhePheIleargaspillelelvsproaspProProthrasnleu 220
 |||||||
 DB 601 AACTACACGAGAGCTTCTTCATCAGGACATCATCAACCGACCCACCAAGAACCTG 660
 QY 221 GlnLeuLysProLeuLysasnSerArgHisValGluValSerTrpGluTrpProaspThr 240
 |||||||
 DB 661 CAACGTGAAGCCATTAAAAATTTCTGGCATGTGGAGAGTACGTGGGAATACCTTGACACC 720
 QY 241 TrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnIleLysasn 260
 |||||||
 DB 721 TGCAGACACCCCATCTCTACTTCTCTTACATTGGCGTACAGGTCCAGGGCAAGAAC 780
 QY 261 AsnArgGluLysLysAspArgLeucysValAspLysThrSerAlaLysValValCysHis 280
 |||||||
 DB 781 AACAGAGAAAGAAAGACAGACTCTCCGTGACAAAGCTCAGCCAAAGTCTGTGCCAC 840
 QY 281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsp 300
 |||||||
 DB 841 AAGGATGCCAAGATCCGCGTGCAGAGCCAGACCGCTACTATAGCTCATCTCGAGCAAC 900
 QY 301 TrpAlaSerValSerCysSer 307
 |||||||
 DB 901 TGGGCATCCGTCTCTCTGAGT 921

RESULT 13

US-09-917-265-29

; Sequence 29, Application US/09917265
 ; Patent No. US20020052030A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wonderling, Ramani S.
 ; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
 ; FILE REFERENCE: IM-5
 ; CURRENT APPLICATION NUMBER: US/09/917,265
 ; CURRENT FILING DATE: 2001-07-27
 ; PRIOR APPLICATION NUMBER: 60/223,016
 ; PRIOR FILING DATE: 2000-08-04
 ; NUMBER OF SEQ ID NOS: 109
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 29
 ; LENGTH: 987
 ; TYPE: DNA
 ; ORGANISM: Felis catus
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(987)
 ; OTHER INFORMATION:
 ; US-09-917-265-29

Alignment Scores:

Pred. No.: 5 97e-182 Length: 987
 Score: 1554.00 Matches: 288
 Percent Similarity: 96.74% Conservative: 9
 Best Local Similarity: 93.81% Mismatches: 10
 Query Match: 94.01% Indels: 0
 DB: 10 Gaps: 0

US-09-917-265-53 (1-307) x US-09-917-265-29 (1-987)

QY 1 IletPgluleuglulysaspValTyrValValGluLeuAspTrpHisProaspAlapro 20
 |||||||
 DB 67 ATATGGAACTGGAGAAAAACGTTATGTGTAGAGTTGAGTGGACCTGATGCCCC 126
 QY 21 GlyGluMetValValLeuThrCysHisThrProGluGluAspAspIleThrTrpThrSer 40
 |||||||
 DB 127 GGAGAAATGGTGTCTCTCAGCTGCAATACTCTGGAAGAGATGACATCAGTGGACCTCT 186
 QY 41 AlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60

DB 187 GACCAGAGAGAGTGAAGTCTAGGCTCTGTAAACCTGACCATCAAGTCAAAAGATT 246
 |||||||
 QY 61 GlyAspAlaGlnTyrThrCysHisLysGlyGlyLysValLeuSerArgSerleu 80
 |||||||
 DB 247 GCAGATGCTGGCCATATACCTGTCATTAAGACGCGAGGTTCTAGCCATTCTGCTCTC 306
 QY 81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGlnIleLysGlu 100
 |||||||
 DB 307 CTGATATACCAAAAAGAGAGATGGAATTGGTCTCAGTATATCTTAAGGAGCAAGAAAGA 366
 QY 101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
 |||||||
 DB 367 TCCAAAAATTAAGATCTTTCTAAATGTAGGCAAGAAATTAATTCGGACGTTTCACCTGC 426
 QY 121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerLysSerArgGlyPhe 140
 |||||||
 DB 427 TGTGTGCTGAGCGCAATGATCCATTTGAAATTCAGTGTCAAAAGACAGAGAGCTCC 486
 QY 141 SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgVal 160
 |||||||
 DB 487 TCTGACCCCAAGGGGTGACTTGTGAGCAGCAGCACTCTCAGCAGAAAGTCCAGAGTG 546
 QY 161 AsnAsnArgAspTyrLysLysTyrThrValGluCysGlnGluLysSerAlaCysProSer 180
 |||||||
 DB 547 GACAACAGGATTAATAGAGTACACAGTGGAGTCCAGAGGCGAGTGCCTGCCGCT 606
 QY 181 Alaglugluserleuproilegluvalvalaspaalielehislusleustyrslu 200
 |||||||
 DB 607 GCCGAGAGAGCCATCCCATAGTCGTGGAGCGATTACACAGCTCAAGTACGAA 666
 QY 201 AsnTYrThrSerSerPhePheIleargaspillelelvsproaspProProthrasnleu 220
 |||||||
 DB 667 AACTACACGAGAGCTTCTTCATCAGGACATCATCAACCGACCCACCAAGAACCTG 726
 QY 221 GlnLeuLysProLeuLysasnSerArgHisValGluValSerTrpGluTrpProaspThr 240
 |||||||
 DB 727 CAACGTGAAGCCATTAAAAATTTCTGGCATGTGGAGAGTACGTGGGAATACCTTGACACC 786
 QY 241 TrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnIleLysasn 260
 |||||||
 DB 787 TGCAGACACCCCATCTCTACTTCTCTTACATTGGCGTACAGGTCCAGGGCAAGAAC 846
 QY 261 AsnArgGluLysLysAspArgLeucysValAspLysThrSerAlaLysValValCysHis 280
 |||||||
 DB 847 AACAGAGAAAGAAAGACAGACTCTCCGTGACAAAGCTCAGCCAAAGTCTGTGCCAC 906
 QY 281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsp 300
 |||||||
 DB 907 AAGGATGCCAAGATCCGCGTGCAGAGCCAGACCGCTACTATAGCTCATCTCGAGCAAC 966
 QY 301 TrpAlaSerValSerCysSer 307
 |||||||
 DB 967 TGGGCATCCGTCTCTCTGAGT 987

RESULT 14

US-09-917-265-31/c

; Sequence 31, Application US/09917265
 ; Patent No. US20020052030A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wonderling, Ramani S.
 ; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
 ; FILE REFERENCE: IM-5
 ; CURRENT APPLICATION NUMBER: US/09/917,265
 ; CURRENT FILING DATE: 2001-07-27
 ; PRIOR APPLICATION NUMBER: 60/223,016
 ; PRIOR FILING DATE: 2000-08-04
 ; NUMBER OF SEQ ID NOS: 109
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 31
 ; LENGTH: 987
 ; TYPE: DNA

ORGANISM: Felis catus
US-09-917-265-31

Alignment Scores:

Pred. No.: 5 97e-182 Length: 987
Score: 1534.00 Matches: 288
Percent Similarity: 96.74% Conservative: 9
Best Local Similarity: 93.81% Mismatches: 10
Query Match: 94.01% Indels: 0
DB: 10 Gaps: 0

US-09-917-265-53 (1-307) x US-09-917-265-31 (1-987)

```

QY      1  ILETpGluLeuGluLysAspValTyrValValGluLeuAspTrpHisProAspAlaPro 20
Db      921 ATATGGGAAGCTGGAGAAAACGTTATGTTGTAGAGTTGGACCTGGACCTGATGCCCC 862

QY      21  G1yGluMeValValLeuThrCysHisThrProGluLysAspP1eThrTrpThrSer 40
Db      861 GGAGAAATGGTGGCTCCTCACCCTGCATCTCTGAAGAAGATGACATCACCCTGGACCTCT 802

QY      41  AlAGInSerSerGluValLeuGlySerGlyLysThrLeuThr11eGlnValLysGluPhe 60
Db      801 GACCAGAGCAGTGAAGCTTGAAGCTCTGCTAAACCTGACCATCCAAAGTCAAGAAATT 742

QY      61  G1yAspAlaGlyInTyrThrCysHisLysGlyLysValLeuSerArgSerLeuLeu 80
Db      741 GCAGATCTGCGCCAGCTTACTCTGCATTAAGAGCCAGGTTCTTGAGCCATTCCTCTCTC 682

QY      81  Leu11eHisLysLysGluAspGly11eTrpSerThrAsp11eLeuLysGluLysGlu 100
Db      681 CTGATACACAAAAGAGATGGAATTGCTCCACTGATATCTTAAGGAGACAGAAAGAA 622

QY      101 SerLysAspLys11ePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
Db      621 TCCAAAATTAAGATCTTTTAAATGAGGCAAGAAATTAATTCGACGTTTACCTGC 562

QY      121 TrpTrpLeuThrAla11eSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
Db      561 TGTGTGCTGACGGCAATCAGTACGATTGAAATTCATCTGCAAAACAGCAGAGCGCTCC 502

QY      141 SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgVal 160
Db      501 TCTGACCCCAAGCGGCTGACTTGTGGAGCGCAGCTCTCAGCAGAGAGTCAAGTGA 442

QY      161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProSer 180
Db      441 GACAACAGGATTAATAGAGTACACAGTGCAGTGTGAGAGGCGCAGTGCCTGCCGCT 382

QY      181 AlAG1uGluSerLeuPro11eGluValValValAspAla11eHisLysLeuLysTyrGlu 200
Db      381 GCGGAGAGAGCTTACCATTGGAAGTCTGCTGGACCTTATTCACAAGCTCAAACTACGAA 322

QY      201 AsnTyrThrSerSerPhePhe11eArgAsp11eLeuLysProAspProProThrAsnLeu 220
Db      321 AACTACACCGCAGCTTCTTCATCAGGACATCATCAACCGGACCCACCAAGAAGACTG 262

QY      221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
Db      261 CAACGTGAAGCATTAATAAAATTCGCGCATGTGGAATGTGGAATGCCCTGCAGACCC 202

QY      241 TrpSerThrProHisSerTyrPheSerLeuThrPheCys11eGlnAlaGlnLysAsn 260
Db      201 TGGAGCAGCCACCATTCCTTCTCTTAACATTTTGGCGTACAGGTCCAGGAGCAAAAC 142

QY      261 AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValCysHis 280
Db      141 AACAGAGAAAGAGACAGACTCTCTCGACAAAGCCTCAGCCAGAGTGTGCTGCAC 82

QY      281 LysAspAlaLysLysLeuArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsp 300
Db      81 AAGGATGTCCAAAGATCCCGTCAAGCCAGAGACCGCTACTATACCTATCATCTGAGAAC 22

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QY      301 TrpAlaSerValSerCysSer 307
Db      21 TGGGATCCGTGCTCTGCAGT 1

RESULT 15
US-10-079-616-5
: Sequence 5, Application US/10079616
: Publication No. US20020107366A1
: GENERAL INFORMATION:
:   APPLICANT: IMAMURA, Takayuki
:   MAEDA, Hiroaki
:   FUJISAWA, Takeshi
:   IMAGAWA, Yoshitaka
:   TOKIYOSHI, Sachio
:   TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
:   NUMBER OF SEQUENCES: 26
:   CORRESPONDENCE ADDRESS:
:   ADDRESSEE: BROWDY AND NEWMARK
:   STREET: 419 Seventh Street, N.W., Suite 300
:   CITY: Washington
:   STATE: D.C.
:   COUNTRY: USA
:   ZIP: 20004
:   COMPUTER READABLE FORM:
:   MEDIUM TYPE: Floppy disk
:   COMPUTER: IBM PC compatible
:   OPERATING SYSTEM: PC-DOS/MS-DOS
:   SOFTWARE: Patentin Release #1.0, Version #1.30
:   CURRENT APPLICATION DATA:
:   APPLICATION NUMBER: US/10/079, 616
:   FILING DATE: 22-Feb-2002
:   CLASSIFICATION: <Unknown>
:   PRIOR APPLICATION DATA:
:   APPLICATION NUMBER: 09/011,143
:   FILING DATE: 04-FEB-1998
:   APPLICATION NUMBER: PCT/jp97/01824
:   FILING DATE: 29-MAY-1997
:   APPLICATION NUMBER: JP 165249/1996
:   FILING DATE: 04-JUN-1996
:   ATTORNEY/AGENT INFORMATION:
:   NAME: BROWDY, Roger L.
:   REGISTRATION NUMBER: 25,618
:   REFERENCE/DOCKET NUMBER: IMAMURA-1
:   TELECOMMUNICATION INFORMATION:
:   TELEPHONE: 202-737-3528
:   TELEFAX: 202-628-5197
:   INFORMATION FOR SEQ ID NO: 5:
:   SEQUENCE CHARACTERISTICS:
:   LENGTH: 2193 base pairs
:   TYPE: nucleic acid
:   STRANDEDNESS: single
:   TOPOLOGY: linear
:   MOLECULE TYPE: cDNA
:   SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-079-616-5

Alignment Scores:
Pred. No.: 1.92e-181 Length: 2193
Score: 1534.00 Matches: 288
Percent Similarity: 96.74% Conservative: 9
Best Local Similarity: 93.81% Mismatches: 10
Query Match: 94.01% Indels: 0
DB: 15 Gaps: 0

US-09-917-265-53 (1-307) x US-10-079-616-5 (1-2193)

QY      1  ILETpGluLeuGluLysAspValTyrValValGluLeuAspTrpHisProAspAlaPro 20
Db      130 ATATGGGAAGCTGGAGAAAACGTTATGTTGTAGAGTTGGACCTGGACCTGATGCCCC 189

QY      21  G1yGluMeValValLeuThrCysHisThrProGluLysAspP1eThrTrpThrSer 40
Db      190 GGAGAAATGGTGGCTCCTCACCCTGCATCTCTGAAGAAGATGACATCACCCTGGACCTCT 249

```

```
QY 41 AlaGlnSerSerGluValIleuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
    |||
Db 250 GACCAGAGCAGTAGTAAGTCTAGGCTGTGTAATAACTCTGACCATCCAAAGTCAAGAATTT 309
QY 61 GlyAspAlaGlyGlnTyrrThrcysHisLysGlyGlyLysValIleuSerArgSerLeuLeu 80
    |||
Db 310 GCAGATGCTGGCCAGTATACCTGTATACATAAAGAGGCGAGGTCTGTAGCCATTCGTTCTC 369
QY 81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGlu 100
    |||
Db 370 CTGATACACAAAAGAAAGAAATGGAAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 429
QY 101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrrSerGlyArgPheThrCys 120
    |||
Db 430 TCCAAAATTAAGATCTTCTTAAAAATGTAGAGCAAAAGAAATTAATCTGAGCGTTTCACCTGC 489
QY 121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
    |||
Db 490 TGGTGGCTGAGGCAATCAGTACCGATTGTAATTCACGTCTCAAAAGCAGCAGAGGCTCC 549
QY 141 SerAspProGlnGlyValIleThrCysGlyAlaValIleThrLeuSerAlaGluArgValArgVal 160
    |||
Db 550 TCTGACCCCAAGGGGTGACTGTGGAGCAGCGACTCTCAGCAGAAAGTCTAGAGTG 609
QY 161 AspAsnArgAspTyrrLysLysTyrrThrValGluCysGlnGlySerAlaCysProSer 180
    |||
Db 610 GACAAACAGGATTATTAAGAAATGACACAGTGAGTGTGAGAGGCGACTGCTGCCCGCT 669
QY 181 AlagluGlnSerLeuProIleGluValValAspAlaIleHisLysLeuLysTyrrGlu 200
    |||
Db 670 GCCGAGGAGAGCTACCCATTGAAGTGTGTGACGCTATTCACAAGCTCAAGTACGAA 729
QY 201 AsnTyrrThrSerSerPhePheIleArgAspIleIleLysProAspPropThrAsnLeu 220
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Db 730 AACTACACACAGAGCTTCTTCATCAGGACATCATCAACCGAGCCACCCAGAACCTG 789
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Search completed: July 17, 2003, 09:56:14
Job time : 213.737 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 13:00:49 : Search time 2742.43 Seconds

(without alignments)
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Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 974 | 98.7 | 990 | 6 | AR151071 | AR151071 Sequence |
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| 5 | 580 | 58.8 | 588 | 4 | AF349536 | AF349536 Canis fam |
| 6 | 444 | 45.0 | 452 | 4 | AF333121 | AF333121 Canis fam |
| 7 | 387 | 39.2 | 446 | 4 | AF091134 | AF091134 Canis fam |
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| 9 | 128 | 13.0 | 984 | 6 | AX154599 | AX154599 Sequence |
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ALIGNMENTS

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ACCESSION AR151071
VERSION AR151071.1 GI:15117121
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 990)
AUTHORS Okano, F., Saitoh, M. and Yamada, K.
TITLE Canine Interleukin 12
JOURNAL Patent: US 6231850-A 11 15-MAY-2001;
FEATURES location/Qualifiers
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LOCUS      E15017          990 bp      DNA          linear      PAT 28-JUL-1999
DEFINITION Canine mRNA for Interleukin 12 40kDa subunit, complete cds.
ACCESSION  E15017
VERSION    E15017.1 GI:5709700
KEYWORDS   JP 1998036397-A/1.
SOURCE     Canis sp.
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE  1 (bases 1 to 990)
AUTHORS   Okano,F.
TITLE     CANINE INTERLEUKIN 12 AND ITS PRODUCTION
JOURNAL   Patent: JP 1998036397-A 1 10-FEB-1998;
          TORAY IND INC
COMMENT    OS   Canis sp. (dog)
          PN   JP 1998036397-A/1
          PD   10-FEB-1998
          PR   08-NOV-1996 JP 1996296789
          PR   08-NOV-1995 JP 95P 289729, 23-MAY-1996 JP 96P 128104 PI
          ORANO FUMIYOSHI
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Query Match     98.7%; Score 974; DB 6; Length 990;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 974; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ACCESSION U49100
VERSION U49100.1 GI:1223907
KEYWORDS
SOURCE
ORGANISM
Canis familiaris.
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
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1 (bases 1 to 1015)
Belke-Louis, G.F. and Bueltner, M.
Cloning and sequence analysis of the p35 and p40 subunits of canine
Interleukin-12
TITLE
JOURNAL
REFERENCE
AUTHORS
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TITLE
JOURNAL
Microbiology, Veterinärstr. 13, Muenchen, D-80539, Germany
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DEFINITION
ACCESSION AR151061
VERSION   AR151061.1 GI:15117111
KEYWORDS
SOURCE   Unknown.
ORGANISM Unclassified.
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AUTHORS   Okano, F., Satoh, M., and Yamada, K.
TITLE     Canine Interleukin 12
JOURNAL   Patent: US 6231850-A 1 15-MAY-2001;
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Best Local Similarity 99.7%; Pred. No. 0;
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QY      568 TACACAGTGAAGTGTAGAGAGGAGTGTGCTGCTGCGAGAGAGACCTTACCATC 627
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Db      568 TACACAGTGAAGTGTAGAGAGGAGTGTGCTGCTGCGAGAGAGACCTTACCATC 627
QY      628 GAGTGTGTGTGATCTATTTCACAAAGCTCAAGTATGAAAACTACACACAGCTTCTTC 687

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Db      628 GAGTGTGTGTGATCTATTTCACAAAGCTCAAGTATGAAAACTACACACAGCTTCTTC 687
QY      688 ATCAGAGACATCATCAACACAGACCCACCAACACTGACGTGAGGCATGAAAGAT 747
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Db      688 ATCAGAGACATCATCAACACAGACCCACCAACACTGACGTGAGGCATGAAAGAT 747
QY      748 TCTGCGACGTGAGGTGACGCTGGAATACCCGACACCTGAGACACCCACATTCCTAC 807
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Db      748 TCTGCGACGTGAGGTGACGCTGGAATACCCGACACCTGAGACACCCACATTCCTAC 807
QY      808 TTCTCCCTGACATTTTTCATACAGGCCGACGAGCAAGACAAATAGAAAAAGATAGA 867
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Db      808 TTCTCCCTGACATTTTTCATACAGGCCGACGAGCAAGACAAATAGAAAAAGATAGA 867
QY      868 CTCGTGGTGAGCAAGACCTCAGCCAGAGGTGTGTGCGACAAAGATGCCGATCCGCTG 927
        |||||||
Db      868 CTCGTGGTGAGCAAGACCTCAGCCAGAGGTGTGTGCGACAAAGATGCCGATCCGCTG 927
QY      928 CAAGCCCGAGACCGCTACTATAGTTCATCCTGAGAGGAGCTGGCATCTGTG 978
        |||||||
Db      928 CAAGCCCGAGACCGCTACTATAGTTCATCCTGAGAGGAGCTGGCATCTGTG 978
RESULT 5
AF349536
LOCUS   588 bp mRNA linear MAN 17-MAY-2001
DEFINITION
ACCESSION AF349536
VERSION   AF349536.1 GI:14133584
KEYWORDS
SOURCE   Canis familiaris.
ORGANISM Canis familiaris.
          Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 588)
AUTHORS   Fontana, S., Groene, A., Koenig, M., and Baumgaertner, W.
TITLE     Sequence of canine Interleukin-12 p40 mRNA in DH82-cells
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 588)
AUTHORS   Fontana, S., Groene, A., Koenig, M., and Baumgaertner, W.
TITLE     Direct Submission
JOURNAL   Submitted (15-FEB-2001) Institute of Pathology,
          Justus-Liebig-University, Frankfurt Str. 96, Giessen 35392,
          Germany
FEATURES
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                        Location/Qualifiers
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                        /organism="Canis familiaris"
                        /db_xref="taxon:9615"
                        /cell_line="DH82"
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                        /codon_start=3
                        /product="Interleukin-12 subunit p40"
                        /protein_id="AAK54070.1"
                        /db_xref="GI:14133585"
                        /translation="QQVLISWSEVLVLASPLMAIWELEKDYVVELDMHPADGEMV
                        LKHPEDDITWTSQSSSEVLGSKTLIOVEFDAQOYCHKGKVLRSLLIR
                        KKEGDIWSTDLIKEOKESKNKIFLKCEANYSGRFTCMWLTAISTDLKFSVSRGFS
                        DPQVTCGAVTISAERVYDNRNDNRKRYTECGEGS"
BASE COUNT  167 a 124 c 155 g 142 t
ORIGIN
Query Match      58.8%; Score 580; DB 4; Length 588;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 580; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CTGACAGTGTGTCATCTCTGTTTCCCTGTTTTCGCGGCTCCCTCATGAGCA 67
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Db      1 CTCAGCAGTTGTCATCTCTGTTTCCCTGTTTTCGCGGCTCCCTCATGAGCA 60
QY      68 TATGGGAACGTGGAGAAAGATTTATGTGTAGAGTTGAGTGGACAGCCCGATGAGCCCG 127
        |||||||
Db      61 TATGGGAACGTGGAGAAAGATTTATGTGTAGAGTTGAGTGGACAGCCCGATGAGCCCG 120

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| Query Match | 45.0% | Score 444 | DB 4 | Length 452 |
|-----------------------|--|---|----------|-----------------|
| Best Local Similarity | 100.0% | Pred. No. 2,4e-238 | | |
| Matches 444 | Conservative 0 | Mismatches 0 | Indels 0 | Gaps 0 |
| QY | 144 | CACCGCCCATACCCCTGAGAAAGATGACATCATCTTGGACCTCAGCGCAGACAGTGAAGT | 203 | |
| Db | 1 | CACCTGCCATACCCCTGAGAAAGATGACATCATCTTGGACCTCAGCGCAGACAGTGAAGT | 60 | |
| QY | 204 | CTTAGGTTCTGGTAAACCTCTGACCATCCAAAGAAATTTTGAGATGCTGGCCAGTA | 263 | |
| Db | 61 | CCTAGGTTCTGGTAAACCTCTGACCATCCAAAGAAATTTTGAGATGCTGGCCAGTA | 120 | |
| QY | 264 | TACCTGCCATTAAGAGGACGAAGTTCTGAGCCGCTCACTCTGTGATTACAAAAAGA | 323 | |
| Db | 121 | TACCTGCCATTAAGAGGACGAAGTTCTGAGCCGCTCACTCTGTGATTACAAAAAGA | 180 | |
| QY | 324 | AGATGGAAATTTGGTGCACATGATTCCTTAAAGCAAGAAAGATCCAAAAATAGATCTT | 383 | |
| Db | 181 | AGATGGAAATTTGGTGCACATGATTCCTTAAAGCAAGAAAGATCCAAAAATAGATCTT | 240 | |
| QY | 384 | TCTGAAATGTGAGGCCAAAGAAATTAATCTGACGCTTTGACATGCTGGTGCAGCGCAAT | 443 | |
| Db | 241 | TCTGAAATGTGAGGCCAAAGAAATTAATCTGACGCTTTGACATGCTGGTGCAGCGCAAT | 300 | |
| QY | 444 | CAGTACGATTTTGAATTCACATGTCACAAAGTCAGAGAGCTTCTCTGACCCCAAGGGT | 503 | |
| Db | 301 | CAGTACGATTTTGAATTCACATGTCACAAAGTCAGAGAGCTTCTCTGACCCCAAGGGT | 360 | |
| QY | 504 | GACATGTCAGCAGCAGACACTTTAGCAGAGAGGGTCAGAGTGGACCAACAGGATTTAA | 563 | |
| Db | 361 | GACATGTCAGCAGCAGTGGACACTTTTACCGAGAGGGTCAGAGTGGACCAACAGGATTTAA | 420 | |
| QY | 564 | GAAGTACACAGCTGGAGTGTGAGA | 587 | |
| Db | 421 | GAAGTACACAGCTGGAGTGTGAGA | 444 | |
| RESULT 7 | | | | |
| AF091134 | 446 bp | mrna | linear | MAM 04-AUG-1999 |
| LOCUS | | | | |
| DEFINITION | Canis familiaris Interleukin-12 p40 mRNA, partial cds. | | | |
| ACCESSION | AF091134 | | | |
| VERSION | AF091134.1 | GI:5690205 | | |
| KEYWORDS | | | | |
| SOURCE | | | | |
| ORGANISM | Canis familiaris. | | | |
| REFERENCE | | | | |
| AUTHORS | German,A.J., Helps,C.R., Harley,R., Hall,E.J. and Day,M.J. | | | |
| TITLE | 1 (bases 1 to 446) | | | |
| JOURNAL | German,A.J., Helps,C.R., Harley,R., Hall,E.J. and Day,M.J. | | | |
| REFERENCE | 2 (bases 1 to 446) | | | |
| AUTHORS | German,A.J., Helps,C.R., Harley,R., Hall,E.J. and Day,M.J. | | | |
| TITLE | Direct Submission | | | |
| JOURNAL | Submitted (12-SEP-1998) Department of Clinical Veterinary Science, | | | |
| AUTHORS | University of Bristol, Langford House, Langford, Bristol, North | | | |
| TITLE | Somerset BS40 5DU, United Kingdom | | | |
| JOURNAL | Location/Qualifiers | | | |
| FEATURES | | | | |
| SOURCE | 1..446 | | | |
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| | /codon_start=1 | | | |
| | /product="Interleukin-12 p40" | | | |
| | /protein_id="AAD6992.1" | | | |
| | /db_xref="GI:5690206" | | | |
| | /translation="TGAAGTLLTIOVKEFFGDAGQYTCCHKGKVLRSLLTHKKEDGIV | | | |
| | STDLIRKESKNIKFLKCEAKNYSGRFTCMWLTALISTDLKFSVKSRRGSPDGQYTC | | | |
| | GAVTLSAEIRVDRDVRNXYTVCEQESACPSAEESLPIEVVDAIP" | | | |

ORIGIN

Query Match 39.2%; Score 387; DB 4; Length 446;
Best Local Similarity 99.8%; Pred. No. 3.3e-206;
Matches 437; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 212 CTGTAACCTCTACCATCCAAATTTGGAGATGCTGGCCAGTATACCTGCC 271
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Db 8 CTGTAACCTCTACCATCCAAATTTGGAGATGCTGGCCAGTATACCTGCC 67

QY 272 ATAAGAGGCAAGCTCTGAGCGCTCACCTCGTTGATTACAAAAAGAAATGGA 331
|||||
Db 68 ATAAGAGGCAAGCTCTGAGCGCTCACCTCGTTGATTACAAAAAGAAATGGA 127

QY 332 TTGGTCCACTGATATCTTAAAGACAGAAAGATCAAAATATAGATCTTTGAAAT 391
|||||
Db 128 TTGGTCCACTGATATCTTAAAGACAGAAAGATCAAAATATAGATCTTTGAAAT 187

QY 392 GTGAGCAAGAAATATTTCTGAGCTTTCACATGCTGTGGCTGAGGCAATGACTG 451
|||||
Db 188 GTGAGCAAGAAATATTTCTGAGCTTTCACATGCTGTGGCTGAGGCAATGACTG 247

QY 452 ATTGAATTCAGTGTCAAAAGTACAGAGGCTTCTGACCCCAAGGGGTGACATGTG 511
|||||
Db 248 ATTGAATTCAGTGTCAAAAGTACAGAGGCTTCTGACCCCAAGGGGTGACATGTG 307

QY 512 GAGCAGTGACACTTTCAGCAGAGAGGCTCAGAGTGAACAACAGGATTTAAGAACTACA 571
|||||
Db 308 GAGCAGTGACACTTTCAGCAGAGAGGCTCAGAGTGAACAACAGGATTTAAGAACTACA 367

QY 572 CAGTGAGTGTACAGAGGAGGAGTCCCTGCTGCTGCGGAGAGAGCTTACCATGAGG 631
|||||
Db 368 CAGTGAGTGTACAGAGGAGGAGTCCCTGCTGCTGCGGAGAGAGCTTACCATGAGG 427

QY 632 TCGTGTGATGCTATTC 649
|||||
Db 428 TCGTGTGATGCTATTC 445

RESULT 8
AX154603 990 bp DNA linear PAT 22-JUN-2001
LOCUS Sequence 7 from Patent WO0140257.
DEFINITION AX154603
ACCESSION AX154603
VERSION AX154603.1 GI:14536186
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
synthetic construct
artificial sequences.
REFERENCE
1 (bases 1 to 990)
AUTHORS
Leong, S.R. and Punnonen, J.
TITLE
Cytokine polypeptides and nucleic acids
JOURNAL
Patent: WO 0140257-A 7 07-JUN-2001;
Maxygen, Inc. (US)
location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

BASE COUNT 270 a 250 c 254 g 216 t

ORIGIN

Query Match 14.5%; Score 143; DB 6; Length 990;
Best Local Similarity 100.0%; Pred. No. 1.1e-68;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 565 AAGTACACAGTGTGATGTCAGAGGCGAGTGCCTGCGCGAGAGAGCCTAACCC 624
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Db 565 AAGTACACAGTGTGATGTCAGAGGCGAGTGCCTGCGCGAGAGAGCCTAACCC 624

QY 625 ATCGAGGTGTGTGATGCTATTCACAAAGCTCAAGTATGAAACTACACAGCAGCTTC 684
|||||
Db 625 ATCGAGGTGTGTGATGCTATTCACAAAGCTCAAGTATGAAACTACACAGCAGCTTC 684

QY 685 TTCATCAGACATCATCAAAACC 707
|||||
Db 685 TTCATCAGACATCATCAAAACC 707

RESULT 9
AX154599 984 bp DNA linear PAT 22-JUN-2001
LOCUS Sequence 3 from Patent WO0140257.
DEFINITION AX154599
ACCESSION AX154599
VERSION AX154599.1 GI:14536182
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
synthetic construct
artificial sequences.
REFERENCE
1 (bases 1 to 984)
AUTHORS
Leong, S.R. and Punnonen, J.
TITLE
Cytokine polypeptides and nucleic acids
JOURNAL
Patent: WO 0140257-A 3 07-JUN-2001;
Maxygen, Inc. (US)
location/Qualifiers
FEATURES
source
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

BASE COUNT 267 a 246 c 254 g 217 t

ORIGIN

Query Match 13.0%; Score 128; DB 6; Length 984;
Best Local Similarity 100.0%; Pred. No. 1.3e-60;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 565 AAGTACACAGTGTGATGTCAGAGGCGAGTGCCTGCGCGAGAGAGCCTAACCC 624
|||||
Db 565 AAGTACACAGTGTGATGTCAGAGGCGAGTGCCTGCGCGAGAGAGCCTAACCC 624

QY 625 ATCGAGGTGTGTGATGCTATTCACAAAGCTCAAGTATGAAACTACACAGCAGCTTC 684
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Db 625 ATCGAGGTGTGTGATGCTATTCACAAAGCTCAAGTATGAAACTACACAGCAGCTTC 684

QY 685 TTCATCAG 692
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Db 685 TTCATCAG 692

RESULT 10
AX154600 984 bp DNA linear PAT 22-JUN-2001
LOCUS Sequence 4 from Patent WO0140257.
DEFINITION AX154600
ACCESSION AX154600
VERSION AX154600.1 GI:14536183
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
synthetic construct
artificial sequences.
REFERENCE
1 (bases 1 to 984)
AUTHORS
Leong, S.R. and Punnonen, J.
TITLE
Cytokine polypeptides and nucleic acids
JOURNAL
Patent: WO 0140257-A 4 07-JUN-2001;
Maxygen, Inc. (US)
location/Qualifiers
FEATURES
source
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

BASE COUNT 272 a 254 c 247 g 211 t

ORIGIN

Query Match 9.6%; Score 95; DB 6; Length 984;
Best Local Similarity 100.0%; Pred. No. 1.3e-41;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 586 GAGGGCACTGCTGCCCTCTGCCGAGAGAGACCTACCATTGAGTGTGATGCT 645
|||||
Db 586 GAGGGCACTGCTGCCCTCTGCCGAGAGAGACCTACCATTGAGTGTGATGCT 645
Oy 646 ATTCACAGCTCAAGTATGAAACTACACGACG 680
|||||
Db 646 ATTCACAGCTCAAGTATGAAACTACACGACG 680

RESULT 11

AX154601
LOCUS AX154601 5 969 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 5 from Patent WO0140257.
ACCESSION AX154601
VERSION AX154601.1 GI:14536184
KEYWORDS

SOURCE

ORGANISM synthetic construct.
artificial sequences.

REFERENCE

1 (bases 1 to 969)
AUTHORS Leong,S.R. and Punnonen,J.
TITLE Cytokine polypeptides and nucleic acids
JOURNAL Patent: WO 0140257-A 5 07-JUN-2001;
Maxygen, Inc. (US)

FEATURES

Location/Qualifiers
1..969
/organism="synthetic construct"
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/note="Synthetic Sequence"

BASE COUNT 263 a 249 c 251 g 206 t
ORIGIN

Query Match 7.6%; Score 75; DB 6; Length 969;
Best Local Similarity 100.0%; Pred. No. 2.4e-30;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 900 CTGCCACAGCATCCGCTGCCAAGCCCGAGCCGCTACTAGTTCATCCTG 959
|||||

Db 879 CTGCCACAGCATCCGCTGCCAAGCTCCGCTGCCAAGCCCGAGCCGCTACTAGTTCATCCTG 938

Oy 960 GAGCGACTGGCGATC 974
|||||

Db 939 GAGCGACTGGCGATC 953

RESULT 12

AX154597
LOCUS AX154597 1 975 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1 from Patent WO0140257.
ACCESSION AX154597
VERSION AX154597.1 GI:14536180
KEYWORDS

SOURCE

ORGANISM synthetic construct.
artificial sequences.

REFERENCE

1 (bases 1 to 975)
AUTHORS Leong,S.R. and Punnonen,J.
TITLE Cytokine polypeptides and nucleic acids
JOURNAL Patent: WO 0140257-A 1 07-JUN-2001;
Maxygen, Inc. (US)

FEATURES

Location/Qualifiers
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/note="Synthetic Sequence"

BASE COUNT 269 a 252 c 250 g 204 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.2e-28;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 647 TTCAACAAGCTCAAGTATGAAACTACACGACGCTTCTTCATGAGACATCATCAAC 706

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Db 632 TTCAACAAGCTCAAGTATGAAACTACACGACGCTTCTTCATGAGACATCATCAAC 691
Oy 707 CAGACCCACCA 718
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Db 692 CAGACCCACCA 703

RESULT 13

AF054607
LOCUS AF054607 431 bp mRNA linear MAM 26-JUL-2000
DEFINITION Fells catus interleukin 12 p40 subunit mRNA, partial cds.
ACCESSION AF054607
VERSION AF054607.1 GI:3126822
KEYWORDS

SOURCE

ORGANISM Fells catus.

REFERENCE

1 (bases 1 to 431)
AUTHORS Harley,R., Helps,C.R., Harbour,D.A., Gruffydd-Jones,T.J. and Day,M.J.
TITLE Cytokine mRNA expression in lesions in cats with chronic gingivostomatitis
JOURNAL Clin. Diagn. Immunol. 6 (4), 471-478 (1999)

MEETING 10391845
PUBMED 99322318
REFERENCE 2 (bases 1 to 431)
AUTHORS Harley,R., Helps,C.R., Gruffydd-Jones,T.J., Day,M.J. and Harbour,D.A.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1998) Clinical Veterinary Science, University of Bristol, Langford House, Langford, Bristol BS40 7DU, U.K.
LOCATION/Qualifiers
1..431

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/db_xref="GI:3126823"
/translation="CHKXEVLSHSXYLIHXKDGIMSTDILRQKSKNKPIPKCEAKNSGRFTCMWLTAISTDLKFTVKSRSRSDPQVTCGAATLSAEKVRVDMRDYKKYTVCEQBSACPAEESLPIEVVVDAIHKLIKENYTSFPIRD"

CDS

BASE COUNT 129 a 93 c 114 g 91 t 4 others
ORIGIN

Query Match 6.7%; Score 66; DB 4; Length 431;
Best Local Similarity 100.0%; Pred. No. 2.9e-25;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 537 GGTGAGTGGACACAGGATTAATAAGTATACAGTGTGAGGAGGACATGCG 596
|||||

Db 270 GGTGAGTGGACACAGGATTAATAAGTATACAGTGTGAGGAGGACATGCG 329

Oy 597 CTGCC 602
|||||
Db 330 CTGCC 335

RESULT 14

FCU83184
LOCUS FCU83184 990 bp mRNA linear MAM 16-JUL-1999
DEFINITION Fells catus interleukin-12 p40 subunit (IL-12) mRNA, complete cds.
ACCESSION U83184
VERSION U83184.1 GI:2735050
KEYWORDS

BASE COUNT 269 a 252 c 250 g 204 t
ORIGIN

Query Match 7.3%; Score 72; DB 6; Length 975;
Best Local Similarity 100.0%; Pred. No. 1.2e-28;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE 1 (bases 1 to 990)
AUTHORS Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W., Pedersen,N.C., and Lutz,H.
TITLE Nucleotide and predicted peptide sequence of feline interleukin-12 (IL-12)
JOURNAL DNA Seq. 8 (1-2), 77-82 (1997)
MEDLINE 98182592
PUBMED 952125
REFERENCE 2 (bases 1 to 990)
AUTHORS Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W., Pedersen,N.C., and Lutz,H.
TITLE Direct Submission
JOURNAL Submitted (24-DEC-1996) Clinical Laboratory, Department of Internal Veterinary Medicine, University of Zurich, Winterthurerstrasse 260, Zurich, ZH 8057, Switzerland
FEATURES
source Location/Qualifiers
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BASE COUNT 283 a 251 c 249 g 207 t
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Query Match 6.7%; Score 66; DB 4; Length 990;
Best Local Similarity 100.0%; Pred. No. 2.9e-25;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 537 GGTGAGAGTGACACAGGAGGATTATTAAGAGTACACAGTGCAGGAGGCGAGTGC 596
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DB 537 GGTGAGAGTGACACAGGAGGATTATTAAGAGTACACAGTGCAGGAGGCGAGTGC 596
QY 597 CTGCCC 602
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DB 597 CTGCCC 602
RESULT 15
AX076200 990 bp DNA linear PAT 06-FEB-2001
LOCUS AX076200
DEFINITION Sequence 1 from Patent WO0104155.
ACCESSION AX076200
VERSION AX076200.1 GI:12710825
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 990)
AUTHORS Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
TITLE Feline interleukin-12 as an immune stimulant
JOURNAL Patent: WO 0104155-A 1 18-JAN-2001;
Mojoen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)
FEATURES
source Location/Qualifiers
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/note="feline IL-12 p40"
BASE COUNT 283 a 249 c 248 g 210 t
ORIGIN

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Job time : 2743.63 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 06:46:54 ; Search time 254.001 Seconds
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Searched: 2185239 seqs, 1125999159 residues

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Minimum DB seq length: 0

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20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 974 | 98.7 | 990 | 19 | AAV13817 |
| 2 | 974 | 98.7 | 990 | 20 | AAV35625 |
| 3 | 974 | 98.7 | 990 | 20 | AAV35625 |
| 4 | 974 | 98.7 | 990 | 22 | AAV35625 |
| 5 | 900 | 91.2 | 990 | 19 | AAV35625 |
| 6 | 900 | 91.2 | 990 | 20 | AAV35625 |
| 7 | 900 | 91.2 | 990 | 20 | AAV35625 |
| 8 | 900 | 91.2 | 990 | 22 | AAV35625 |
| 9 | 658 | 66.7 | 924 | 20 | AAV35625 |

| | | | | | |
|----|-----|------|------|----|----------|
| 10 | 658 | 66.7 | 2154 | 20 | AAV18176 |
| 11 | 143 | 14.5 | 990 | 22 | AAD15209 |
| 12 | 128 | 13.0 | 984 | 22 | AAD15205 |
| 13 | 95 | 9.6 | 984 | 22 | AAD15206 |
| 14 | 75 | 7.6 | 969 | 22 | AAD15207 |
| 15 | 72 | 7.3 | 975 | 22 | AAD15203 |
| 16 | 66 | 6.7 | 921 | 19 | AAV56626 |
| 17 | 66 | 6.7 | 990 | 22 | AAV26082 |
| 18 | 66 | 6.7 | 990 | 22 | AAV26085 |
| 19 | 66 | 6.7 | 2193 | 19 | AAV56625 |
| 20 | 66 | 6.7 | 4522 | 22 | AAV26076 |
| 21 | 66 | 6.7 | 4522 | 22 | AAV26094 |
| 22 | 63 | 6.4 | 921 | 19 | AAV56627 |
| 23 | 60 | 6.1 | 540 | 20 | AAV27732 |
| 24 | 60 | 6.1 | 540 | 21 | AAV13801 |
| 25 | 46 | 4.7 | 906 | 11 | AAQ04701 |
| 26 | 46 | 4.7 | 975 | 22 | AAD15208 |
| 27 | 46 | 4.7 | 979 | 12 | AAQ12149 |
| 28 | 46 | 4.7 | 987 | 16 | AAQ97484 |
| 29 | 46 | 4.7 | 987 | 19 | AAV07273 |
| 30 | 46 | 4.7 | 987 | 19 | AAV07217 |
| 31 | 46 | 4.7 | 987 | 20 | AAV40404 |
| 32 | 46 | 4.7 | 987 | 20 | AAV85199 |
| 33 | 46 | 4.7 | 987 | 22 | AAD15210 |
| 34 | 46 | 4.7 | 1007 | 22 | AAD18585 |
| 35 | 46 | 4.7 | 1018 | 15 | AAQ67879 |
| 36 | 46 | 4.7 | 1018 | 20 | AAQ08510 |
| 37 | 46 | 4.7 | 1389 | 22 | AAV76880 |
| 38 | 46 | 4.7 | 1397 | 18 | AAV00401 |
| 39 | 46 | 4.7 | 1397 | 18 | AAV79699 |
| 40 | 46 | 4.7 | 1397 | 18 | AAV79699 |
| 41 | 46 | 4.7 | 1397 | 19 | AAV37767 |
| 42 | 46 | 4.7 | 1399 | 21 | AAZ40021 |
| 43 | 46 | 4.7 | 2300 | 21 | AAV92406 |
| 44 | 46 | 4.7 | 2362 | 13 | AAQ23586 |
| 45 | 46 | 4.7 | 2362 | 17 | AAV48098 |

ALIGNMENTS

```
RESULT 1
AAV13817
ID AAV13817 standard; cDNA to mRNA; 990 BP.
AC AAV13817;
DT 14-MAY-1998 (first entry)
DE Canine IL-12 P40 subunit cDNA.
KW Canine; interleukin-12 P40 subunit; IL-12 P40 subunit; antitumour;
  antiviral; vaccine adjuvant; ds.
OS Canis sp.
FT key Location/Qualifiers
FT CDS 1..990 /tag= a /product= interleukin-12_P40_subunit
PD 10-FEB-1998.
PP 08-NOV-1996; 96JP-0296789.
PR 23-MAY-1996; 96JP-0128104.
PR 08-NOV-1995; 95JP-0289729.
PA (TORA ) TORAY IND INC.
PA 1998-174914/16.
DR
```

| | |
|----|--|
| DR | P-PSDB; AAM1791. |
| XX | |
| PT | Canine interleukin 12 - comprises P40 and P35 subunits; useful in |
| PT | veterinary medicine, e.g. antitumour, antiviral and vaccine adjuvant |
| PT | activities are expected |
| XX | |
| PS | Claim 10: Pages 10-11; 12pp; Japanese. |
| XX | |
| CC | The present sequence encodes a canine interleukin-12 (IL-12) P40 |
| CC | subunit. A canine IL-12 comprising a P40 and P35 subunit is capable |
| CC | of inducing an antiviral activating factor and the expression of |
| CC | class II MHC molecules in canine tumour cells; stimulating |
| CC | proliferation of canine blastogenic lymphocytes and activating |
| CC | canine leukocytes to inhibit canine tumour cells. The canine IL-12 |
| CC | can be used in veterinary medicines, e.g. antitumour, antiviral and |
| CC | vaccine adjuvant activities are expected. |
| XX | |
| SO | Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 other; |

| | | | |
|----|-----|--|-----|
| Db | 72 | CAGCTGAAGCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATATCCCGAGACC | 786 |
| Qy | 787 | TGGAGGACCCCGCAATTCCCTACTTTCGCCGACATTTTCGATACAGGCCGACGGCAAC | 846 |
| Db | 787 | TGGAGCACCCCGCAATTCTACTTCTCCCTGACATTTTCTACACAGGCCGACGGCAAC | 846 |
| Qy | 847 | AATAGGAAAAAGAAATAGACTCTGCGTGGCAAGACCTCAGCCAAAGTGGTGGCAC | 906 |
| Db | 847 | AATAGGAAAAAGAAATAGACTCTGCGTGGCAAGACCTCAGCCAAAGTGGTGGCAC | 906 |
| Qy | 907 | AAGGATGCCACAGATCCGCTGGCAACCCGAGACCGCTACTATAGTTTCATCCTGGAGGAC | 966 |
| Db | 907 | AAGGATGCCCAAGATCCGCGCTGGCAAGCCGAGACCGCTACTATAGTTTCATCCTGGAGGAC | 966 |
| Qy | 967 | TGGGCACTGTCTC 980 | |
| Db | 967 | TGGGCACTGTCTC 980 | |

| | | | | |
|-----------------------|--------------|-----------|------------|------------|
| Query Match | 98.7% | Score 974 | DB 19 | Length 990 |
| Best Local Similarity | 100.0% | Pred. Nc. | 0 | |
| Matches 974 | Conservative | 0 | Mismatches | 0 |
| | | | Indels | 0 |
| | | | Gaps | 0 |

RESULT 2
AAX35625
ID AAX35625 standard; CDNA to mRNA; 990 BP

| | | | |
|----|-----|---|-----|
| OY | 7 | CCTAGCAGTGGTCATATCCCGGTTTCCCGGTTTGGGGCTCCCTCATAGGCG | 66 |
| Db | 7 | CCTACGCGATTGGTCATCTCTGGTTTCCCTCGTTTGGGGCTCCCTCATAGGCG | 66 |
| OY | 67 | ATATGGCACTGGAGAAAGATGTTTATGTTAGATTGGACTGGCACCTCATCCCC | 126 |
| Db | 67 | ATATGGCAACTGGAGAAAGATGTTTATGTTAGATTGGACTGGCACCTCATGCCCC | 126 |
| OY | 127 | GGAGAAATGGTGGTCCCTGACCTGGCATACCCCTGAAAGAAAGATACATGTAACCTCA | 186 |
| Db | 127 | GGAGAAATGGTGGTCTTCCCTGACCTGGCATACCCCTGAAAGAAAGATACATGTAACCTCA | 186 |
| OY | 187 | GGCGAGAGCAGTGAAGTCTAGGTTCTGTTAAACTCTGACCATCAAGTCAAAAGATT | 246 |
| Db | 187 | GGCGAGAGCAGTGAAGTCTAGGTTCTGTTAAACTCTGACCATCAAGTCAAAAGATT | 246 |
| OY | 247 | GGAGATGTTGGCCAGTATACCTGCCATAAAGAGGCAAGGTTCTAGCGCCCTCACTCTG | 306 |
| Db | 247 | GGAGATGTTGGCCAGTATACCTGCCATAAAGAGGCAAGGTTCTAGCGCCCTCACTCTCG | 306 |
| OY | 307 | TTGATTCACAAAAAGAGATGGATTTGGTCCACTGATATCTTAAAGACACAGAAAGAA | 366 |
| Db | 307 | TTGATTCACAAAAAGAGATGGATTTGGTCCACTGATATCTTAAAGACACAGAAAGAA | 366 |
| OY | 367 | TCCAAAATTAAGATCTTTCTGAATGTGAGGCAAGAAATTATCTGGACGTTTCAATGC | 426 |
| Db | 367 | TCCAAAATTAAGATCTTTCTGMAATGTGAGGCAAGAAATTATCTGGACGTTTCAATGC | 426 |
| OY | 427 | TGGTGGCTGAGGGCAATCAGTACGTATTGMAATTCAGTGTCAAAAGTAGAGAGGCTTC | 486 |
| Db | 427 | TGGTGGCTGAGGGCAATCAGTACGTATTGMAATTCAGTGTCAAAAGTAGAGAGGCTTC | 486 |
| OY | 487 | TCTGACCCCCAAGGGGTGACATGTGTGAGCAGTACACTTTCAGCAGAGAGGGTCAAGATG | 546 |
| Db | 487 | TCTGACCCCCAAGGGGTGACATGTGTGAGCAGTACACTTTCAGCAGAGAGGGTCAAGATG | 546 |
| OY | 547 | GACAAACAGGGATTATTAAGAGTACACAGTGTGATGTCAAGAGGGCAGTGCCTGCCCTCT | 606 |
| Db | 547 | GACAAACAGGGATTATTAAGAGTACACAGTGTGATGTCAAGAGGGCAGTGCCTGCCCTCT | 606 |
| OY | 607 | GGCGAGGAGACCTTACCCATCGAGGTCTGTGGGATGCTATTCAACAGTCAAGTATGAA | 666 |
| Db | 607 | GGCGAGGAGACCTTACCCATCGAGGTCTGTGGGATGCTATTCAACAGTCAAGTATGAA | 666 |
| OY | 667 | AACACACACAGAGCTTCTCATCGAGACATCATCAACACAGACCCACCCCAAAACCTG | 726 |
| Db | 667 | AACACACACAGAGCTTCTCATCGAGACATCATCAACACAGACCCACCCCAAAACCTG | 726 |
| OY | 727 | CAGCTGAAGCATTGAAAAATTCTCGCACGTGAAGGTACGCTGGAAATTACCCCGACAC | 786 |
| Db | 727 | CAGCTGAAGCATTGAAAAATTCTCGCACGTGAAGGTACGCTGGAAATTACCCCGACAC | 786 |

| | | |
|----|--|--------------------------------------|
| AC | AXX35625; | |
| XX | | |
| DT | 09-JUL-1999 | (first entry) |
| XX | | |
| XX | | |
| DE | Nucleic acid encoding canine Interleukin-12 (IL-12). | |
| XX | | |
| KW | Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer; | |
| XX | tumour; skin disease; infectious disease; allergic disease; ds. | |
| KX | | |
| OS | Canis sp. | |
| XX | | |
| FH | Key | Location/Qualifiers |
| FT | CDS | 1..990 |
| FT | | /*tag= a |
| XX | | |
| PN | JPI1106350-A. | |
| XX | | |
| PD | 20-APR-1999. | |
| XX | | |
| PF | 15-MAY-1998; | 98JP-0133345. |
| XX | | |
| PR | 07-AUG-1997; | 97JP-0213755. |
| PR | 16-MAY-1997; | 97JP-0127690. |
| XX | | |
| PA | (TORA) TORAY IND INC. | |
| XX | | |
| DR | WPI; 1999-308068/26. | |
| DR | P-PSDB; AAY02342. | |
| PT | | |
| PT | A prevention and treating agent containing Interleukin 12 (CaIL12) - | |
| XX | for prevention and treatment of dog and cat immune diseases | |
| XX | | |
| PS | Claim 1; Page 14-15; 16pp; Japanese. | |
| XX | | |
| CC | | |
| CC | The present sequence encodes canine Interleukin-12 (IL-12). The | |
| CC | specification describes a method for the prevention and treatment | |
| CC | of dog and cat immune diseases. The treatment used an agent comprising | |
| CC | dog IL-12 (CaIL12) proteins to form a heterodimer. The agent is | |
| CC | useful for preventing and treating dog and cat immune diseases, | |
| CC | including tumours, skin diseases, infectious diseases and allergic | |
| CC | diseases. | |
| XX | | |
| SO | Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 other; | |
| | Query Match | 98.7%; Score 974; DB 20; Length 990; |
| | Best Local Similarity | 100.0%; Pred. No. 0; |
| | Matches 974; Conservative 0; Mismatches 0; Indels 0; Gaps 0 | |
| 09 | 7 CCTAGCAGTTGGTCATCTCCTGGTTTCCCTGTTTGGTCAGGCGTCCTCCTCATGGCC 66 | |
| | | |

```
Dh 7 CCTGAGCAGTGGTGCATCTCCCTGGTTTTCCCTCGTTTTGCTGGCTCTCCCTCATGCGC 66
Qy 67 ATATGGAACTGGAGAAAGATGTTATGTTAGAGTTGGACCTGGACCCGATGCCCC 126
Dh 67 ATATGGAACTGGAGAAAGATGTTATGTTAGAGTTGGACCTGGACCCGATGCCCC 126
Qy 127 GGAGAAATGGTGTCTCTACCTGGCCATACCCCTGAGAGAGATGACATCTACTTGGACCTCA 186
Dh 127 GGAGAAATGGTGTCTCTACCTGGCCATACCCCTGAGAGAGATGACATCTACTTGGACCTCA 186
Qy 187 GCGCAGACGACGTGAAGTCTTAGTTCGTGTGTAATAACTGACCAATCCAAAGTCAAGAAATTT 246
Dh 187 GCGCAGACGACGTGAAGTCTTAGTTCGTGTGTAATAACTGACCAATCCAAAGTCAAGAAATTT 246
Qy 247 GGACATGCTGGCCGATGTTACTGCTTAAGAGAGCAAGTTCGAGCGCTGACTCTG 306
Dh 247 GGACATGCTGGCCGATGTTACTGCTTAAGAGAGCAAGTTCGAGCGCTGACTCTG 306
Qy 307 TTGATTCACAAAAAAGAAAGATGCAATTTGTCCTCATATATCTTAAAGAACAGAAAGAA 366
Dh 307 TTGATTCACAAAAAAGAAAGATGCAATTTGTCCTCATATATCTTAAAGAACAGAAAGAA 366
Qy 367 TCCAAAAATAGATCTTTCTGAAATGTGAGGCAAAAGATTAATCTGACGTTTCACATGC 426
Dh 367 TCCAAAAATAGATCTTTCTGAAATGTGAGGCAAAAGATTAATCTGACGTTTCACATGC 426
Qy 427 TGGTGGCTGAGCGGCATCTAGTATGTTGAAATTCAGTGTCAAAAGTACGAGAGGCTTC 486
Dh 427 TGGTGGCTGAGCGGCATCTAGTATGTTGAAATTCAGTGTCAAAAGTACGAGAGGCTTC 486
Qy 487 TCTGACCCCAAGGGGTGACATGTGAGACAGTGCACATTCAGAGAGAGGCTCAGAGTG 546
Dh 487 TCTGACCCCAAGGGGTGACATGTGAGACAGTGCACATTCAGAGAGAGGCTCAGAGTG 546
Qy 547 GACACACAGGATTAATGAAGTACACAGTGTGAGGCAAGGAGGCTGCCCCCTCT 606
Dh 547 GACACACAGGATTAATGAAGTACACAGTGTGAGGCAAGGAGGCTGCCCCCTCT 606
Qy 607 GCGGAGAGAGGCTTACCCTATGAGTGTGTGATCTTATTCACAAAGCTCAAGTATGAA 666
Dh 607 GCGGAGAGAGGCTTACCCTATGAGTGTGTGATCTTATTCACAAAGCTCAAGTATGAA 666
Qy 667 AACTACACAGCAGCTTCTTCATCAGAGACATCATCAAACCCAGACCACCAACCTG 726
Dh 667 AACTACACAGCAGCTTCTTCATCAGAGACATCATCAAACCCAGACCACCAACCTG 726
Qy 727 CAGCTGAAGCCATTGAAAAATTTCTGCGACGTGAGGTGACGTGGAAATACCCGACACC 786
Dh 727 CAGCTGAAGCCATTGAAAAATTTCTGCGACGTGAGGTGACGTGGAAATACCCGACACC 786
Qy 787 TGGAGCAGCCGACATCTCTACTTCTGCTGACATTTTGCAATACAGGCCAGGGAAGAAC 846
Dh 787 TGGAGCAGCCGACATCTCTACTTCTGCTGACATTTTGCAATACAGGCCAGGGAAGAAC 846
Qy 847 AATAGAGAAAAAGAAAGATAGACTCTGCGTGACAAAGCCTGAGCAAGGTCGTGGCAC 906
Dh 847 AATAGAGAAAAAGAAAGATAGACTCTGCGTGSAACAAGCCTGAGCAAGGTCGTGGCAC 906
Qy 907 AAGGATGCCAAGATCCCGCTGCAAGCCCGAGACCGCTACTACTATCTCTGAGCGAC 966
Dh 907 AAGGATGCCAAGATCCCGCTGCAAGCCCGAGACCGCTACTACTATCTCTGAGCGAC 966
Qy 967 TGGGCACTGTGTC 980
Dh 967 TGGGCACTGTGTC 980
Db 967 TGGGCACTGTGTC 980
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RESULT 3
ID AAX03162 standard: cDNA to mRNA: 990 BP.
XX AAX03162:
XX AAX03162:
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```
DT 30-MAR-1999 (first entry)
XX Nucleic acid encoding canine Interleukin 12.
DE
XX Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
XX skin disease; viral infection; allergic disease; breast tumour;
XX oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
XX otomatoma; pneumonodema; skin soft pedicled soft tumour; anal tumour;
XX oitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
XX allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
XX dog Parvovirus infection; distemper virus; cat plaque virus infection;
XX feline leukaemia; allergy; pollinosis; ds.
OS
XX Canis sp.
XX
XX Key Location/Qualifiers
XX CDS 1..990
XX FT /tag= a
XX FT /product= interleukin_12
XX
XX W09851327-A1.
XX
XX 19-NOV-1998.
XX
XX 07-MAY-1998; 98WO-JP02031.
XX
XX 16-MAY-1997; 97JP-0127690.
XX
XX (TORA ) TORAY IND INC.
XX
XX Okano F, Satoh M, Yamada K;
XX WPI: 1999-070100/06.
XX DR P-PSDB: AAM84373.
XX
XX New therapeutic and prophylactic agents - comprise
XX PT genetically-engineered canine interleukin 12, used to treat, e.g.
XX canine and feline immunological diseases
XX
XX Claim 1: Page 30-32; 45pp; Japanese.
XX
XX The present sequence encodes a canine interleukin 12 (IL-12) protein.
XX CC The IL-12 protein can be used in therapeutic or prophylactic agents.
XX CC The agents can be used to prevent and treat canine and feline
XX CC immunological diseases, including dog and cat tumours, skin diseases,
XX CC viral infections and allergic diseases, especially tumours, breast
XX CC tumour, oesinophilic granuloma, epidermoid tumour, skin tumour, lipoma,
XX CC otomatoma, pneumonodema, skin soft pedicled soft tumour and anal
XX CC tumour; skin diseases, oitis externa, dermatitis, eczema, fungal
XX CC diseases of the skin, pyoderma, allergic dermatitis, nettle rash,
XX CC traumatic dermatitis and hair loss; infections; dog parvovirus infection
XX CC and distemper virus; cat plaque virus infection and feline leukaemia, and
XX CC allergic diseases, e.g. pollinosis.
XX
XX Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 other;
XX
XX Query March 98.7%; Score 974; DB 20; Length 990;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 974; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 7 CCTGAGAGTGGTGCATCTCTGTTTCCCTGTTTGGTGGGCTCCCTCATGAGCC 66
Qy 7 CCTGAGAGTGGTGCATCTCTGTTTCCCTGTTTGGTGGGCTCCCTCATGAGCC 66
Dh 7 CCTGAGAGTGGTGCATCTCTGTTTCCCTGTTTGGTGGGCTCCCTCATGAGCC 66
Qy 67 ATATGGAACTGGAGAAAGATGTTATGTTAGAGTTGGACCTGGACCCGATGCCCC 126
Dh 67 ATATGGAACTGGAGAAAGATGTTATGTTAGAGTTGGACCTGGACCCGATGCCCC 126
Qy 127 GGAGAAATGGTGTCTCTACCTGGCCATACCCCTGAGAGAGATGACATCTACTTGGACCTCA 186
Dh 127 GGAGAAATGGTGTCTCTACCTGGCCATACCCCTGAGAGAGATGACATCTACTTGGACCTCA 186
Qy 187 GCGCAGACGACGTGAAGTCTTAGTTCGTGTGTAATAACTGACCAATCCAAAGTCAAGAAATTT 246
Dh 187 GCGCAGACGACGTGAAGTCTTAGTTCGTGTGTAATAACTGACCAATCCAAAGTCAAGAAATTT 246
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Db      ||| 187 GCGAGAGCAGTGAAGTCTAGTTCGTGTAAGAACTGTGACATCCAAAGTCAAGAAATTT 246
Oy      ||| 247 GGAGATGCTGGCCGATTAACCTGCAATAAAGGAGGCAAGGTTTCAGCCGCTCCTCTG 306
Db      ||| 247 GGAGATGCTGGCCGATTAACCTGCAATAAAGGAGGCAAGGTTTCAGCCGCTCCTCTG 306
Oy      ||| 307 TTGATTCACAAAAAAGAAAGATGAAATTTGGTCCATGATATCTTAAAGAAACAGAAAGAA 366
Db      ||| 307 TTGATTCACAAAAAAGAAAGATGAAATTTGGTCCATGATATCTTAAAGAAACAGAAAGAA 366
Oy      ||| 367 TCCAAAAATTAAGATCTTTCTGAATGTGAGGCAAAAGATTATTTGAGACGTTTCAATGC 426
Db      ||| 367 TCCAAAAATTAAGATCTTTCTGAATGTGAGGCAAAAGATTATTTGAGACGTTTCAATGC 426
Oy      ||| 427 TGGTGGCTGAGCGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGAGAGAGGCTTC 486
Db      ||| 427 TGGTGGCTGAGCGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGAGAGAGGCTTC 486
Oy      ||| 487 TCTGACCCCAAGGGGTGACATGTGAGCAGTGCACCTTTCAGCAGAGAGAGGTCAGAGTG 546
Db      ||| 487 TCTGACCCCAAGGGGTGACATGTGAGCAGTGCACCTTTCAGCAGAGAGAGGTCAGAGTG 546
Oy      ||| 547 GACAAACAGGATTTAAGAAATAGACAGTGTGAGGAGGAGGAGGAGGCTGCTGCTCT 606
Db      ||| 547 GACAAACAGGATTTAAGAAATAGACAGTGTGAGGAGGAGGAGGAGGCTGCTGCTCT 606
Oy      ||| 607 GCCGAGAGAGCTTAACCATGAGGTGTGTGATGCTATTCACAAAGCTCAATATGAA 666
Db      ||| 607 GCCGAGAGAGCTTAACCATGAGGTGTGTGATGCTATTCACAAAGCTCAATATGAA 666
Oy      ||| 667 AACTACACACGACCTTCTTCATCAGACATCATCAAAACAGCCACCCCAAAACCTG 726
Db      ||| 667 AACTACACACGACCTTCTTCATCAGACATCATCAAAACAGCCACCCCAAAACCTG 726
Oy      ||| 727 CAGTGAAGCCATTGAATAATTCGCGACGCTGAGAGTGCAGCTGGGAATACCCGACACC 786
Db      ||| 727 CAGTGAAGCCATTGAATAATTCGCGACGCTGAGAGTGCAGCTGGGAATACCCGACACC 786
Oy      ||| 787 TGGAGACCCCACTTCTACTCTCTGATCTGATTTGATACAGGCGCCAGGCAAAAC 846
Db      ||| 787 TGGAGACCCCACTTCTACTCTCTGATCTGATTTGATACAGGCGCCAGGCAAAAC 846
Oy      ||| 847 AATAGAGAAAAGAAAGATAGACTGTGCTGAGCAAGACCTCAGCCAAAGTGTGCTCAC 906
Db      ||| 847 AATAGAGAAAAGAAAGATAGACTGTGCTGAGCAAGACCTCAGCCAAAGTGTGCTCAC 906
Oy      ||| 907 AAGGATGCCAAGATCCGCTGCAAGCCGAGACCCGCTACTATTTATCTCTGAGAGAC 966
Db      ||| 907 AAGGATGCCAAGATCCGCTGCAAGCCGAGACCCGCTACTATTTATCTCTGAGAGAC 966
Oy      ||| 967 TGGGATCTGTGTC 980
Db      ||| 967 TGGGATCTGTGTC 980

RESULT 4
AA164388 standard; DNA; 990 BP.
XX
XX AA164388;
XX
XX 23-NOV-2001 (first entry)
XX
XX Canine coding sequence #3.
XX
XX Canine: dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
XX
XX Canis familiaris.
XX
XX Key 1. 990 Location/Qualifiers
XX CDS /*tag= a
FT

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FT      /product= "Canine protein #1"
FT      sig_peptide 1..66
FT      /*tag= b
FT      mat_peptide 67..987
FT      /*tag= c
XX
XX JP2001161378-A.
XX
XX 19-JUN-2001.
XX
XX 26-SEP-2000; 2000JP-0292946.
XX
XX 01-OCT-1999; 99JP-0281234.
XX
XX (TORA ) TORAY IND INC.
XX
XX WPT: 2001-592466/67.
XX
XX P-PSDB: AAG66482.
XX
XX Preparation of a highly pure protein, interleukin 12, a protein
XX inhibiting the activity of interleukin 12, and a treating agent and a
XX treating method for immunopathy of mammalian
XX
XX Claim 6; Page 16-17; 21pp; Japanese.
XX
XX The present invention relates to a method for the preparation of a highly
XX pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
XX the activity of IL12 is contacted to an ion exchanging carrier and/or a
XX pigment carrier to get IL12 and/or a protein inhibiting the activity of
XX IL12. The protein is used as a preventive agent for dog immunopathy. The
XX present sequence was used in the method of the present invention.
XX
XX Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 other;
XX
XX Query Match 98.7%; Score 974; DB 22; Length 990;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 974; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy      7 CCTCAGCAGTTGGTCATCTCCTGTTTCCCTGTTTGGTGGCGTCTCCCTCATAGGCC 66
Db      7 CCTCAGCAGTTGGTCATCTCCTGTTTCCCTGTTTGGTGGCGTCTCCCTCATAGGCC 66
Oy      67 ATATGGGAAGTGGAGAAAGATGTTTATGTTGAGAGTTGACATGCGACCTGATGCCCC 126
Db      67 ATATGGGAAGTGGAGAAAGATGTTTATGTTGAGAGTTGACATGCGACCTGATGCCCC 126
Oy      127 GGAAGAAATGGTGCCCTCACCTGCAATACCCCTGAAGAAAGATGATCATCTGAGACCTCA 186
Db      127 GGAAGAAATGGTGCCCTCACCTGCAATACCCCTGAAGAAAGATGATCATCTGAGACCTCA 186
Oy      187 GCGCAGAGCAGTGAAGTCTAGGTTCTGTTAAACTCTGACATCCAAAGTCAAAAGATTT 246
Db      187 GCGCAGAGCAGTGAAGTCTAGGTTCTGTTAAACTCTGACATCCAAAGTCAAAAGATTT 246
Oy      247 GGAGATGCTGGCCAGTATTAACCTGCCATAAAGGAGCGAAGTTTGTAGCCGCTCACTCTG 306
Db      247 GGAGATGCTGGCCAGTATTAACCTGCCATAAAGGAGCGAAGTTTGTAGCCGCTCACTCTG 306
Oy      247 GGAGATGCTGGCCAGTATTAACCTGCCATAAAGGAGCGAAGTTTGTAGCCGCTCACTCTG 306
Db      247 GGAGATGCTGGCCAGTATTAACCTGCCATAAAGGAGCGAAGTTTGTAGCCGCTCACTCTG 306
Oy      307 TTGATTCACAAAAAAGAAAGATGAAATTTGGTCCATGATATCTTAAAGAAACAGAAAGAA 366
Db      307 TTGATTCACAAAAAAGAAAGATGAAATTTGGTCCATGATATCTTAAAGAAACAGAAAGAA 366
Oy      367 TCCAAAAATTAAGATCTTTCTGAATGTGAGGCAAAAGATTATTTGAGACGTTTCAATGC 426
Db      367 TCCAAAAATTAAGATCTTTCTGAATGTGAGGCAAAAGATTATTTGAGACGTTTCAATGC 426
Oy      427 TGGTGGCTGAGCGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGAGAGAGGCTTC 486
Db      427 TGGTGGCTGAGCGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGAGAGAGGCTTC 486
Oy      487 TCTGACCCCAAGGGGTGACATGTGAGCAGTGCACCTTTCAGCAGAGAGAGGTCAGAGTG 546
Db      487 TCTGACCCCAAGGGGTGACATGTGAGCAGTGCACCTTTCAGCAGAGAGAGGTCAGAGTG 546

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OY 547 GACACAGGATTATACAGTACAGAGTGCAGGAGGAGTGGCTGCTCT 506
DB 547 GACACAGGATTATACAGTACAGAGTGCAGGAGGAGTGGCTGCTCT 506
OY 607 GCCGAGAGAGCCATCCGAGTGTGTGATGCTATTCAGCAAGCTCACTATGAA 566
DB 607 GCCGAGAGAGCCATCCGAGTGTGTGATGCTATTCAGCAAGCTCACTATGAA 566
OY 667 AACTACACGAGCAGCTTCTTCATCAGAGACATCATCAACCAAGCCCAAACTCG 726
DB 667 AACTACACGAGCAGCTTCTTCATCAGAGACATCATCAACCAAGCCCAAACTCG 726
OY 727 CAGCTGAGAGCCATCAAAAATCTCGGACGCTGAGAGTACCTGGAAATACCCGACAC 786
DB 727 CAGCTGAGAGCCATCAAAAATCTCGGACGCTGAGAGTACCTGGAAATACCCGACAC 786
OY 787 TCGAGCACCACCATCTTCTTCTCCCTGACATTTTGCATACAGGCCCGGCAAGAAC 846
DB 787 TCGAGCACCACCATCTTCTTCTCCCTGACATTTTGCATACAGGCCCGGCAAGAAC 846
OY 847 AATAGAGAAAGAAAGATAGACTCTGCGTGGACAAAGACCTCAGCCAAAGTGTGCTCAC 906
DB 847 AATAGAGAAAGAAAGATAGACTCTGCGTGGACAAAGACCTCAGCCAAAGTGTGCTCAC 906
OY 907 AAGCATGCCAAGATCGCGCTGCAGAGCCGCTACTATAGTTTCATCCTGGAGCGAC 966
DB 907 AAGCATGCCAAGATCGCGCTGCAGAGCCGCTACTATAGTTTCATCCTGGAGCGAC 966
OY 967 TCGGCATCTGTGTC 980
DB 967 TCGGCATCTGTGTC 980
```

RESULT 5
AAV13816

ID AAV13816 standard; cDNA to mRNA; 990 BP.

AC AAV13816;

DT 14-MAY-1998 (first entry)

XX Canine IL-12 P40 subunit cDNA.

KM Canine; interleukin-12 P40 subunit; IL-12 P40 subunit; antitumour;

KW antiviral; vaccine adjuvant; ds.

XX Canis sp.

OS Canis sp.

FH Key Location/Qualifiers

FT CDS 1..990 /*tag= a

FT /product= interleukin-12_P40_subunit

PN JP10036397-A.

PD 10-FEB-1998.

PE 08-NOV-1996; 96JP-0296789.

PR 23-MAY-1996; 96JP-0128104.

XX 08-NOV-1995; 95JP-0289729.

PA (TORAY) TORAY IND INC.

DR WPI; 1998-174914/16.

DR P-PSDB; AAM41790.

PT Canine interleukin 12 - comprises P40 and P35 subunits; useful in

PS Claim 8; Page 8; 12pp; Japanese.

XX The present sequence encodes a canine interleukin-12 (IL-12) P40 subunit. A canine IL-12 comprising a P40 and P35 subunit is capable of inducing an antiviral activating factor and the expression of CC class II MHC molecules in canine tumour cells, stimulating CC proliferation of canine blastogenic lymphocytes and activating CC canine leukocytes to inhibit canine tumour cells. The canine IL-12 can be used in veterinary medicines, e.g. antitumour, antiviral and vaccine adjuvant activities are expected.

SQ Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 other;

Query Match 91.2%; Score 900; DB 19; Length 990;

Best Local Similarity 99.9%; Pred No. 0;

Matches 950; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
OY 28 TGGTTTCCCTGTTTGGCTGGCGTCCCTCATATGGCCATATGGGAATGAGAAAGAT 87
DB 28 TGGTTTCCCTGTTTGGCTGGCGTCCCTCATATGGCCATATGGGAATGAGAAAGAT 87
OY 88 GTTTATGTTGTAGACTTGCACCTGATGCCCGGAGAAATGTTGCTCTCAC 147
DB 88 GTTTATGTTGTAGACTTGCACCTGATGCCCGGAGAAATGTTGCTCTCAC 147
OY 148 TGGCATACCCCTGGAAGAAGATGACATCACTTGGACCTCAGCGCAGAGTGAAGTCCTA 207
DB 148 TGGCATACCCCTGGAAGAAGATGACATCACTTGGACCTCAGCGCAGAGTGAAGTCCTA 207
OY 208 GGTTCGTGTAACACTCTGACCATCCAGTCAAAGAAATTTGAGATGCTGGCAGTATACC 267
DB 208 GGTTCGTGTAACACTCTGACCATCCAGTCAAAGAAATTTGAGATGCTGGCAGTATACC 267
OY 268 TGGCATAAAGAGGAGGAGTGTGAGCCGCTACCTCGTTGATTTACAAAAAAGAGAT 327
DB 268 TGGCATAAAGAGGAGGAGTGTGAGCCGCTACCTCGTTGATTTACAAAAAAGAGAT 327
OY 328 GGAATTTGGTCCACATGATCTTTAAAGAACAGAAAGAAATCCAAAAATAGATCTTCTG 387
DB 328 GGAATTTGGTCCACATGATCTTTAAAGAACAGAAAGAAATCCAAAAATAGATCTTCTG 387
OY 388 AAATGTGAGGCAAAAGATTTATCTGAGCTTTCACATGCTGTGCTGAGGCAATCACT 447
DB 388 AAATGTGAGGCAAAAGATTTATCTGAGCTTTCACATGCTGTGCTGAGGCAATCACT 447
OY 448 ACTGATTTGAAATTCAGTGTCAAAAGTACAGAGGCTCTCTGACCCCAAGGGGTGACA 507
DB 448 ACTGATTTGAAATTCAGTGTCAAAAGTACAGAGGCTCTCTGACCCCAAGGGGTGACA 507
OY 508 TGTGAGCAGTGACACTTTCACGACAGAGGTCAGAGTGACAGCAGGATTAAGAAG 567
DB 508 TGTGAGCAGTGACACTTTCACGACAGAGGTCAGAGTGACAGCAGGATTAAGAAG 567
OY 568 TACACAGTGAGAGTGTGACAGAGGAGTGCCTCTGCCGAGAGAGCTTACCATC 627
DB 568 TACACAGTGAGAGTGTGACAGAGGAGTGCCTCTGCCGAGAGAGCTTACCATC 627
OY 628 GAGGTGAGTGTGATGATTCATTCAGAGGTCAGAGTGTGAGAAATACACACGAGTCTTC 687
DB 628 GAGGTGAGTGTGATGATTCATTCAGAGGTCAGAGTGTGAGAAATACACACGAGTCTTC 687
OY 688 ATCAGAGACATCATCAAAACACAGCCACCAAAACCTGACCTGAAGCATTTGGAANAAT 747
DB 688 ATCAGAGACATCATCAAAACACAGCCACCAAAACCTGACCTGAAGCATTTGGAANAAT 747
OY 748 TCTCGGCACTGAGAGTGTGAGGATTAACCCGACACCTGAGAGCACCACATTCCTAC 807
DB 748 TCTCGGCACTGAGAGTGTGAGGATTAACCCGACACCTGAGAGCACCACATTCCTAC 807
OY 808 TTCTCCCTGACATTTTTCATACAGGCCCAAGGCAAGAAATATGAGAAAGAAATATGA 867
DB 808 TTCTCCCTGACATTTTTCATACAGGCCCAAGGCAAGAAATATGAGAAAGAAATATGA 867
OY 868 CTCTGCTGTGACAAAGACCTCAGCCCAAGGTCGTGCTCCCAAGGATGCCAAGTCGCGTG 927
```

```
Db      |||
868 CTCTGCGGACAGACCTCAGCCAGGTGCTGTGCCACAGAGATGCCAAGATCCGCGTG 927
QY      928 CAAGCCGAGACCCCTACTATAGTTTCATCTGAGAGCACTGGCATCTGTG 978
      |||
Db      928 CAAGCCGAGACCCCTACTATAGTTTCATCTGAGAGCACTGGCATCTGTG 978

RESULT 6
AAK35615
ID      AAK35615 standard; cDNA to mRNA; 990 BP.
XX
AC      AAK35615;
XX
DT      09-JUL-1999 (first entry)
XX
DE      Nucleic acid encoding canine Interleukin-12 (IL-12).
XX
KW      Interleukin-12; IL-12; dog; cat; immune disease; Call12; heterodimer;
KW      tumour; skin disease; infectious disease; allergic disease; ds.
XX
OS      Canis sp.
XX
FH      Key location/Qualifiers
FT      CDS 1..990
          /*tag= a
XX
PN      JP1106350-A.
PD      20-APR-1999.
XX
PF      15-MAY-1998; 98JP-0133345.
XX
PR      07-AUG-1997; 97JP-0213755.
PR      16-MAY-1997; 97JP-0127690.
XX
PA      (TORA ) TORAY IND INC.
XX
DR      WPI; 1999-308068/26.
DR      P-PSDB; AAY02339.
XX
PT      A prevention and treating agent containing interleukin 12 (Call12) -
PT      for prevention and treatment of dog and cat immune diseases
XX
PS      Claim 1; Page 12; 16pp; Japanese.
XX
CC      The present sequence encodes canine interleukin-12 (IL-12). The
CC      specification describes a method for the prevention and treatment
CC      of dog and cat immune diseases. The treatment used an agent comprising
CC      dog IL-12 (Call12) proteins to form a heterodimer. The agent is
CC      useful for preventing and treating dog and cat immune diseases,
CC      including tumours, skin diseases, infectious diseases and allergic
CC      diseases.
XX
SQ      Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 other;

Query Match 91.28; Score 900; DB 20; Length 990;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 950; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Db      |||
208 GGTTCGTGTAACACTGTGACCATTCACAGTCAAGAAATTGGAAATGCTGGCCAGTATACC 267
QY      268 TGCCATTAAGAGAGAGCAAGGTTCTGAGCCGCTCACTCTCTGTTGATTCACAAAAAAGAGAT 327
      |||
Db      268 TGCCATTAAGAGAGCAAGGTTCTGAGCCGCTCACTCTCTGTTGATTCACAAAAAAGAGAT 327
QY      328 GGAATTTGGTCCACTGATATCTTAAAGAACAGAAAGAAATCAAAAAATAGATCTTTCTG 387
      |||
Db      328 GGAATTTGGTCCACTGATATCTTAAAGAACAGAAAGAAATCAAAAAATAGATCTTTCTG 387
QY      388 AAATGTAGGCAAAAGAAATTTCTGTGACGTTTCACATGCTGTGCGCTGAGAGCAATCAGT 447
      |||
Db      388 AAATGTAGGCAAAAGAAATTTCTGTGACGTTTCACATGCTGTGCGCTGAGAGCAATCAGT 447
QY      448 ACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTCTCTGACCCCAAGGGGTGACA 507
      |||
Db      448 ACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTCTCTGACCCCAAGGGGTGACA 507
QY      508 TGTGAGACAGTACACTTTTCAGCAGAGAGGGTCAAGAGTGCACAACAGGGATTATTAAGAA 567
      |||
Db      508 TGTGAGACAGTACACTTTTCAGCAGAGAGGGTCAAGAGTGCACAACAGGGATTATTAAGAA 567
QY      568 TACACAGTGAAGTGTGAGAGGAGGAGGCTGCGCCCTGCGCAGAGAGACCTTACCCATC 627
      |||
Db      568 TACACAGTGAAGTGTGAGAGGAGGAGGCTGCGCCCTGCGCAGAGAGACCTTACCCATC 627
QY      628 GAGTGTGATGATGCTATTCACAAAGCTCAAGTATGAAATACACACAGACCTTCTTC 687
      |||
Db      628 GAGTGTGATGATGCTATTCACAAAGCTCAAGTATGAAATACACACAGACCTTCTTC 687
QY      688 ATCAGAGACATCATCAACACAGACCCACACAACTGCAGCTGAAGCCATTGAAAAT 747
      |||
Db      688 ATCAGAGACATCATCAACACAGACCCACACAACTGCAGCTGAAGCCATTGAAAAT 747
QY      748 TCTGCGAGGTGAGAGGTCAAGTACCAGCAGCTGAGAGCCACCACTTCCTAC 807
      |||
Db      748 TCTGCGAGGTGAGAGGTCAAGTACCAGCAGCTGAGAGCCACCACTTCCTAC 807
QY      808 TTCTCCCTGACATTTTGCATACAGAGCCAGGCAAGAACATAGAGAAAAAGAAATAGA 867
      |||
Db      808 TTCTCCCTGACATTTTGCATACAGAGCCAGGCAAGAACATAGAGAAAAAGAAATAGA 867
QY      868 CTCTGCGTGACAAAGACCTTACAGCAAGTGTGTGCCACAGAGATGCCAAGATCCGCTG 927
      |||
Db      868 CTCTGCGTGACAAAGACCTTACAGCAAGTGTGTGCCACAGAGATGCCAAGATCCGCTG 927
QY      928 CAAGCCGAGACCGCTACTATAGTTCATCTCTGAGAGGACTGGGCATCTGTG 978
      |||
Db      928 CAAGCCGAGACCGCTACTATAGTTCATCTCTGAGAGGACTGGGCATCTGTG 978

RESULT 7
AAK03152
ID      AAK03152 standard; cDNA to mRNA; 990 BP.
XX
AC      AAK03152;
XX
DT      30-MAR-1999 (first entry)
XX
DE      Nucleic acid encoding canine interleukin 12.
XX
KW      Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW      skin disease; viral infection; allergic disease; breast tumour;
KW      oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW      othematoma; pneumoedema; skin soft pedicled soft tumour; anal tumour;
KW      otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW      allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW      dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW      feline leukaemia; allergy; pollinosis; ds.
XX
OS      Canis sp.
```

Key Location/Qualifiers
CDS 1..990
/*tag= a
/product= interleukin_12

MO9851327-A1.
19-NOV-1998.
07-MAY-1998; 98WO-JP02031.
16-MAY-1997; 97JP-0127690.
(TORA) TORAY IND INC.
Okano F, Satoh M, Yamada K:
WPI: 1999-070100/06.
P-PSDB: AAM84371.

New therapeutic and prophylactic agents - comprise genetically-engineered canine interleukin 12, used to treat, e.g. canine and feline immunological diseases

Claim 1: Page 23-25; 45pp; Japanese.

The present sequence encodes a canine interleukin 12 (IL-12) protein. The IL-12 protein can be used in therapeutic or prophylactic agents. The agents can be used to prevent and treat canine and feline immunological diseases including dog and cat tumours, skin diseases, viral infections and allergic diseases, especially tumours, breast tumour, eosinophilic granuloma, epidermoid tumour, skin tumour, lipoma, otomastoma, pneumoedema, skin soft pedicled soft tumour and anal tumour; skin diseases, otitis externa, dermatitis, eczema, fungal diseases of the skin, pyoderma, allergic dermatitis, nettle rash, traumatic dermatitis and hair loss; infections; dog parvovirus infection and distemper virus; cat plaque virus infection and feline leukaemia, and allergic diseases, e.g. pollinosis.

Sequence 990 BP: 278 A; 243 C; 251 G; 218 T; 0 other:

Query Match 91.2%; Score 900; DB 20; Length 990;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 950; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

28 TCGTTTCCCTGCTTTCCTGGCGTCCCTCATGGCCATATGGAGCACTGGAGAAAGAT 87
|||
28 TGGTTTCCCTGCTTTCCTGGCGTCCCTCATGGCCATATGGAGCACTGGAGAAAGAT 87

88 GTTATCTGTAGAGTTGAGATGACATGACCTGATGCCCGGAGAAATGGTGCCTCACC 147
|||
88 GTTATCTGTAGAGTTGAGATGACATGACCTGATGCCCGGAGAAATGGTGCCTCACC 147

148 TGCCATACCCCTGAAGAAGATGACATCATTGGACCTTCAGCGCAGAGCAATGAAGTCTTA 207
|||
148 TGCCATACCCCTGAAGAAGATGACATCATTGGACCTTCAGCGCAGAGCAATGAAGTCTTA 207

148 TGCCATACCCCTGAAGAAGATGACATCATTGGACCTTCAGCGCAGAGCAATGAAGTCTTA 207
|||
148 TGCCATACCCCTGAAGAAGATGACATCATTGGACCTTCAGCGCAGAGCAATGAAGTCTTA 207

208 GGTTCGTGTAACCTGACCATGCAAGTCAAGATTTGAGATTCGTGGCCAGATATACC 267
|||
208 GGTTCGTGTAACCTGACCATGCAAGTCAAGATTTGAGATTCGTGGCCAGATATACC 267

208 GGTTCGTGTAACCTGACCATGCAAGTCAAGATTTGAGATTCGTGGCCAGATATACC 267
|||
208 GGTTCGTGTAACCTGACCATGCAAGTCAAGATTTGAGATTCGTGGCCAGATATACC 267

268 TGCCATTAAGAGAGCAAGTTCAGCGCTCACTCCGTGATTGATTCACAAAAAAGAGAT 327
|||
268 TGCCATTAAGAGAGCAAGTTCAGCGCTCACTCCGTGATTGATTCACAAAAAAGAGAT 327

328 GGAATTTGGTCACTGATCTTAAGAGACAGAAAGATCCAAAAATAGATCTTCTCG 387
|||
328 GGAATTTGGTCACTGATCTTAAGAGACAGAAAGATCCAAAAATAGATCTTCTCG 387

328 GGAATTTGGTCACTGATCTTAAGAGACAGAAAGATCCAAAAATAGATCTTCTCG 387
|||
328 GGAATTTGGTCACTGATCTTAAGAGACAGAAAGATCCAAAAATAGATCTTCTCG 387

388 AAATGTGAGCGCAAGATTAATTCGACGTTTCACATCTGCTGACCGCAATCGT 447
|||
388 AAATGTGAGCGCAAGATTAATTCGACGTTTCACATCTGCTGACCGCAATCGT 447

QY 448 ACTGATTTGAATTCAGTGTCAAAAGTAGACAGAGCTTCTGTGACCCCAAGGGGTGACA 507
|||
Db 448 ACTGATTTGAATTCAGTGTCAAAAGTAGACAGAGCTTCTGTGACCCCAAGGGGTGACA 507

QY 508 TGTGGAGCAGTGCACCTTTCAGACAGAGAGGCTCAGAGTGCACAAACAGGATTTATTAAGAG 567
|||
Db 508 TGTGGAGCAGTGCACCTTTCAGACAGAGAGGCTCAGAGTGCACAAACAGGATTTATTAAGAG 567

QY 568 TACACAGTGCAGTGCAGAGAGGCAAGTCCCTGCTGCTGCGGAGAGAGAGCTTACCCATTC 627
|||
Db 568 TACACAGTGCAGTGCAGAGAGGCAAGTCCCTGCTGCTGCGGAGAGAGAGCTTACCCATTC 627

QY 628 GAGTCTGCTGATGATTCATTCACAGTCAAGTATGAAGAACTACACAGCAGCTTCTTC 687
|||
Db 628 GAGTCTGCTGATGATTCATTCACAGTCAAGTATGAAGAACTACACAGCAGCTTCTTC 687

QY 688 ATCAGAGACATCATCAAAACAGAGCCACCCACAAACCTGCAGCTGAAGCCATTGAAAAAT 747
|||
Db 688 ATCAGAGACATCATCAAAACAGAGCCACCCACAAACCTGCAGCTGAAGCCATTGAAAAAT 747

QY 748 TCTGCGCAGCTGAGAGTACGCTGGAAATACCCCGACACCTGAGCAGCCCATTTCTTAC 807
|||
Db 748 TCTGCGCAGCTGAGAGTACGCTGGAAATACCCCGACACCTGAGCAGCCCATTTCTTAC 807

QY 808 TTCTCCCTGACATTTTGCATACAGGCCCGCAAGCAACATAGAGAAAGAGATAGA 867
|||
Db 808 TTCTCCCTGACATTTTGCATACAGGCCCGCAAGCAACATAGAGAAAGAGATAGA 867

QY 868 CTCTGCGTGGACAAAGACCTCAGCCAAAGTCTGTGCCCAAGAGATGCCAAGATCCGCGTG 927
|||
Db 868 CTCTGCGTGGACAAAGACCTCAGCCAAAGTCTGTGCCCAAGAGATGCCAAGATCCGCGTG 927

QY 928 CAAGCCGAGACCGCTACTATAGTTCACTCTGGAGCGAGCTGGCATCTGTG 978
|||
Db 928 CAAGCCGAGACCGCTACTATAGTTCACTCTGGAGCGAGCTGGCATCTGTG 978

RESULT 8
AA164378
ID AA164378 standard; DNA: 990 BP.

XX AA164378;
AC XX
AC XX
DT 23-NOV-2001 (first entry)
XX XX
DE Canine coding sequence #1.
XX Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
XX OS Canis familiaris.

Key Location/Qualifiers
CDS 1..990
/*tag= a
/product= "Canine protein #1"
sig_peptide 1..66
FT /*tag= b
FT mat_peptide 67..987
FT /*tag= c

JP2001161378-A.
19-JUN-2001.
26-SEP-2000; 2000JP-0292946.
01-OCT-1999; 99JP-0281234.
(TORA) TORAY IND INC.
WPI: 2001-592466/67.
P-PSDB: AAG66480.

PT Preparation of a highly pure protein, interleukin 12, a protein
 PT inhibiting the activity of interleukin 12, and a treating agent and a
 PT treating method for immunopathy of mammalian

PS Claim 6; Page 14; 21pp: Japanese.

XX The present invention relates to a method for the preparation of a highly
 CC pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
 CC the activity of IL12 is contacted to an ion exchanging carrier and/or a
 CC pigment carrier to get IL12 and/or a protein inhibiting the activity of
 CC IL12. The protein is used as a preventive agent for dog immunopathy. The
 CC present sequence was used in the method of the present invention.

XX Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 other;

Query Match 91.2%; Score 900; DB 22; Length 990;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 950; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

OY 28 TGGTTTTCCCTGTTTGGCTGGCGTCTCCCTCATGGCCATATGGAACTGGAGAAAGAT 87
DB 28 TGGTTTTCCCTGTTTGGCTGGCGTCTCCCTCATGGCCATATGGAACTGGAGAAAGAT 87
OY 88 GTTATGTTTACAGTTGAGCTGGCACTCCCTGATGCCCGGAGAAAATGGTCTCTACC 147
DB 88 GTTATGTTTACAGTTGAGCTGGCACTCCCTGATGCCCGGAGAAAATGGTCTCTACC 147
OY 148 TGGCATACCCCTAAGAAAGATGACATCTTGGACCTCAGCGAGACATGAAATCTTA 207
DB 148 TGGCATACCCCTAAGAAAGATGACATCTTGGACCTCAGCGAGACATGAAATCTTA 207
OY 208 GGTTCGTGTAACACTCTGACATCAAGTCAAGAAATTTGGAGTGTGCGCAGTATACC 267
DB 208 GGTTCGTGTAACACTCTGACATCAAGTCAAGAAATTTGGAGTGTGCGCAGTATACC 267
OY 268 TGCCATAAAGAGGAGCAAGTTTGTGAGCGGCTCACTCTGTTGATTCAGAAAAGAAAT 327
DB 268 TGCCATAAAGAGGAGCAAGTTTGTGAGCGGCTCACTCTGTTGATTCAGAAAAGAAAT 327
OY 328 GGAATTTGGTCACTGATATCTTAAAGAAAGAAAGAAATCAAAAATAAGATCTTCTG 387
DB 328 GGAATTTGGTCACTGATATCTTAAAGAAAGAAAGAAATCAAAAATAAGATCTTCTG 387
OY 388 AATGTGAGGCAAGAAATTTCTGAGACGTTTCACTGCTGTGCTGAGCGCAATCATAGT 447
DB 388 AATGTGAGGCAAGAAATTTCTGAGACGTTTCACTGCTGTGCTGAGCGCAATCATAGT 447
OY 448 ACTGATTTGAAATTCAGTGTCAAAAGTAGAGAGGCTTCTGTACCCCAAGGGGTGACA 507
DB 448 ACTGATTTGAAATTCAGTGTCAAAAGTAGAGAGGCTTCTGTACCCCAAGGGGTGACA 507
OY 508 TGTGAGAGTAGTACACTTTTACAGAGAGGGTGTAGAGTGTGACAGAGATTTAAGAG 567
DB 508 TGTGAGAGTAGTACACTTTTACAGAGAGGGTGTAGAGTGTGACAGAGATTTAAGAG 567
OY 568 TACACAGTGTGAGTGTGAGAGGGGAGTGTGCTGCTGCTGCTGAGAGAGACCTTACCATC 627
DB 568 TACACAGTGTGAGTGTGAGAGGGGAGTGTGCTGCTGCTGCTGAGAGAGACCTTACCATC 627
OY 628 GAGTGTGTGTGATCTATTCACAGGCTCAAGTATGAAAGTAACTACACACAGCTTCTTC 687
DB 628 GAGTGTGTGTGATCTATTCACAGGCTCAAGTATGAAAGTAACTACACACAGCTTCTTC 687
OY 688 ATGAGAGACATCATCAAAACAGAGACCAACCAAAACCTGACGCTGAAGCCATTGAAAT 747
DB 688 ATGAGAGACATCATCAAAACAGAGACCAACCAAAACCTGACGCTGAAGCCATTGAAAT 747
OY 748 TCTCGGAGGTGAGGTCAGCTGGAATACCCCGAGACCTGTGAGACACCCACATCTCTAC 807
DB 748 TCTCGGAGGTGAGGTCAGCTGGAATACCCCGAGACCTGTGAGACACCCACATCTCTAC 807
OY 808 TTCTCCCTGACATTTTGCATACAGGCCCAAGGCAAGAAATAGAGAAAAGAAATAGA 867
DB 808 TTCTCCCTGACATTTTGCATACAGGCCCAAGGCAAGAAATAGAGAAAAGAAATAGA 867

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DB 808 TTCTCCCTGACATTTTGCATACAGGCCCAAGGCAAGAAATAGAGAAAAGAAATAGA 867
OY 868 CTCTGCGTGAGACAAGACCTCAGCCAAAGTGTGTGTCACAAAGATGCCAAGATCCGCGTG 927
DB 868 CTCTGCGTGAGACAAGACCTCAGCCAAAGTGTGTGTCACAAAGATGCCAAGATCCGCGTG 927
OY 928 CAAGCCGAGACCGCTACTATTAATCTTCTGAGCGAGCTGGGCAATCTGTG 978
DB 928 CAAGCCGAGACCGCTACTATTAATCTTCTGAGCGAGCTGGGCAATCTGTG 978

RESULT 9
AAK18177
ID AAK18177 standard; cDNA; 924 BP.
XX
XX AAK18177;
AC
XX 07-MAY-1999 (first entry)
DT
XX
XX Canine mature CLAF p40 subunit coding sequence.
DE
XX CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
XX viral disease; canine distemper; canine parvovirus; autoimmune disease;
XX canine infectious hepatitis; ds.
XX
XX Canis sp.
OS
XX
XX WO9855511-A1.
XX
XX 10-DEC-1998.
PD
XX
XX 26-MAY-1998; 98WO-JP02295.
XX
XX 03-JUN-1997; 97JP-0161936.
XX
XX (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
XX Eda Y, Imanura T, Maeda H, Tokiyoshi S;
XX
XX WPI; 1999-070260/06.
XX
XX P-PDB; AAW74323.
XX
XX Canine cytokine protein which activates canine cytotoxic T
XX lymphocytes is useful for treatment of viral and autoimmune
XX diseases in dogs
XX
XX Claim 8; Page 32; 51pp: Japanese.
XX
XX This sequence encodes the canine lymphocyte activation factor (CLAF) of
XX the invention. CLAF activates lymphocytes, especially canine cytotoxic
XX T cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
XX recognising it may be used in the treatment of viral diseases in dogs
XX (such as canine distemper, canine parvovirus and canine infectious
XX hepatitis). The antibodies may also be used in isolation of CLAF from
XX culture of the transformant host cells by affinity chromatography. The
XX p40 homodimer can be used for the treatment of autoimmune diseases in
XX dogs.
XX
XX Sequence 924 BP; 273 A; 222 C; 234 G; 195 T; 0 other;
XX
XX Query Match 66.7%; Score 658; DB 20; Length 924;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 658; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 323 AAGATGGAATTTGTCACACTGATATCTTAAAGAGAGAAAGAAATCAAAATAGATCT 382
DB 260 AAGATGGAATTTGTCACACTGATATCTTAAAGAGAGAAAGAAATCAAAATAGATCT 319
OY 383 TTCTGAAATGTGAGCAAGCAATTAATTTCTGAGAGTTTCACTGCTGTGCTGACGCA 442
DB 320 TTCTGAAATGTGAGCAAGCAATTAATTTCTGAGAGTTTCACTGCTGTGCTGACGCA 379
OY 443 TCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGAGAGGCTTCTGTGACCCCAAGGG 502

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|||||
Db 380 TCAGTACTGATTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTCTGTGACCCCAAGGGG 439
QY 503 TGACATGTGGAGCCAGTCACTTTCAGACAGAGGGCTCAGANTGCAACAAGGATTATA 562
Db 440 TGACATGTGGAGCCAGTCACTTTCAGACAGAGGGCTCAGANTGCAACAAGGATTATA 499
QY 563 AGAAGTACACAGAGTGTGTGAGAGGAGGAGGAGTGTGCTGCTCCAGAGAGAGCCCTAC 622
Db 500 AGAAGTACACAGAGTGTGTGAGAGGAGGAGGAGTGTGCTGCTCCAGAGAGAGCCCTAC 559
QY 623 CCATGAGAGTGTGTGATGATCTATTCACAAAGCTCAAGTATGAAAACTACACAGCAGCT 682
Db 560 CCATGAGAGTGTGTGATGATGCTATTCACAAAGCTCAAGTATGAAAACTACACAGCAGCT 619
QY 683 TCTTCATCAGAGACATCATCAAAACCAGACCCACCAAAAGCTGAGAGCTGAAGCATTGA 742
Db 620 TCTTCATCAGAGACATCATCAAAACCAGACCCACCAAAAGCTGAGAGCTGAAGCATTGA 679
QY 743 AAAATTCTGGCAGCTGAGAGTCACTGGGAATACCCGACACCTGGAGCACCACATT 802
Db 680 AAAATTCTGGCAGCTGAGAGTCACTGGGAATACCCGACACCTGGAGCACCACATT 739
QY 803 CCTACTCTCCCTGACATTTTGCATACAGGCCAGGCAAGAACATAGAGAAAAAAG 862
Db 740 CCTACTCTCCCTGACATTTTGCATACAGGCCAGGCAAGAACATAGAGAAAAAAG 799
QY 863 ATACACTCTGGCTGACAAAGACCTGAGCAAGGCTGTGCCACAAAGATGCCAAGATCC 922
Db 800 ATACACTCTGGCTGACAAAGACCTGAGCAAGGCTGTGCCACAAAGATGCCAAGATCC 859
QY 923 GCGTGCAAGCCCGAGACCGCTACTATAGTTCATCTGAGGAGCTGGGCATCTGTGTC 980
Db 860 GCGTGCAAGCCCGAGACCGCTACTATAGTTCATCTGAGGAGCTGGGCATCTGTGTC 917
```

RESULT 10
AA18176
ID AA18176 standard; cDNA: 2154 BP.

```
AC AAX18176:
DT 07-MAY-1999 (first entry)
DE Canine full length CLAF p40 subunit coding sequence.
KM CLAF; canine lymphocyte activation factor; p35 subunit; dog;
KW viral disease; canine distemper; canine parvovirus; autoimmune disease;
OS canine infectious hepatitis; ds.
XX
XX Canis sp.
XX WO9855511-A1.
XX 10-DEC-1998.
XX 26-MAY-1998; 98WO-JP02295.
XX 03-JUN-1997; 97JP-0161936.
XX
XX (KAGA ) CHERO-SERO-THERAPEUTIC RES INST.
XX Eda Y, Imamura T, Maeda H, Tokiyoshi S;
XX WPI: 1999-070260/06.
XX P-PSDB: AAW74322.
XX
XX Canine cytokine protein which activates canine cytotoxic T
XX lymphocytes - is useful for treatment of viral and autoimmune
XX diseases in dogs
XX
XX Claim 8; Page 30-31; 51pp; Japanese.
```

CC This sequence encodes the canine lymphocyte activation factor (CLAF) of
CC the invention. CLAF activates lymphocytes, especially canine cytotoxic
CC T cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC recognising it may be used in the treatment of viral diseases in dogs
CC (such as canine distemper, canine parvovirus and canine infectious
CC hepatitis). The antibodies may also be used in isolation of CLAF from
CC culture of the transformant host cells by affinity chromatography. The
CC p40 homodimer can be used for the treatment of autoimmune diseases in
CC dogs.

SQ Sequence 2154 BP: 663 A; 448 C; 477 G; 566 T; 0 other;

Query Match 66.7%; Score 658; DB 20; Length 2154;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 658; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 323 AAGATGAATTTGGTCCACTGATATCTTAAAGAAACAGAAAGATCCAAAATAAGATCT 382
Db 377 AAGATGAATTTGGTCCACTGATATCTTAAAGAAACAGAAAGATCCAAAATAAGATCT 436
QY 383 TTCTGAATGTGAGGCAAAAGATTTATCTGAGAGCTTTTCACATGCTGGTGGCTGAGGGCA 442
Db 437 TTCTGAATGTGAGGCAAAAGATTTATCTGAGAGCTTTTCACATGCTGGTGGCTGAGGGCA 496
QY 443 TCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTCTGTGACCCCAAGGG 502
Db 497 TCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTCTGTGACCCCAAGGG 556
QY 503 TGACATGTGAGACCTGACACTTTTCAGCAGAGAGGCTCAGAGTGCACAAACAGGATTATA 562
Db 557 TGACATGTGAGACCTGACACTTTTCAGCAGAGAGGCTCAGAGTGCACAAACAGGATTATA 616
QY 563 AGAAGTACACAGTGTGAGTGTGAGAGGGAGGAGGCTGCTCCAGGAGAGAGCTAC 622
Db 617 AGAAGTACACAGTGTGAGTGTGAGAGGGAGGAGGCTGCTCCAGGAGAGAGCTAC 676
QY 623 CCATGAGAGTGTGTGATGCTATTCACAAAGCTCAAGTATGAAAACTACACAGCAGCT 682
Db 677 CCATGAGAGTGTGTGATGCTATTCACAAAGCTCAAGTATGAAAACTACACAGCAGCT 736
QY 683 TCTTCATCAGAGACATCATCAAAACCAGACCCACCAAAAGCTGCAGCTGAAGCATTGA 742
Db 737 TCTTCATCAGAGACATCATCAAAACCAGACCCACCAAAAGCTGCAGCTGAAGCATTGA 796
QY 743 AAAATTCTGGCAGCTGAGAGTCACTGGGAATACCCGACACCTGGAGAGCCACCAATT 802
Db 797 AAAATTCTGGCAGCTGAGAGTCACTGGGAATACCCGACACCTGGAGAGCCACCAATT 856
QY 803 CCTACTCTCCCTGACATTTTGCATACAGGCCAGGCAAGAACATAGAGAAAAAAG 862
Db 857 CCTACTCTCCCTGACATTTTGCATACAGGCCAGGCAAGAACATAGAGAAAAAAG 916
QY 863 ATAGACTGTGCTGAGACAAAGACCTGACCAAGAGTGTGCCACAAGATGCCAAGATCC 922
Db 917 ATAGACTGTGCTGAGACAAAGACCTGACCAAGAGTGTGCCACAAGATGCCAAGATCC 976
QY 923 GCGTGCAAGCCCGAGACCGCTACTATAGTTCATCTGAGGAGCTGGGCATCTGTGTC 980
Db 977 GCGTGCAAGCCCGAGACCGCTACTATAGTTCATCTGAGGAGCTGGGCATCTGTGTC 1034
```

RESULT 11

AD15209
ID AD15209 standard; DNA: 990 BP.

AD15209;

01-NOV-2001 (first entry)

Modified human cytokine p40 encoding DNA from clone R16-51.

Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection;
KW AIDS; diabetic retinopathy; cancer; vaccine; cell-mediated immunity;

| Query Match | 14.5% | Score 143 | DB 22 | Length 990 |
|-----------------------|----------------|---|----------|------------|
| Best Local Similarity | 100.0% | Pred. No. 1.5e-62 | | |
| Matches 143 | Conservative 0 | Mismatches 0 | Indels 0 | Gaps 0 |
| QY | 565 | AAAGTACACAGTGGAGTGTCTCAGAGAGGAGAGTGGCTGCCCTGTGCGAGAGAGCCTACCC | 624 | |
| DB | 565 | AAAGTACACAGTGGAGTGTCTCAGAGAGGAGAGTGGCTGCCCTGTGCGAGAGAGCCTACCC | 624 | |
| QY | 625 | ATCGAGGTGCTGGTGGATGATCTATTTCACAAGCTCAAGTATGAAAGTACACCGACGCTTC | 684 | |
| DB | 625 | ATCGAGGTGCTGGTGGATGATCTATTTCACAAGCTCAAGTATGAAAGTACACCGACGCTTC | 684 | |
| QY | 685 | TTCATCAGACGACATCATCAAAAC | 707 | |
| DB | 685 | TTCATCAGACGACATCATCAAAAC | 707 | |

RESULT 12

AAD15205

1D AAD15205 standard: DNA: 984 BP.

XX AAD15205;

XX

| | | | |
|----|---|--|--|
| DT | | 01-NOV-2001 | (first entry) |
| XX | | | |
| DE | | | Modified human cytokine p40 encoding DNA from clone B2-52. |
| KW | Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; | | |
| KM | AIDS; diabetic retinopathy; cancer; vaccine; cell-mediated immunity; | | |
| KW | human; p40; mutant; ds. | | |
| XX | | | |
| OS | Homo sapiens. | | |
| XX | Synthetic. | | |
| FH | Key | Location/Qualifiers | |
| FT | CDS | 1..984 | |
| FT | | /tag= a | |
| FT | | /product= "Modified p40 protein precursor" | |
| FT | sig_peptide | 1..66 | |
| FT | | /tag= b | |
| FT | mat_peptide | 67..981 | |
| FT | | /tag= c | |
| FT | | /product= "Mature modified p40 protein" | |
| PX | | | |
| PN | MO200140257-AZ. | | |
| PD | | | |
| PF | 07-JUN-2001. | | |
| XX | | | |
| PF | 30-NOV-2000; 2000WO-US32664. | | |
| XX | | | |
| PR | 02-DEC-1999; 99US-0169035. | | |
| PR | 28-NOV-2000; 2000US-0169035. | | |
| XX | | | |
| PA | (MAXY-) MAXYGEN INC. | | |
| XX | | | |
| PI | Leong SR, Punnonen J; | | |
| DR | WPI: 2001-502381/55. | | |
| DR | P-PSDB: AAE08598. | | |
| PT | Nucleic acids encoding modified cytokine polypeptides (i.e. modified | | |
| PT | p40 and p35 polypeptides), useful for treating various diseases e.g. | | |
| PT | diabetic retinopathy and cancer - | | |
| XX | | | |
| PS | Claim 1; Page 136-137; 223pp; English. | | |
| XX | | | |
| CC | The invention relates to nucleic acids encoding modified cytokine | | |
| CC | polypeptides (i.e. modified p40 and p35 polypeptides). The modified | | |
| CC | cytokine polypeptides have T-cell proliferative and interferon (IFN)- | | |
| CC | gamma induction activities. The polypeptides and polynucleotides of the | | |
| CC | invention are useful for treating various diseases e.g. bacterial | | |
| CC | infections, AIDS, diabetic retinopathy and cancer. The polypeptide and | | |
| CC | polynucleotide may also be useful as a vaccine adjuvant, to enhance a | | |
| CC | vaccinated host's cell-mediated immunity for protective response to a | | |
| CC | pathogen. The present sequence is a modified human p40 protein encoding | | |
| CC | DNA. | | |
| XX | | | |
| SQ | Sequence 984 BP; 267 A; 246 C; 254 G; 217 T; 0 other; | | |
| | | | |
| | Query Match | 13.0%; Score 128; DB 22; Length 984; | |
| | Best local Similarity | 100.0%; Pred. NO. 6.7e-55; | |
| | Matches 128; Conservative | 0; Mismatches 0; Indels 0; Gaps 0; | |
| OY | 565 AAGTACACAGGAGGTCTCAGAGGGCGAGTCCTGCCCTCTGCAGAGAGGCTTACC | 624 | |
| | | | |
| Db | 565 AAGTACACAGGAGGTCTCAGAGGGCGAGTCCTGCCCTCTGCAGAGAGGCTTACC | 624 | |
| | | | |
| OY | 625 ATGCAGGTCGTGGTGATGCTATTTCACAAGCTCAAGTWTGAATACTACACAGCATTC | 684 | |
| | | | |
| Db | 625 ATGCAGGTCGTGGTGATGCTATTTCACAAGCTCAAGTWTGAATACTACACAGCATTC | 684 | |
| | | | |
| OY | 685 TTTCATCAG 692 | | |
| | | | |
| Db | 685 TTTCATCAG 692 | | |
| | | | |

```
RESULT 13
AADI5206
ID AADI5206 standard; DNA: 984 BP.
XX
AC AADI5206;
XX
DT 01-NOV-2001 (first entry)
XX
DE Modified human cytokine p40 encoding DNA from clone B1-81.
XX
KW Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection;
KW AIDS; diabetic retinopathy; cancer; vaccine; cell-mediated immunity;
KW human; p40; mutant; ds.
XX
OS Homo sapiens.
XX
XX Synthetic.
XX
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FH /product= "Modified p40 protein precursor"
FT sig_peptide 1..66
FT /*tag= b
FT mat_peptide 67..981
FT /*tag= c
FT /product= "Mature modified p40 protein"
XX
PN MO200140257-A2.
XX
PD 07-JUN-2001.
XX
PF 30-NOV-2000; 2000WO-US12664.
XX
PR 02-DEC-1999; 99US-0169035.
PR 28-NOV-2000; 2000US-0169035.
XX
PA (MAXY-) MAXYGEN INC.
XX
PI Leong SR, Punnonen J;
XX
DR WPI: 2001-502381/55.
DR P-PSDB: AAE08599.
XX
XX Nucleic acids encoding modified cytokine polypeptides (i.e. modified
PT p40 and p35 polypeptides), useful for treating various diseases e.g.
PT diabetic retinopathy and cancer -
XX
XX Claim 1; Page 137; 223pp; English.
XX
PS The invention relates to nucleic acids encoding modified cytokine
CC polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC gamma induction activities. The polypeptides and polynucleotides of the
CC invention are useful for treating various diseases e.g. bacterial
CC infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC vaccinated host's cell-mediated immunity for protective response to a
CC pathogen. The present sequence is a modified human p40 protein encoding
CC DNA.
XX
SQ Sequence 984 BP; 272 A; 254 C; 247 G; 211 T; 0 other;
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Query Match 9.6%; Score 95; DB 22; Length 984;
Best Local Similarity 100.0%; Pred. No. 4.7e-38;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 586 GAGGGAGTGCCTGCCCTCTGCCGAGAGAGAGCTTACCATCGAGTCTGTGTCGATGCT 645
DB 586 GAGGGAGTGCCTGCCCTCTGCCGAGAGAGAGAGCTTACCATCGAGTCTGTGTCGATGCT 645
QY 646 ATTCACAGCTCAAGTATGAAGAACTACACGACGAG 680
DB 646 ATTCACAGCTCAAGTATGAAGAACTACACGACGAG 680
```

```
RESULT 14
AADI5207
ID AADI5207 standard; DNA: 969 BP.
XX
AC AADI5207;
XX
DT 01-NOV-2001 (first entry)
XX
DE Modified human cytokine p40 encoding DNA from clone A3-48.
XX
KW Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection;
KW AIDS; diabetic retinopathy; cancer; vaccine; cell-mediated immunity;
KW human; p40; mutant; ds.
XX
OS Homo sapiens.
XX
XX Synthetic.
XX
FH Key Location/Qualifiers
FH CDS 1..969
FH /*tag= a
FH /product= "Modified p40 protein precursor"
FT sig_peptide 1..66
FT /*tag= b
FT mat_peptide 67..966
FT /*tag= c
FT /product= "Mature modified p40 protein"
XX
PN MO200140257-A2.
XX
PD 07-JUN-2001.
XX
PF 30-NOV-2000; 2000WO-US32664.
XX
PR 02-DEC-1999; 99US-0169035.
PR 28-NOV-2000; 2000US-0169035.
XX
PA (MAXY-) MAXYGEN INC.
XX
PI Leong SR, Punnonen J;
XX
DR WPI: 2001-502381/55.
DR P-PSDB: AAE08599.
XX
XX Nucleic acids encoding modified cytokine polypeptides (i.e. modified
PT p40 and p35 polypeptides), useful for treating various diseases e.g.
PT diabetic retinopathy and cancer -
XX
XX Claim 1; Page 137; 223pp; English.
XX
PS The invention relates to nucleic acids encoding modified cytokine
CC polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC gamma induction activities. The polypeptides and polynucleotides of the
CC invention are useful for treating various diseases e.g. bacterial
CC infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC vaccinated host's cell-mediated immunity for protective response to a
CC pathogen. The present sequence is a modified human p40 protein encoding
CC DNA.
XX
SQ Sequence 969 BP; 263 A; 249 C; 251 G; 206 T; 0 other;
```

```
Query Match 7.6%; Score 75; DB 22; Length 969;
Best Local Similarity 100.0%; Pred. No. 7.6e-28;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 900 GTGCCACAAGATCCCAAGATCCCGGTGCAGAGCCCGGACCGCTACTATAGTTGATCTCG 959
DB 879 GTGCCACAAGATCCCAAGATCCCGGTGCAGAGCCCGGACCGCTACTATAGTTGATCTCG 938
QY 960 GAGGAGCTGGGCAATC 974
```

Db 939 GAGCGACTGGGCAATC 953

RESULT 15
AADI5203

ID AADI5203 standard; DNA: 975 BP.

AC AADI5203:

DT 01-NOV-2001 (first entry)

DE Modified human cytokine p40 encoding DNA from clone C2-22.

KW Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection;
KW AIDS; diabetic retinopathy; cancer; vaccine; cell-mediated immunity;
KW human; p40; mutant; ds.

OS Homo sapiens.
OS Synthetic.

Key Location/Qualifiers
CDS 1..975

FT sig_peptide 1..66 /product= "Modified p40 protein precursor"

FT mat_peptide 67..972 /tag= b

FT /tag= c /product= "Mature modified p40 protein"

PN WO200140257-A2.

PD 07-JUN-2001.

PF 30-NOV-2000; 2000MO-US32664.

PR 02-DEC-1999; 99US-0169035.

PR 28-NOV-2000; 2000US-0169035.

PA (MAXY-) MAXYGEN INC.

PI Leong SR, Punnonen J;

DR WPI; 2001-502381/55.

DR P-PSDB; AAE08596.

PT Nucleic acids encoding modified cytokine polypeptides (i.e. modified
PT p40 and p35 polypeptides), useful for treating various diseases e.g.
PT diabetic retinopathy and cancer -

PS Claim 1; Page 136; 223pp; English.

CC The invention relates to nucleic acids encoding modified cytokine
CC polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC gamma induction activities. The polypeptides and polynucleotides of the
CC invention are useful for treating various diseases e.g. bacterial
CC infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC vaccinated host's cell-mediated immunity for protective response to a
CC pathogen. The present sequence is a modified human p40 protein encoding
CC DNA.

CC Sequence 975 BP; 269 A; 252 C; 250 G; 204 T; 0 other;

Query Match 7.3%; Score 72; DB 22; Length 975;
Best Local Similarity 100.0%; Pred. No. 2.6e-26;

Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 647 TTCACAAGCTCAAGTATGAAACTACACGAGCTTCTTCATGAGACATCATCAAC 706
|||||
Db 632 TTCACAAGCTCAAGTATGAAACTACACGAGCTTCTTCATGAGACATCATCAAC 691

OY 707 CAGACCCACCCA 718
|||||
Db 692 CAGACCCACCCA 703

Search completed: July 16, 2003, 13:41:42
Job time : 255.001 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 10:34:53 ; Search time 1695.97 Seconds
(without alignments)
9425.275 Million cell updates/sec

Title: US-09-917-265-58

Perfect score: 987

Sequence: 1 atgcaccctcagcagctgtg.....gggcacatcgtgcatcagct 987

Scoring table: OLIGO_NGC

Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Database :

EST: *
1: em_estba: *
2: em_esthum: *
3: em_estin: *
4: em_estnu: *
5: em_estrov: *
6: em_estrpl: *
7: em_estro: *
8: em_hlc: *
9: gb_est1: *
10: gb_est2: *
11: gb_hlc: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estrom: *
17: gb_gss: *
18: em_gss_hum: *
19: em_gss_inu: *
20: em_gss_pln: *
21: em_gss_vrt: *
22: em_gss_fun: *
23: em_gss_mam: *
24: em_gss_mus: *
25: em_gss_other: *
26: em_gss_pro: *
27: em_gss_rtd: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|-------------|
| 1 | 2.2 | 662 | 17 | AG049786 | Pan trogl |
| 2 | 2.1 | 369 | 21 | AZ884788 | RCIC-23.1 |
| 3 | 2.1 | 564 | 13 | BJ030774 | BJ030774 |
| 4 | 2.1 | 571 | 13 | BJ032049 | BJ032049 |
| 5 | 2.1 | 638 | 13 | BI099266 | IP1_40_GO |
| 6 | 2.1 | 646 | 10 | BB038225 | BB038225 |

| | | | | | |
|----|-----|------|----|----------|---------------------|
| 7 | 2.1 | 667 | 13 | BJ042592 | BJ042592 |
| 8 | 2.1 | 975 | 17 | CNS04WYT | AL310995 Tetradon |
| 9 | 2.0 | 173 | 13 | BJ006287 | BJ006287 |
| 10 | 2.0 | 239 | 17 | BH870361 | BH870361 hme1B07.b |
| 11 | 2.0 | 374 | 14 | T99581 | T99581 ye55d08.r1 |
| 12 | 2.0 | 436 | 10 | AV792889 | AV792889 AV792889 |
| 13 | 2.0 | 475 | 12 | BF704417 | BF704417 M1-P-E6-a |
| 14 | 2.0 | 527 | 17 | BH780306 | BH780306 f2mb015-f0 |
| 15 | 2.0 | 530 | 14 | BM884387 | BM884387 rcl0f05.y |
| 16 | 2.0 | 536 | 10 | AV554146 | AV554146 |
| 17 | 2.0 | 550 | 17 | B75609 | B75609 RPI111-11L1 |
| 18 | 2.0 | 569 | 17 | AZ853726 | AZ853726 2M0157M01 |
| 19 | 2.0 | 605 | 17 | AO544128 | AO544128 RPI-11-3 |
| 20 | 2.0 | 637 | 9 | A1982112 | A1982112 pat.pk007 |
| 21 | 2.0 | 690 | 17 | AZ424475 | AZ424475 1M0204A12 |
| 22 | 2.0 | 707 | 14 | BU002016 | BU002016 QG62912.Y |
| 23 | 2.0 | 855 | 17 | AO893069 | AO893069 HS_3072_A |
| 24 | 2.0 | 862 | 13 | BI830737 | BI830737 603075132 |
| 25 | 2.0 | 1637 | 14 | BO056451 | BO056451 AGENCOURT |
| 26 | 1.9 | 268 | 10 | BB427690 | BB427690 BB427690 |
| 27 | 1.9 | 313 | 10 | BB471339 | BB471339 BB471339 |
| 28 | 1.9 | 334 | 17 | AZ396610 | AZ396610 1M0161B18 |
| 29 | 1.9 | 352 | 17 | AZ799073 | AZ799073 2M0056D24 |
| 30 | 1.9 | 360 | 14 | C47397 | C47397 C47397 Yuj1 |
| 31 | 1.9 | 380 | 17 | AO141956 | AO141956 HS_3173_A |
| 32 | 1.9 | 383 | 13 | BJ283928 | BJ283928 |
| 33 | 1.9 | 390 | 10 | BE424991 | BE424991 WHE0079_H |
| 34 | 1.9 | 408 | 17 | AO118163 | AO118163 HS_3003_A |
| 35 | 1.9 | 432 | 12 | BG513467 | BG513467 dae11B06. |
| 36 | 1.9 | 448 | 10 | AW513679 | AW513679 x087e09.x |
| 37 | 1.9 | 453 | 14 | BM868100 | BM868100 mgcs013.x1 |
| 38 | 1.9 | 476 | 17 | AO766175 | AO766175 HS_5477.B |
| 39 | 1.9 | 477 | 14 | BM750317 | BM750317 K-EST0025 |
| 40 | 1.9 | 478 | 13 | BI450211 | BI450211 dae76811. |
| 41 | 1.9 | 480 | 17 | AZ457253 | AZ457253 1M0260E06 |
| 42 | 1.9 | 481 | 9 | A1545879 | A1545879 fb76e12.y |
| 43 | 1.9 | 505 | 17 | AZ635629 | AZ635629 1M0493D09 |
| 44 | 1.9 | 508 | 14 | BU002504 | BU002504 OCG31119. |
| 45 | 1.9 | 509 | 13 | BJ068319 | BJ068319 |

ALIGNMENTS

RESULT 1
AG049786
LOCUS
DEFINITION
ACCESSION
KEYWORDS
SOURCE

ORGANISM
Pan troglodytes male lymphoblast DNA, clone: PTB-030A07.R, genomic survey sequence.
BAC library clone: PTB-030A07.R.
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

TITLE
JOURNAL
REFERENCE
AUTHORS

COMMENT
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: chimpbes@sc.riken.go.jp, url: http://hnp.gsc.riken.go.jp/). Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.

PRIMERS

Sequencing: M13rev
LIBRARY

Vector : PKS145
R.Site 1 : SacI
R.Site 2 : SacI

FEATURES

Source

Location/Qualifiers
1..662

/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-030A07.R"
/sex="male"

/cell_type="lymphoblast"

BASE COUNT 197 a 118 c 140 g 206 t
ORIGIN 1 others

Query Match

Best Local Similarity 2.1%; Score 22; DB 17; Length 662;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY

307 TTGATTCACAAAAAAGAGATG 328
|||||

Db

345 TTGATTCACAAAAAAGAGATG 366

RESULT 2

LOCUS

AZ884788 369 bp DNA linear GSS 05-MAR-2001

DEFINITION RPI-23-182A5.TV RPI-23 Mus musculus genomic clone RPI-23-182A5,
DNA sequence.

ACCESSION

AZ884788
GSS.
GI:13203733

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Zhao, S., Nieman, W., Feldblyum, T., Malek, J., Shatsman, S., Akınret,
B., Levins, M., McGam, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.
and Fraser, C.M.
Mouse BAC End Sequences from Library RPI-23
Unpublished (1999)
Other_GSSs: RPI-23-182A5.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tifg.org

Clones are derived from the mouse BAC library RPI-23. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (<http://www.choi.org/bacpac/orderinframe.htm>). BAC end
plate: 182 row: A column: 5
Seq primer: T7
Class: BAC ends.

TITLE

JOURNAL

COMMENT

Source

Location/Qualifiers
1..369

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="RPI-23-182A5"

/clone_lib="RPI-23"

/sex="female"

/lab_host="DH10B"

/note="Organ: Kidney/Brain; Vector: pBAC3.6; Site: 1;
ECORI; Site: 2: EcorI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcorI and EcorI Methylase. Size

BASE COUNT

97 a 76 c 86 g 110 t
ORIGIN

Query Match

Best Local Similarity 2.1%; Score 21; DB 17; Length 369;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY

484 TTCTGTGACCCCAAGGGGTG 504
|||||

Db

121 TTCTGTGACCCCAAGGGGTG 141

RESULT 3

LOCUS

Bj030774 564 bp mRNA linear EST 05-DEC-2001

DEFINITION Bj030774 N1BB Mochii normalized Xenopus neurula library Xenopus
laevis cDNA clone Xl005c01 5', mRNA sequence.

ACCESSION

Bj030774
EST.
GI:17377868

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Source

Expressed genes in X. laevis embryo
Unpublished (2001)
Contact: Tadasu Shin-i
Center for Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshtn@genes.nig.ac.jp.

FEATURES

Source

Location/Qualifiers

1..564

/organism="Xenopus laevis"

/db_xref="taxon:8355"

/clone="Xl005c01"

/clone_lib="N1BB Mochii normalized Xenopus neurula
library"

/tissue_type="whole embryo"

/dev_stage="stage 15"

/note="Vector: pBSRN3; Site: 1: NotI; Site: 2: EcorI; cDNAs
were oligo-dT primed and directionally cloned. Staging
according to Nieuwkoop and Faber. Library is subtracted
and was constructed by N. Garrett and A.M. Zorn,
(Wellcome/CRC Institute)."

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 2.1%; Score 21; DB 13; Length 564;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY

250 GATCTGGCCAGTATACCTGC 270
|||||

Db

178 GATCTGGCCAGTATACCTGC 198

RESULT 4

LOCUS

Bj032049 571 bp mRNA linear EST 05-DEC-2001

DEFINITION Bj032049 N1BB Mochii normalized Xenopus neurula library Xenopus
laevis cDNA clone Xl015h03 5', mRNA sequence.

ACCESSION

Bj032049
GI:17375617

KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
Xenopodinae; Xenopus.
REFERENCE 1 (bases 1 to 571)
AUTHORS Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-I,T. and Kohara,Y.

TITLE Expressed genes in X. laevis embryo
JOURNAL Unpublished (2001)
COMMENT Contact: Tadasi Shin-I
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6695
Fax: 81-559-81-6685
Email: tshin@genes.nig.ac.jp.

FEATURES
source Location/Qualifiers
1..571
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone_lib="NIBB Mochii normalized Xenopus neurula library"
/tissue_type="whole embryo"
/dev_stage="stage 15"
/note="Vector: pBSRN3. Site_1: NotI; Site_2: EcoRI; cDNAs were oligo-dT primed and directionally cloned. Staging according to Nieukoop and Faber. Library is subcloned and was constructed by N. Garrett and A.M. Zorn, (Wellcome/CRC Institute)."

BASE COUNT 142 a 142 c 143 g 144 t
ORIGIN

Query Match 2.1%; Score 21; DB 13; Length 571;
Best local Similarity 100.0%; Pred. No. 18;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 CATGCTGGCCACTATACCTGC 270
|||||
Db 140 GATGCTGGCCACTATACCTGC 160

RESULT 5
BI099266/c 638 bp mRNA linear EST 26-JUN-2001
LOCUS IP1_40.G03.g1_A002 Immature pannicle 1 (IP1) Sorghum bicolor cDNA,
DEFINITION mRNA sequence.
ACCESSION BI099266
VERSION BI099266.1 GI:14570848
KEYWORDS EST.
SOURCE Sorghum.
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoidae; Andropogoneae; Sorghum.
1 (bases 1 to 638)
Klein,R.R., Cordonnier-Pratt,M.-M., Gingle,A., Sudhan,M. and Pratt,L.H.
An EST database from Sorghum: developing preanthesis pannicles
Unpublished (2001)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Km. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude polyA, vector and regions below Phred quality 16. The threshold for high quality sequence is 20. Three-prime sequences, which are obtained with PolyTmix or T7 sequencing primer, are presented as the reverse complement.

Seq primer: T7
High quality sequence start: 8
High quality sequence stop: 638
POLY-A-Tes.
FEATURES
source Location/Qualifiers
1..638
/organism="Sorghum bicolor"
/cultivar="BTx623"
/db_xref="taxon:4558"
/clone_lib="Immature pannicle 1 (IP1)"
/note="Organ: Developing preanthesis pannicles; Vector: pBluescript II SK(-) from Lambda Zap II; Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda Zap II. Clones to be sequenced were prepared by mass excision."

BASE COUNT 143 a 134 c 179 g 182 t
ORIGIN

Query Match 2.1%; Score 21; DB 13; Length 638;
Best local Similarity 100.0%; Pred. No. 18;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 725 TGCAGCTGAAGCCATTGAAAA 745
|||||
Db 135 TGCAGCTGAAGCCATTGAAAA 115

RESULT 6
BB038225 646 bp mRNA linear EST 18-OCT-2001
LOCUS BB038225 RIKEN full-length enriched, 13 days embryo forelimb Mus
DEFINITION musculus cDNA clone 5930435K16 3', mRNA sequence.
ACCESSION BB038225
VERSION BB038225.2 GI:16258473
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 646)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
On Jun 10, 2000 this sequence version replaced gi:8444611.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watanabe,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)
 Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
 Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences *Mamm. Genome*, 12, 673-677 (2001)
 Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

FEATURES

source

Location/Qualifiers
 1. 646
 /organism="Mus musculus"
 /strain="C57Bl/6J"
 /db_xref="taxon:10090"
 /clone="5930435K16"
 /clone_lib="RIKEN full-length enriched, 13 days embryo forelimb"
 /sex="mixed"
 /tissue_type="forelimb"
 /dev_stage="13 days embryo"
 /lab_host="DH10B"
 /note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
 GAGAGAGAGAGATCCCAAGAGCTTTTCTTTTCTTTT 3'], cDNA was prepared by using trehalose thermoactivated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCGAGTTAATTAATTCCTCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda PUC I. Cloning sites, 5' end: SalI; 3' end: BamHI."

BASE COUNT 181 a 137 c 153 g 175 t
 ORIGIN

Query Match 2.1%; Score 21; DB 10; Length 646;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 484 TTCTCTGACCCCAAGGGGTG 504
 ||||||||||||||||||||
 Db 341 TTCTCTGACCCCAAGGGGTG 361

RESULT 7 667 bp mRNA linear EST 06-DEC-2001
 BJO42592
 LOCUS BJO42592 NIBB Mochii normalized Xenopus neurula library Xenopus
 DEFINITION laevis cDNA clone XL03C23 5', mRNA sequence.
 ACCESSION BJO42592
 VERSION BJO42592.1 GI:17392768
 KEYWORDS EST.
 SOURCE African clawed frog.
 ORGANISM *Xenopus laevis*

REFERENCE
 AUTHORS Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae; Xenopodinae; Xenopus.
 1 (bases 1 to 667)
 Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara, Y.

TITLE
 JOURNAL Expressed genes in X. laevis embryo
 COMMENT Unpublished (2001)
 Contact: Tadasu Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tsuhit@genes.nig.ac.jp.

FEATURES

source

Location/Qualifiers
 1. 667
 /organism="Xenopus laevis"
 /db_xref="taxon:8355"
 /clone="XL03C23"
 /clone_lib="NIBB Mochii normalized Xenopus neurula library"
 /tissue_type="whole embryo"
 /dev_stage="stage 15"
 /note="Vector: pBSRN3; Site 1: NotI; Site 2: EcoRI; cDNAs were oligo-dT primed and directionally cloned. Staging according to Nieuwkoop and Faber. Library is subtracted and was constructed by N. Garrett and A.M. Zorn, (Wellcome/CRC Institute)."

BASE COUNT 151 a 186 c 166 g 164 t
 ORIGIN

Query Match 2.1%; Score 21; DB 13; Length 667;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 250 GATGCTGGCCAGTATACCTGC 270
 ||||||||||||||||||||
 Db 281 GATGCTGGCCAGTATACCTGC 301

RESULT 8 975 bp DNA linear GSS 26-JUL-2000
 CNS04WYI
 LOCUS CNS04WYI/c
 DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone 053B09 of library A from Tetraodon nigroviridis, genomic survey sequence.

ACCESSION AL310995
 VERSION AL310995.1 GI:9543863
 KEYWORDS GSS: genome survey sequence.
 SOURCE Tetraodon nigroviridis.
 ORGANISM *Tetraodon nigroviridis*

REFERENCE
 AUTHORS Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.
 1 (bases 1 to 975)
 Roest Crolius, H., Jallion, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brothier, P., Quetier, F., Saurin, W. and Weissenbach, J.
 Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence

Nat. Genet. 25 (2), 235-238 (2000)
 JOURNAL Nat. Genet.
 MEDLINE 20296633
 PUBMED 10835645

2 (bases 1 to 975)
 Crolius, H., Jallion, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.

Characterization and repeat analysis of the compact genome of the freshwater pufferfish *Tetraodon nigroviridis*
 Genome Res. 10 (7), 939-949 (2000)

JOURNAL Genome Res.
 MEDLINE 20359837
 PUBMED 10899143

3 (bases 1 to 975)
 Genoscope.
 Direct Submission
 Submitted (12-APR-2000)
 COMMENT This sequence is a single read and was generated as part of a large

scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.

FEATURES

source
1. .975
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="053809"
/clone_lib="A"
/notes="Genoscope sequence ID : C0MA053CA05C1-end : 77"

BASE COUNT 188 a 289 c 279 g 197 t 22 others
ORIGIN

Query Match 2.1%: Score 21; DB 17; Length 975;
Best Local Similarity 100.0%: Pred. No. 20;

Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 949 AGTTCATCCTGAGCGACTGG 969
|||||
590 AGTTCATCCTGAGCGACTGG 570

RESULT 9
BJ006287 173 bp mRNA linear EST 05-DEC-2001
LOCUS BJ006287 MF01SSA cDNA Oryzias latipes cDNA clone MF01SSA051H02 5',
DEFINITION mRNA sequence.
ACCESSION BJ006287 GI:17362447
VERSION BJ006287
KEYWORDS EST.
SOURCE Japanese medaka.
ORGANISM Oryzias latipes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorphi; Acanthopterygii; Perciformes; Atherinomorpha; Belontiiformes; Adrianiichthyidae; Oryziinae; Oryzias.

REFERENCE 1 (bases 1 to 173)
Kohara,Y., Shin-I,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H.
Medaka EST Project in Takeda's lab
Unpublished (2001)
COMMENT Contact: Tadasu Shin-I
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.

FEATURES
source
1. .173
/organism="Oryzias latipes"
/strain="Hd-rf"
/db_xref="taxon:8090"
/clone="MF01SSA091H02"
/clone_lib="MF01SSA cDNA"
/sex="mixture of female and male"
/tissue_type="whole embryo"
/dev_stage="segmentation stage 20 - 25"
/dev_stage="segmentation stage 20 - 25"
Location/Qualifiers

BASE COUNT 36 a 53 c 50 g 31 t 3 others
ORIGIN

Query Match 2.0%: Score 20; DB 13; Length 173;
Best Local Similarity 100.0%: Pred. No. 47;

Matches 20: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 586 GAGGCGAGTCCTGCCCTC 605
|||||
85 GAGGCGAGTCCTGCCCTC 104

RESULT 10
BH870361 239 bp DNA linear GSS 05-AUG-2002
LOCUS BH870361/c
DEFINITION hm61b07.b1 WGS-Zmaysf (JM107 adapted methyl filtered) zea mays

genomic clone hm61b07 5', DNA sequence.

ACCESSION BH870361 GI:22106258
VERSION BH870361.1
KEYWORDS GSS.
SOURCE zea mays.
ORGANISM zea mays

REFERENCE 1 (bases 1 to 239)
Rabinowicz,P.D., O'Shaughnessy,A.L., Balija,V., Dedhia,N., Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L., Zulaewen,T., McCombie,W.R. and Martienssen,R.A.
Genomic shotgun sequences from zea mays (methyl-filtered)
Unpublished (2002)
CONTACT: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org

Plate: hm61 row: b column: 07
Seq primer: -21M13univrev
Class: shotgun
High quality sequence stop: 239.

FEATURES

source

1. .239
Location/Qualifiers

/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="hm61b07"
/clone_lib="WGS-Zmaysf (JM107 adapted methyl filtered)"
/lab_host="JM107 or DH5a"

/note="Organ: immature ears; Site_1: Xba I; Site_2: Xba I;
The vector was digested with XbaI and one nucleotide was added by fill in in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (x/y reads in M13mp19, b/g reads in pUC19). The same ligation was transformed in either JM107 or DH5a."

BASE COUNT 66 a 44 c 38 g 91 t

Query Match 2.0%: Score 20; DB 17; Length 239;
Best Local Similarity 100.0%: Pred. No. 50;
Matches 20: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 309 GATTCACAAAAGAGATG 328
|||||
31 GATTCACAAAAGAGATG 12

RESULT 11
T99581 374 bp mRNA linear EST 31-MAR-1995
LOCUS T99581/c
DEFINITION ye65d08.r1 Soares fetal liver spleen JNPLS Homo sapiens cDNA clone
IMAGE:122607 5', mRNA sequence.
ACCESSION T99581
VERSION T99581.1 GI:749318
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 374)
Hillier,L., Clark,N., Dubuque,T., Ellison,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevisakis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)

COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
Insert Size: 954
High quality sequence stops: 243 Source: IMAGE Consortium, LLNL This
clone is available royalty-free through LLNL; contact the IMAGE
Consortium (info@image.llnl.gov) for further information.
Insert Length: 954 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 243.

FEATURES
Source Location/Qualifiers
1. 374
/organism="Homo sapiens"
/db_xref="GDB:475152"
/db_xref="taxon:9606"
/clone="IMAGE:122607"
/clone_1lb="Soares fetal liver spleen INFLS"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
1st strand cDNA was primed with a Pac I - oligo(dT) primer
15' AACCTGAGAGATTAAATTAAGATCTTTTCTTTTCTTTT 3',
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 89 a 80 c 79 g 121 t 5 others

ORIGIN

Query Match 2.0%; Score 20; DB 14; Length 374;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 388 AAATGTGAGCCAAAGAAATTA 407
|||||
83 AAATGTGAGCCAAAGAAATTA 64

Db

RESULT 12
AV792889 436 bp mRNA linear EST 29-MAR-2002
LOCUS AV792889 RAFL7 Arabidopsis thaliana cDNA clone RAFL07-17-C16 3',
DEFINITION mRNA sequence.
ACCESSION AV792889
VERSION AV792889.1 GI:19826872
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 436)
Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,
Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,
Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.
and Shinozaki,K.
Large scale analysis of Arabidopsis full-length cDNA (2002b)
Unpublished (2002)
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rkc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI

TITLE
JOURNAL
COMMENT

and XhoI was ligated to modified lambda FIC-1 vector (Carinici et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified Bluescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
details.

FEATURES
Source Location/Qualifiers
1. 436
/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/clone="RAFL07-17-C16"
/clone_1lb="RAFL7"
/dev_stage="roselite plants"
/lab_host="DH10B"
/note="Site_1: BamHI; Site_2: SalI; subjected to
cold-treated (1, 2, 5, 10, 24 hr)"

BASE COUNT 121 a 72 c 103 g 140 t

ORIGIN

Query Match 2.0%; Score 20; DB 10; Length 436;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 684 CTTGATCAGACATCATCA 703
|||||
Db 424 CTTGATCAGACATCATCA 405

Db

RESULT 13
BF704417 475 bp mRNA linear EST 22-DEC-2000
LOCUS BF704417
DEFINITION M1-P-E6-acc-g-09-1-UM.s1 M1-P-E6 Sus scrofa cDNA clone
M1-P-E6-acc-g-09-1-UM 3', mRNA sequence.
ACCESSION BF704417
VERSION BF704417.1 GI:11989825
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 475)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery.
Genome Res. 6 (9), 791-806 (1996)
JOURNAL
MEDLINE
COMMENT Contact: Tugale CK
97044477
Molecular Genetics Laboratory, Department of Animal Science
Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
Tel: 5152944252
Fax: 5152944201
Email: cktugale@iastate.edu
Oligo-dT track not found. Not 1 site shown in beginning of sequence
is likely internal to the message. cDNA library Preparation: RJ
Woods, JA Green, RS Prather S142 Animal Science Research Center,
Department of Animal Science, University of Missouri-Columbia,
65211 Clone distribution: clones will be available through Research
genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA=No.

FEATURES
Source Location/Qualifiers
1. 475
/organism="Sus scrofa"
/strain="crossbred"
/db_xref="taxon:9823"
/clone="M1-P-E6-acc-g-09-1-UM"
/clone_1lb="M1-P-E6"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: EcoRI; The M1-P-E6
library is derived from fetus at gestational day 20. For
a detailed description of the library from which this
clone was derived, please visit our web site at

http://pigest.genome.iastate.edu/
TAG_SEQ=None found"

BASE COUNT 129 a 120 c 121 g 104 t 1 others

Query Match 2.0%: Score 20; DB 12; Length 475;
Best Local Similarity 100.0%: Pred. No. 57;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 157 CCTGACAGATGATCATC 176
11111111111111111111
Db 202 CCTGAGAGATGATCATC 221

RESULT 14

LOCUS BH780306 527 bp DNA linear GSS 28-MAR-2002
DEFINITION f2mb015f001a07f0 f2mb filtered library zea mays genomic clone
f2mb015f001a07 5', DNA sequence.

ACCESSION BH780306
VERSION BH780306.1 GI:19783255

KEYWORDS GSS.
SOURCE Zea mays.
ORGANISM Zea mays

REFERENCE 1 (bases 1 to 527)
AUTHORS Budlman,M.A., Freese,R.G., Bedell,J.A., Nunberg,A.N. and Lakey,N.D.
TITLE Genethresher methylation filtered genomic sequences from maize
JOURNAL Unpublished (2002)
COMMENT Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: f2mb015f001 row: a column: 07
Seq primer: M13 forward
Class: Shotgun
High quality sequence stop: 527.

FEATURES
Location/Qualifiers
1..527

source
/organism="Zea mays"
/cultivar="M017"
/db_xref="taxon:4577"
/clone="f2mb015f001a07"
/note="f2mb filtered library"
/note="Organ: leaf; Vector: pBCSK(-); Site: 1; HindII: DNA
prepared from purified nuclei was randomly sheared,
end-repaired, size fractionated to enrich for the 0.5 to
5 kb fraction, ligated into HindII-digested pBCSK(-)
vector and electroporated into E. coli cells."

BASE COUNT 181 a 77 c 108 g 161 t

Query Match 2.0%: Score 20; DB 17; Length 527;
Best Local Similarity 100.0%: Pred. No. 58;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 309 GATTCCACAAAAGAGATG 328
11111111111111111111
Db 141 GATTCCACAAAAGAGATG 160

RESULT 15

LOCUS BM884387 530 bp mRNA linear EST 08-MAR-2002
DEFINITION rcl0f05.y1 Meloidogyne hapla egg PAMP1 v1 Meloidogyne hapla cDNA 5'

ACCESSION BM884387
VERSION BM884387.1 GI:19268131

KEYWORDS EST.

SOURCE
ORGANISM Meloidogyne hapla.
Meloidogyne hapla
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.

REFERENCE

1 (bases 1 to 530)
AUTHORS McCarter,J., Clifton,S., Chappel11,B., Pape,D., Martin,J., Wylie,T.,
Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y.,
Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagarisvilli,R.,
Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Septeoe
, M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.,
, Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
Wilson,R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)

JOURNAL
COMMENT The Washington Univ. Nematode EST Project, 1999
Contact: McCarter, JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu
The library was constructed by Claire Murphy and Dr. James McCarter
at Washington University, St. Louis. DNA Sequencing by: Washington
University Genome Sequencing Center
Seq primer: -40RP from Gibco
High quality sequence stop: 426..

FEATURES
Location/Qualifiers
1..530

source
/organism="Meloidogyne hapla"
/db_xref="taxon:6305"
/clone_lib="Meloidogyne hapla egg PAMP1 v1"
/dev_stage="parasitic adult females"
/lab_host="DH10B"
/note="Vector: PAMP1 (Gibco); Site: 1; NotI; Site: 2; SalI;
The library was constructed by Claire Murphy and Dr. James
McCarter at Washington University, St. Louis. The cDNA was
made by using Dynabead oligo-dT priming (Dynal). PCR based
library using a modified protocol from the SMART PCR cDNA
Synthesis kit from Clontech. Directionally cloned into the
UD6 sites ofPAMP1."

BASE COUNT 156 a 118 c 161 g 95 t

Query Match 2.0%: Score 20; DB 14; Length 530;
Best Local Similarity 100.0%: Pred. No. 58;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 TCATCTCTGCGTTTCCCTC 39
11111111111111111111
Db 386 TCATCTCTGCGTTTCCCTC 367

Search completed: July 16, 2003, 15:58:25
Job time : 1695.97 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 13:16:38 ; Search time 52.4162 Seconds
(without alignments)
5774.736 Million cell updates/sec

Title: US-09-917-265-58

Perfect score: 987

Sequence: 1 atgacacctcagcagctgtgtc.....gggcattctgtctatgcagt 987

Scoring table:

OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Issued_Patents_NA: *
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2: /cgn2_6/pdata/1/ina/5B.COMB.seq: *
3: /cgn2_6/pdata/1/ina/6A.COMB.seq: *
4: /cgn2_6/pdata/1/ina/6B.COMB.seq: *
5: /cgn2_6/pdata/1/ina/PC105.COMB.seq: *
6: /cgn2_6/pdata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 974 | 98.7 | 990 | 4 | US-09-079-984A-11 |
| 2 | 798 | 80.9 | 990 | 4 | US-09-079-984A-1 |
| 3 | 46 | 4.7 | 987 | 1 | US-08-186-529-1 |
| 4 | 46 | 4.7 | 987 | 1 | US-08-640-386A-1 |
| 5 | 46 | 4.7 | 987 | 4 | US-08-848-760B-24 |
| 6 | 46 | 4.7 | 1018 | 2 | US-08-184-009-194 |
| 7 | 46 | 4.7 | 1018 | 2 | US-08-458-356-194 |
| 8 | 46 | 4.7 | 1018 | 4 | US-08-460-736-194 |
| 9 | 46 | 4.7 | 1399 | 2 | US-08-751-767A-3 |
| 10 | 46 | 4.7 | 1560 | 2 | US-08-751-767A-11 |
| 11 | 46 | 4.7 | 1623 | 2 | US-08-751-767A-9 |
| 12 | 46 | 4.7 | 1870 | 4 | US-09-310-842-4 |
| 13 | 46 | 4.7 | 2318 | 4 | US-09-851-062-3 |
| 14 | 46 | 4.7 | 2362 | 1 | US-08-265-087-1 |
| 15 | 46 | 4.7 | 2362 | 1 | US-08-621-493-1 |
| 16 | 46 | 4.7 | 2362 | 2 | US-08-965-688-1 |
| 17 | 46 | 4.7 | 2362 | 4 | US-09-260-173-1 |
| 18 | 46 | 4.7 | 6139 | 2 | US-08-751-767A-7 |
| 19 | 24 | 2.4 | 39 | 4 | US-09-079-984A-13 |
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| 21 | 20 | 2.0 | 20 | 4 | US-09-851-062-23 |
| 22 | 20 | 2.0 | 20 | 4 | US-09-851-062-33 |
| 23 | 20 | 2.0 | 39 | 4 | US-09-079-984A-14 |
| 24 | 20 | 2.0 | 1061 | 2 | US-08-385-335A-13 |
| 25 | 20 | 2.0 | 6295 | 2 | US-08-659-206A-4 |
| 26 | 20 | 2.0 | 7287 | 2 | US-08-659-206A-1 |
| 27 | 19 | 1.9 | 25 | 2 | US-08-751-767A-19 |

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| 28 | 19 | 1.9 | 1002 | 2 | US-08-359-850-3 | Sequence 3, Appl |
| 29 | 19 | 1.9 | 3207 | 1 | US-07-946-497-1 | Sequence 1, Appl |
| 30 | 19 | 1.9 | 3207 | 1 | US-08-483-322-1 | Sequence 1, Appl |
| 31 | 19 | 1.9 | 3207 | 2 | US-08-478-882-1 | Sequence 1, Appl |
| 32 | 18 | 1.8 | 20 | 4 | US-09-851-062-22 | Sequence 22, Appl |
| 33 | 18 | 1.8 | 39 | 4 | US-09-079-984A-8 | Sequence 8, Appl |
| 34 | 18 | 1.8 | 926 | 4 | US-08-936-169A-8 | Sequence 118, App |
| 35 | 18 | 1.8 | 1375 | 2 | US-08-993-738A-2 | Sequence 2, Appl |
| 36 | 18 | 1.8 | 1375 | 4 | US-08-713-354C-2 | Sequence 2, Appl |
| 37 | 18 | 1.8 | 1375 | 4 | US-09-241-266-2 | Sequence 2, Appl |
| 38 | 18 | 1.8 | 1375 | 4 | US-09-495-562-2 | Sequence 2, Appl |
| 39 | 18 | 1.8 | 1640 | 1 | US-07-807-043B-11 | Sequence 11, Appl |
| 40 | 18 | 1.8 | 1640 | 1 | US-08-299-849B-11 | Sequence 11, Appl |
| 41 | 18 | 1.8 | 1640 | 2 | US-08-142-368A-11 | Sequence 11, Appl |
| 42 | 18 | 1.8 | 1640 | 3 | US-08-967-727-11 | Sequence 11, Appl |
| 43 | 18 | 1.8 | 1640 | 4 | US-08-037-230D-11 | Sequence 11, Appl |
| 44 | 18 | 1.8 | 8257 | 4 | US-09-484-970B-65 | Sequence 65, Appl |
| 45 | 18 | 1.8 | 13953 | 4 | US-09-738-884-3 | Sequence 3, Appl |

ALIGNMENTS

RESULT 1
US-09-079-984A-11
Sequence 11, Application US/09079984A
Patent No. 6231850
GENERAL INFORMATION:
APPLICANT: Okano, Fumiyoshi, Satoh, Masahiro,
APPLICANT: Yamada, Katsumige
TITLE OF INVENTION: Canine interleukin 12, a production method
TITLE OF INVENTION: thereof, an immune disease treatment method and preventive
TITLE OF INVENTION: method using it
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Miller & Christenbury Intellectual Property
ADDRESSER: Department of Schneider, Harrison, Segal and Lewis, LLP
STREET: 1600 Market Street, 39th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,984A
FILING DATE: 15-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Austin R. Miller
REGISTRATION NUMBER: 16,602
REFERENCE/DOCKET NUMBER: 1051-98
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-1810
TELEFAX: (215) 568-6946
INFORMATION FOR SEO ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 990 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: Canine IL12
LOCATION: 1 to 987
IDENTIFICATION METHOD: Similarity
US-09-079-984A-11
Query Match 98.7%: Score 974: DB 4: Length 990:

Best Local Similarity 100.0%; Pred. No. 0;
Matches 974; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 7 CCTCAGAGTGGTGCATCTCTGGTCTTCCCTGTTTGGTGGGCGTCCCTCCATGAGCC 66
QY 67 ATATGGAGACTGGAGAAAGATGTTTATGTTAGAGTTGAGCTGGACCCCTGATGCCCC 126
Db 67 ATATGGAGACTGGAGAAAGATGTTTATGTTAGAGTTGAGCTGGACCCCTGATGCCCC 126
QY 127 GGAGAAATGGTGGTCTCACCCTGCAATACCCCTGAAAGATGACATCACTTGGACCTCA 186
Db 127 GGAGAAATGGTGGTCTCACCCTGCAATACCCCTGAAAGATGACATCACTTGGACCTCA 186
QY 187 GCGCAGACAGTGAAGTCTAGTGTCTGTTAAACCTGACCATCCCAAGTCAAGAAATTT 246
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QY 427 TGGTGGCTGACGGCAATCACTGATTTGAATTCAGTGTCAAAAGTAGCAGAGGCTTC 486
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QY 487 TCTGACCCCAAGGGGGTACATGTGAGCAGTGCACCTTTCAGAGAGAGGGGTAGAGTG 546
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QY 547 GACAAACAGGATTTAAGAGTACACAGTGAAGTGTGAGAGGCGCATGCTGCCCCCTCT 606
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QY 607 GCGGAGAGAGCTTACCCATCGAGGTGTGGTGGATCTTATTCACAGCTCAAGTATGAA 666
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QY 667 AACTACACAGCAGCTTCTTCATCAGACATCATCAACCCAGACCCACCAACCTG 726
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QY 967 TGGCATCTGTGTC 980
Db 967 TGGCATCTGTGTC 980
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RESULT 2

US-09-079-984A-1
: Sequence 1, Application US/09079984A
: Patent No. 6231850

: GENERAL INFORMATION:
: APPLICANT: Okano, Fumiyoshi, Satoh, Masahiro,
: TITLE OF INVENTION: Canine Interleukin 12, a production method
: TITLE OF INVENTION: thereof, an immune disease treatment method and preventive
: NUMBER OF SEQUENCES: 16
: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Miller & Christenbury Intellectual Property
: ADDRESSEE: Department of Schnader, Harrison, Segal and Lewis, LLP
: STREET: 1600 Market Street, 39th Floor
: CITY: Philadelphia
: STATE: PA
: COUNTRY: USA
: ZIP: 19103

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy Disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Wordperfect 5.1

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/09/079,984A

: FILING DATE: 15-MAY-1998

: ATTORNEY/AGENT INFORMATION:

: NAME: Austin R. Miller

: REGISTRATION NUMBER: 16,602

: REFERENCE/DOCKET NUMBER: 1051-98

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: (215) 561-1810

: TELEFAX: (215) 568-6946

: INFORMATION FOR SEQ ID NO: 1:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 990 base pairs

: TYPE: nucleic acid

: STRANDEDNESS: double

: TOPOLOGY: linear

: MOLECULE TYPE: cDNA to mRNA

: ORIGINAL SOURCE:

: ORGANISM: Canis familiaris

: FEATURE:

: NAME/KEY: Canine IL12

: LOCATION: 1 to 987

: IDENTIFICATION METHOD: Similarity

: US-09-079-984A-1

Query Match 80.9%; Score 798; DB 4; Length 990;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 948; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 88 GTTTATGTTAGAGTTGAGCTGGACCTGATGCCCCGAGAAATGTTGCTTCACC 147
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QY 148 TGGCATACCCCTGAAGAGATGATCATCTTGAACCTCAGCGAGAGCACTGAAGTCTTA 207
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QY 448 ACTGATTTGAATTCAGTCTCAAAAGTAGCAGAGCTTCTGTGACCCCAAGGGGTGACA 507
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Db 508 TGTGGACAGTGAACATTTGACAGAGAGGCTCAGAGTGAACAACAGGATTTATAGAG 567
QY 568 TACACAGTGAAGTTCAGAGAGGCGAGTCCCTGCTCTGCGGAGAGAGCTTACCCATC 627
Db 568 TACACAGTGAAGTTCAGAGAGGCGAGTCCCTGCTCTGCGGAGAGAGCTTACCCATC 627
QY 628 GAGCTCGTGTGATGCTATTCACAGAGCTCAAGTATGAAACTACACGAGCGCTTCTC 687
Db 628 GAGCTCGTGTGATGCTATTCACAGAGCTCAAGTATGAAACTACACGAGCGCTTCTC 687
QY 688 ATCAGAGACATCATCAAAACCAAGACCCCAACCAACCTGCAGCTGAAGCCATTGAAAAAT 747
Db 688 ATCAGAGACATCATCAAAACCAAGACCCCAACCAACCTGCAGCTGAAGCCATTGAAAAAT 747
QY 748 TCTCGGACGTGGAGGTCTAGCTGGGAATACCCCGACACCTGTGAGACCCCATTTCTAC 807
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QY 808 TTCTCCCTGACATTTTGCATACAGGCCAGGGCAAGAAACAATAGAAAAAAGAAATAGA 867
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QY 868 CTCCTGCTGGACAAGACCTCAGCCAGAGTCTGTGCCACAAGATGCCACAGATCCGCGTG 927
Db 868 CTCCTGCTGGACAAGACCTCAGCCAGAGTCTGTGCCACAAGATGCCACAGATCCGCGTG 927
QY 928 CAACGCCGAGCGCTCTACTATAGTTCACTCCTGAGAGCGCACTGGCATCTGTG 978
Db 928 CAACGCCGAGCGCTCTACTATAGTTCACTCCTGAGAGCGCATGGCATCTGTG 978

RESULT 3
US-08-186-529-1
: Sequence 1, Application US/08186529
: Patent No. 5573764
: GENERAL INFORMATION:
: APPLICANT: Sykes, Megan
: APPLICANT: Wolf, Stanley F.
: TITLE OF INVENTION: USE OF INTERLEUKIN-12 TO PREVENT
: TITLE OF INVENTION: GRAFT-VERSUS-HOST DISEASE
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genetics Institute, Inc., Legal Affairs
: STREET: 87 Cambridgepark Drive
: CITY: Cambridge
: STATE: MA
: COUNTRY: USA
: ZIP: 02140
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/186,529
: FILING DATE:
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: McDanielis, Patricia A.
: REGISTRATION NUMBER: 33,194
```

```
: REFERENCE/DOCKET NUMBER: GI 5225
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-498-8401
: TELEFAX: 617-876-5851
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 987 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: ORIGINAL SOURCE:
: ORGANISM: Homo sapiens
: CELL TYPE: Lymphoblast
: CELL LINE: RPMI 8866
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..987
: US-08-186-529-1

Query Match 4 7%; Score 46; DB 1; Length 987;
Best Local Similarity 100.0%; Pred. No. 1,3e-13;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 647 TTCACAGCTCAGATGAAGTAACATACACGACGCTTCTGATCAG 692
Db 644 TTCACAGCTCAGATGAAGTAACATACACGACGCTTCTGATCAG 689

RESULT 4
US-08-640-386A-1
: Sequence 1, Application US/08640386A
: Patent No. 5756085
: GENERAL INFORMATION:
: APPLICANT: Sykes, Megan
: APPLICANT: Wolf, Stanley F.
: TITLE OF INVENTION: USE OF INTERLEUKIN-12 TO PREVENT
: TITLE OF INVENTION: GRAFT-VERSUS-HOST DISEASE
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genetics Institute, Inc., Legal Affairs
: STREET: 87 Cambridgepark Drive
: CITY: Cambridge
: STATE: MA
: COUNTRY: USA
: ZIP: 02140
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/640,386A
: FILING DATE:
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Brown, Scott A.
: REGISTRATION NUMBER: 32,724
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-498-8224
: TELEFAX: 617-876-5851
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 987 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: ORIGINAL SOURCE:
: ORGANISM: Homo sapiens
: CELL TYPE: Lymphoblast
: CELL LINE: RPMI 8866
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FEATURE:
NAME/KEY: CDS
LOCATION: 1..987
US-08-640-386A-1

Query Match
Best Local Similarity 100.0%; Score 46; DB 1; Length 987;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 647 TTCACAGCTCAAGTATGAAACTACACGAGCCTTCTTCATCAG 692
DB 644 TTCACAGCTCAAGTATGAAACTACACGAGCCTTCTTCATCAG 689

RESULT 5
US-08-848-760B-24
Sequence 24, Application US/08848760B
Patent No. 6248721
GENERAL INFORMATION:
APPLICANT: Chang, Lung-Ji
TITLE OF INVENTION: Animal Model For Evaluation Of Vaccines
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: United States of America
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848,760B
FILING DATE: 25-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/838,702
FILING DATE: 09-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: PACE, DORAN R.
REGISTRATION NUMBER: 38,261
REFERENCE/DOCKET NUMBER: CNG-100C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 987 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-08-848-760B-24
Query Match
Best Local Similarity 100.0%; Score 46; DB 4; Length 987;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 647 TTCACAGCTCAAGTATGAAACTACACGAGCCTTCTTCATCAG 692
DB 644 TTCACAGCTCAAGTATGAAACTACACGAGCCTTCTTCATCAG 689

RESULT 6
US-08-184-009-194
Sequence 194, Application US/08184009
Patent No. 5833975
GENERAL INFORMATION:

APPLICANT: Paoletti, Enzo
APPLICANT: Tartaglia, James
APPLICANT: Cox, William I.
TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
NUMBER OF SEQUENCES: 217
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/184,009
FILING DATE: 19-JAN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEX: 425066CURIMS
INFORMATION FOR SEQ ID NO: 194:
SEQUENCE CHARACTERISTICS:
LENGTH: 1018 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-184-009-194

Query Match
Best Local Similarity 100.0%; Score 46; DB 2; Length 1018;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 647 TTCACAGCTCAAGTATGAAACTACACGAGCCTTCTTCATCAG 692
DB 675 TTCACAGCTCAAGTATGAAACTACACGAGCCTTCTTCATCAG 720

RESULT 7
US-08-458-356-194
Sequence 194, Application US/08458356
Patent No. 5942235
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: Tartaglia, James
APPLICANT: Cox, William I.
TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
NUMBER OF SEQUENCES: 217
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,356
FILING DATE: 02-JUN-1995
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/184,009
: FILING DATE: 19-JAN-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Frommer, William S.
: REGISTRATION NUMBER: 25,506
: REFERENCE/DOCKET NUMBER: 454310-2530
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 840-3333
: TELEFAX: (212) 840-0712
: TELEX: 425066CURTMS
: INFORMATION FOR SEQ ID NO: 194:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1018 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: US-08-458-194

Query Match 4.7%; Score 46; DB 2; Length 1018;
Best Local Similarity 100.0%; Pred. No. 1.3e-13;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 647 TTCACAAGCTCAAGTATGAAACATACACGACGACCTTCTTCATCAG 692
|||||
Db 675 TTCACAAGCTCAAGTATGAAACTACACGACGACGACCTTCTTCATCAG 720

RESULT 8
US-08-460-736-194
: Sequence 194, Application US/08460736
: Patent No. 6265189
: GENERAL INFORMATION:
: APPLICANT: Paolelli, Enzo
: APPLICANT: Tartaglia, James
: TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
: NUMBER OF SEQUENCES: 217
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Curtis, Morris & Safford
: STREET: 530 Fifth Avenue
: CITY: New York
: STATE: NY
: COUNTRY: USA
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/460,736
: FILING DATE: 02-JUN-1995
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/184,009
: FILING DATE: 19-JAN-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Frommer, William S.
: REGISTRATION NUMBER: 25,506
: REFERENCE/DOCKET NUMBER: 454310-2530
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 840-3333
: TELEFAX: (212) 840-0712
: TELEX: 425066CURTMS
: INFORMATION FOR SEQ ID NO: 194:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1018 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA

US-08-460-736-194

Query Match 4.7%; Score 46; DB 4; Length 1018;
Best Local Similarity 100.0%; Pred. No. 1.3e-13;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 647 TTCACAAGCTCAAGTATGAAACATACACGACGACCTTCTTCATCAG 692
|||||
Db 675 TTCACAAGCTCAAGTATGAAACTACACGACGACGACCTTCTTCATCAG 720

RESULT 9
US-08-751-767A-3
: Sequence 3, Application US/08751767A
: Patent No. 5994104
: GENERAL INFORMATION:
: APPLICANT: ANDERSON, ROBERT J.
: APPLICANT: GRANT, HUGH
: APPLICANT: MACDONALD, IAN D.
: TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN
: NUMBER OF SEQUENCES: 80
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: NIXON & VANDERHAYE P.C.
: STREET: 1100 NORTH GLEBE ROAD
: CITY: ARLINGTON
: STATE: VA
: COUNTRY: USA
: ZIP: 22201
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/751,767A
: FILING DATE: 08-NOV-1996
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: SADOFF, B.J.
: REGISTRATION NUMBER: 36,663
: REFERENCE/DOCKET NUMBER: 117-221
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 7038164091
: TELEFAX: 7038164100
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1399 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 43..1026
: US-08-751-767A-3

Query Match 4.7%; Score 46; DB 2; Length 1399;
Best Local Similarity 100.0%; Pred. No. 1.3e-13;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 647 TTCACAAGCTCAAGTATGAAACATACACGACGACCTTCTTCATCAG 692
|||||
Db 686 TTCACAAGCTCAAGTATGAAACTACACGACGACGACCTTCTTCATCAG 731

RESULT 10
US-08-751-767A-11
: Sequence 11, Application US/08751767A
: Patent No. 5994104
: GENERAL INFORMATION:
: APPLICANT: ANDERSON, ROBERT J.
: APPLICANT: GRANT, HUGH
: APPLICANT: MACDONALD, IAN D.

TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHUYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,767A
FILING DATE: 08-NOV-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 117-221
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164091
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1560 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1557
US-08-751-767A-11

Query Match 4.7%; Score 46; DB 2; Length 1560;
Best Local Similarity 100.0%; Pred. No. 1.3e-13;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

647 TTCACAAGCTCAAGTATGAAACTACACGAGCGCTTCTTCATCAG 692
|||||
581 TTCACAAGCTCAAGTATGAAACTACACGAGCGCTTCTTCATCAG 626

RESULT 11
US-08-751-767A-9
Sequence 9, Application US/08751767A
Patent No. 5994104
GENERAL INFORMATION:
APPLICANT: ANDERSON, ROBERT J.
APPLICANT: GRANT, HUGH
APPLICANT: MACDONALD, IAN D.
TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHUYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,767A
FILING DATE: 08-NOV-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:

NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 117-221
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164091
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1623 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1620
US-08-751-767A-9

Query Match 4.7%; Score 46; DB 2; Length 1623;
Best Local Similarity 100.0%; Pred. No. 1.3e-13;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

647 TTCACAAGCTCAAGTATGAAACTACACGAGCGCTTCTTCATCAG 692
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644 TTCACAAGCTCAAGTATGAAACTACACGAGCGCTTCTTCATCAG 689

RESULT 12
US-09-310-842-4
Sequence 4, Application US/09310842A
Patent No. 6451593
GENERAL INFORMATION:
APPLICANT: Junghans, Claas
TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Ge
FILE REFERENCE: XI 597/99
CURRENT APPLICATION NUMBER: US/09/310,842A
CURRENT FILING DATE: 1999-05-12
EARLIER APPLICATION NUMBER: DE 196 48 625.4
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver.2.1
SEQ ID NO 4
LENGTH: 1870
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: gene
LOCATION: (1)..(1870)
OTHER INFORMATION: Interleukin-12 (IL-12, p40-subunit); Oligo DNA Dumbbell
FEATURE:
NAME/KEY: misc_binding
LOCATION: (1)..(2)
OTHER INFORMATION: Intramolecular binding site; the T-nucleotides at position 1 t
FEATURE:
NAME/KEY: misc_binding
LOCATION: (1869)..(1870)
OTHER INFORMATION: Intramolecular binding site; the T-nucleotides at position 186
OTHER INFORMATION: to 1870 can be modified with amino or caroxy features
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Strandedness: both; nucle
US-09-310-842-4

Query Match 4.7%; Score 46; DB 4; Length 1870;
Best Local Similarity 100.0%; Pred. No. 1.3e-13;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

647 TTCACAAGCTCAAGTATGAAACTACACGAGCGCTTCTTCATCAG 692
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1276 TTCACAAGCTCAAGTATGAAACTACACGAGCGCTTCTTCATCAG 1321

RESULT 13
US-09-851-062-3
Sequence 3, Application US/09851062
Patent No. 6448081
GENERAL INFORMATION:
APPLICANT: Brenda F. Baker
APPLICANT: Susan M. Freiler
TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
FILE REFERENCE: RTS-0247
CURRENT APPLICATION NUMBER: US/09/851,062
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 3
LENGTH: 2318
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (14)...(1000)
US-09-851-062-3

Query Match
Best Local Similarity 4.7%; Score 46; DB 4; Length 2318;
100.0%; Pred. No. 1.3e-13;
Matches 46: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 647 TTCACAGCTCAAGTATGAAACTACACCAGCAGCTTCTTCATCAG 692
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Db 657 TTCACAGCTCAAGTATGAAACTACACCAGCAGCTTCTTCATCAG 702

RESULT 14
US-08-265-087-1
Sequence 1, Application US/08265087
Patent No. 5571515
GENERAL INFORMATION:
APPLICANT: Scott, Phillip
APPLICANT: Trinchieri, Giorgio
TITLE OF INVENTION: Compositions and Methods for Use of
TITLE OF INVENTION: IL-12 as an Adjuvant
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Center, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/265,087
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/229,282
FILING DATE: 18-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST51AUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2362 base pairs
type: nucleic acid
STRANDEDNESS: double

TOPOLOGY: unknown
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 33..1016
US-08-265-087-1

Query Match
Best Local Similarity 4.7%; Score 46; DB 1; Length 2362;
100.0%; Pred. No. 1.3e-13;
Matches 46: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 647 TTCACAGCTCAAGTATGAAACTACACCAGCAGCTTCTTCATCAG 692
|||||
Db 676 TTCACAGCTCAAGTATGAAACTACACCAGCAGCTTCTTCATCAG 721

RESULT 15
US-08-621-493-1
Sequence 1, Application US/08621493
Patent No. 5723127
GENERAL INFORMATION:
APPLICANT: Scott, Phillip
APPLICANT: Trinchieri, Giorgio
TITLE OF INVENTION: Compositions and Methods for Use of
TITLE OF INVENTION: IL-12 as an Adjuvant
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Center, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,493
FILING DATE: 25-MAR-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/265,087
FILING DATE: 17-JUN-1994
APPLICATION NUMBER: US 08/229,282
FILING DATE: 18-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST51AUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2362 base pairs
type: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 33..1016
US-08-621-493-1

Query Match
Best Local Similarity 4.7%; Score 46; DB 1; Length 2362;
100.0%; Pred. No. 1.3e-13;
Matches 46: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 647 TTCACAGCTCAAGTATGAAACTACACCAGCAGCTTCTTCATCAG 692
|||||
Db 676 TTCACAGCTCAAGTATGAAACTACACCAGCAGCTTCTTCATCAG 721

Thu Jul 17 12:12:44 2003

us-09-917-265-58.oli.mli

Page 8

Search completed: July 16, 2003, 19:43:43
Job time : 52.4162 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 13:21:13 ; Search time 186.875 Seconds
(without alignments)
8432.179 Million cell updates/sec

Title: US-09-917-265-58

Perfect score: 987

Sequence: 1 atgacccctcgcagcttgcgt.....ggcgatctgtcgtcagct 987

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Gapop 60.0 , Gapext 60.0

Searched: 1114047 seqs, 798260406 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2228094

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Published_Applications_NA:*
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12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------------------|-------------------|
| 1 | 987 | 100.0 | 987 | 10 US-09-917-265-58 | Sequence 58, Appl |
| 2 | 987 | 100.0 | 987 | 10 US-09-917-265-60 | Sequence 60, Appl |
| 3 | 987 | 100.0 | 1599 | 10 US-09-917-265-61 | Sequence 61, Appl |
| 4 | 987 | 100.0 | 1599 | 10 US-09-917-265-63 | Sequence 63, Appl |
| 5 | 974 | 98.7 | 2267 | 10 US-09-917-265-107 | Sequence 107, App |
| 6 | 974 | 98.7 | 2267 | 10 US-09-917-265-109 | Sequence 109, App |
| 7 | 921 | 93.3 | 1533 | 10 US-09-917-265-68 | Sequence 68, Appl |
| 8 | 921 | 93.3 | 1533 | 10 US-09-917-265-68 | Sequence 68, Appl |
| 9 | 914 | 92.6 | 921 | 10 US-09-917-265-52 | Sequence 52, Appl |
| 10 | 914 | 92.6 | 921 | 10 US-09-917-265-54 | Sequence 54, Appl |
| 11 | 66 | 6.7 | 921 | 10 US-09-917-265-26 | Sequence 26, Appl |
| 12 | 66 | 6.7 | 921 | 10 US-09-917-265-28 | Sequence 28, Appl |
| 13 | 66 | 6.7 | 921 | 10 US-10-079-616-6 | Sequence 6, Appl |
| 14 | 66 | 6.7 | 985 | 10 US-09-917-265-55 | Sequence 55, Appl |
| 15 | 66 | 6.7 | 985 | 10 US-09-917-265-29 | Sequence 57, Appl |
| 16 | 66 | 6.7 | 987 | 10 US-09-917-265-29 | Sequence 29, Appl |
| 17 | 66 | 6.7 | 987 | 10 US-09-917-265-31 | Sequence 31, Appl |
| 18 | 66 | 6.7 | 1533 | 10 US-09-917-265-43 | Sequence 43, Appl |
| 19 | 66 | 6.7 | 1533 | 10 US-09-917-265-45 | Sequence 45, Appl |

| | | | | | |
|----|----|-----|------|----------------------|-------------------|
| 20 | 66 | 6.7 | 1599 | 10 US-09-917-265-38 | Sequence 38, Appl |
| 21 | 66 | 6.7 | 1599 | 10 US-09-917-265-40 | Sequence 40, Appl |
| 22 | 66 | 6.7 | 2193 | 12 US-10-079-616-5 | Sequence 5, Appl |
| 23 | 63 | 6.4 | 921 | 12 US-10-079-616-7 | Sequence 7, Appl |
| 24 | 46 | 4.7 | 987 | 9 US-09-826-025-24 | Sequence 24, Appl |
| 25 | 46 | 4.7 | 987 | 10 US-09-754-014-2 | Sequence 2, Appl |
| 26 | 46 | 4.7 | 987 | 10 US-09-836-866-2 | Sequence 2, Appl |
| 27 | 46 | 4.7 | 1870 | 9 US-10-1228-811-4 | Sequence 4, Appl |
| 28 | 46 | 4.7 | 2318 | 9 US-10-172-399-7 | Sequence 7, Appl |
| 29 | 46 | 4.7 | 2362 | 10 US-09-924-703-3 | Sequence 3, Appl |
| 30 | 46 | 4.7 | 8578 | 10 US-09-828-825-1 | Sequence 1, Appl |
| 31 | 46 | 4.7 | 8578 | 10 US-09-828-825-3 | Sequence 3, Appl |
| 32 | 46 | 4.7 | 8608 | 10 US-09-828-825-7 | Sequence 7, Appl |
| 33 | 46 | 4.7 | 8623 | 10 US-09-828-825-5 | Sequence 5, Appl |
| 34 | 46 | 4.7 | 8629 | 10 US-09-828-825-15 | Sequence 15, Appl |
| 35 | 46 | 4.7 | 8638 | 10 US-09-828-825-9 | Sequence 9, Appl |
| 36 | 46 | 4.7 | 8644 | 10 US-09-828-825-13 | Sequence 13, Appl |
| 37 | 46 | 4.7 | 8659 | 10 US-09-828-825-11 | Sequence 11, Appl |
| 38 | 27 | 2.7 | 37 | 10 US-09-917-265-99 | Sequence 99, Appl |
| 39 | 24 | 2.4 | 987 | 10 US-09-754-014-3 | Sequence 3, Appl |
| 40 | 24 | 2.4 | 987 | 10 US-09-917-265-97 | Sequence 97, Appl |
| 41 | 22 | 2.2 | 22 | 10 US-09-917-265-100 | Sequence 100, App |
| 42 | 22 | 2.2 | 29 | 10 US-10-079-616-14 | Sequence 14, Appl |
| 43 | 21 | 2.1 | 44 | 12 US-10-172-399-3 | Sequence 3, Appl |
| 44 | 20 | 2.0 | 1840 | 9 US-09-917-265-98 | Sequence 98, Appl |
| 45 | 19 | 1.9 | 19 | 10 US-09-917-265-98 | Sequence 98, Appl |

ALIGNMENTS

```
RESULT 1
US-09-917-265-58
Sequence 58, Application US/09917265
Patent No. US20020052030A1
GENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/09/917,265
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 109
SOFTWARE: PatencIn version 3.1
SEQ ID NO 58
LENGTH: 987
TYPE: DNA
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(987)
OTHER INFORMATION:
US-09-917-265-58

Query Match      100.0%: Score 987; DB 10; Length 987;
Best Local Similarity 100.0%: Pred. No. 0;
Matches 987: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGCACCCCTACACACTTGGTCATCTCCGCTGTTTCCCTGCGCTCCGCC 60
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1 ATGCACCCCTACACACTTGGTCATCTCCGCTGTTTCCCTGCGCTCCGCC 60
1 ATGCACCCCTACACACTTGGTCATCTCCGCTGTTTCCCTGCGCTCCGCC 60
61 ATGCACATATGGAAGTGGTCTCTACCTGCTTATGTTGAGAGTGGAGCTGAT 120
|||||
61 ATGCACATATGGAAGTGGTCTCTACCTGCTTATGTTGAGAGTGGAGCTGAT 120
61 ATGCACATATGGAAGTGGTCTCTACCTGCTTATGTTGAGAGTGGAGCTGAT 120
61 ATGCACATATGGAAGTGGTCTCTACCTGCTTATGTTGAGAGTGGAGCTGAT 120
121 GCCCGGAGGAATGGTGTCTCTACCTGCTTATGTTGAGAGTGGAGCTGAT 180
|||||
121 GCCCGGAGGAATGGTGTCTCTACCTGCTTATGTTGAGAGTGGAGCTGAT 180
121 GCCCGGAGGAATGGTGTCTCTACCTGCTTATGTTGAGAGTGGAGCTGAT 180
181 ACCTCAGCGCAGCAGTGAAGTCTAGTCTGTGTAACACTGACCATCAAGTCAA 240
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|||||
Db 181 ACCTCAGCGACAGAGTGAAGTCTTCTAGTCTGTGTAATACTTGACCATCCAAAGTCAA 240
Qy 241 GAATTTGAGATGCTGGCAGTATACCTGCCATTAAGGAGCAAGGTTCTGAGCCGCTCA 300
Db 241 GAATTTGAGATGCTGGCAGTATACCTGCCATTAAGGAGCAAGGTTCTGAGCCGCTCA 300
Qy 301 CTCCTGTTGATTCACAAAAAAGAGATGGAATTTGGTCCACTGATATCTTAAAGAACAG 360
Db 301 CTCCTGTTGATTCACAAAAAAGAGATGGAATTTGGTCCACTGATATCTTAAAGAACAG 360
Qy 361 AAGAAATCCAAAAATTAAGATCTTCTGAAATGTGAGGCAAGATTAATCTGAGAGTTTC 420
Db 361 AAGAAATCCAAAAATTAAGATCTTCTGAAATGTGAGGCAAGATTAATCTGAGAGTTTC 420
Qy 421 ACATGCTGTTGGTGTACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
Db 421 ACATGCTGTTGGTGTACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
Qy 481 GGGTCTCTGTACCCCCAAGGGGTGACATGTGGAGCAGTACACTTTTCAGAGAGAGGTC 540
Db 481 GGGTCTCTGTACCCCCAAGGGGTGACATGTGGAGCAGTACACTTTTCAGAGAGAGGTC 540
Qy 541 AGAGTGGACAAAGGGATTAAGAAGTACAGTGGAGTGTGAGAGAGAGAGAGAGAGGTC 600
Db 541 AGAGTGGACAAAGGGATTAAGAAGTACAGTGGAGTGTGAGAGAGAGAGAGAGAGGTC 600
Qy 601 CCTCTGCGGAGAGAGAGCTTACCATCGAGTGTGAGTGTGATTCATTCACAGCTCAAG 660
Db 601 CCTCTGCGGAGAGAGAGCTTACCATCGAGTGTGAGTGTGATTCATTCACAGCTCAAG 660
Qy 661 TATGAAAACTACACAGAGAGCTTCTTCACTGAGACATCATCAAAACAGACCCACCA 720
Db 661 TATGAAAACTACACAGAGAGCTTCTTCACTGAGACATCATCAAAACAGACCCACCA 720
Qy 721 AACCTGAGCTGAAGAGCTTGAATAATCTCGGACAGTGGAGGTGAGGTGGGAATPACCC 780
Db 721 AACCTGAGCTGAAGAGCTTGAATAATCTCGGACAGTGGAGGTGAGGTGGGAATPACCC 780
Qy 781 GACACCTGGAGACACCCCATCTTCTTCTCCCTGACATTTTGCATACAGGCCAGAGGC 840
Db 781 GACACCTGGAGACACCCCATCTTCTTCTCCCTGACATTTTGCATACAGGCCAGAGGC 840
Qy 841 AAGAAACATAGAAAAAAGATAGACTTGTGCTGGAGCAAGACCTCAGCCAAAGTGTG 900
Db 841 AAGAAACATAGAAAAAAGATAGACTTGTGCTGGAGCAAGACCTCAGCCAAAGTGTG 900
Qy 901 TGCCACAAGATGCGCAAGATCCGGGTGCAAGCCGAGACCGCTACTATAGTTCAATCCGTG 960
Db 901 TGCCACAAGATGCGCAAGATCCGGGTGCAAGCCGAGACCGCTACTATAGTTCAATCCGTG 960
Qy 961 AGCGACTGGGCATCTGTGTCATGACGT 987
Db 961 AGCGACTGGGCATCTGTGTCATGACGT 987

RESULT 2

US-09-917-265-60/c
; Sequence 60, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Borouhns, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 987

TYPE: DNA
; ORGANISM: Canis familiaris
US-09-917-265-60
Query Match 100.0%; Score 987; DB 10; Length 987;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 987; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGCACCTCAGCAGTGGTGCATCTCTGTTTCCCTGTTTGGTGGGTCCTCCCTC 60
Db 987 ATGCACCTCAGCAGTGGTGCATCTCTGTTTCCCTGTTTGGTGGGTCCTCCCTC 928
Qy 61 ATGGCCATATGGAGACTGGAGAAAGATGTTATGTTGTAAAGTTGACCTGACCTGAT 120
Db 927 ATGGCCATATGGAGACTGGAGAAAGATGTTATGTTGTAAAGTTGACCTGACCTGAT 868
Qy 121 GCCCCGGAGAAATGCGTGTCTACCTGCCATACCCCTGAAGAAGTGAATCAGCTTG 180
Db 867 GCCCCGGAGAAATGCGTGTCTACCTGCCATACCCCTGAAGAAGTGAATCAGCTTG 808
Qy 181 ACCTCAGCGAGAGCAGTGAAGTCCATAGTTTGTGTAATACTGACCATCAAGTCAA 240
Db 807 ACCTCAGCGAGAGCAGTGAAGTCCATAGTTTGTGTAATACTGACCATCAAGTCAA 748
Qy 241 GAATTTGAGATGCTGGCCAGTATACCTGCCATTAAGGAGCAAGGTTCTGAGCCGCTCA 300
Db 747 GAATTTGAGATGCTGGCCAGTATACCTGCCATTAAGGAGCAAGGTTCTGAGCCGCTCA 688
Qy 301 CTCCTGTTGATTCACAAAAAAGAGATGGAATTTGGTCCACTGATTAAGAAGAACAG 360
Db 687 CTCCTGTTGATTCACAAAAAAGAGATGGAATTTGGTCCACTGATTAAGAAGAACAG 628
Qy 361 AAGAAATCCAAAAATTAAGATCTTCTGAAATGTGAGGCAAAAGATTAATCTGAGAGTTTC 420
Db 627 AAGAAATCCAAAAATTAAGATCTTCTGAAATGTGAGGCAAAAGATTAATCTGAGAGTTTC 568
Qy 421 ACATGCTGTTGGTGTGAGAGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
Db 567 ACATGCTGTTGGTGTGAGAGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 508
Qy 481 GGGTCTCTGTACCCCCAAGGGGTGACATGTGGAGCAGTGTGACAGTGTGAGAGAGGTC 540
Db 507 GGGTCTCTGTACCCCCAAGGGGTGACATGTGGAGCAGTGTGACAGTGTGAGAGAGGTC 448
Qy 541 AGAGTGAACAACAGGATTAAGAAGTACACAGTGTGAGTGTGAGAGAGGTCAGTCCCTGC 600
Db 447 AGAGTGAACAACAGGATTAAGAAGTACACAGTGTGAGTGTGAGAGAGGTCAGTCCCTGC 388
Qy 601 CCTCTGCGGAGAGAGAGCTTACCATCGAGTGTGAGTGTGATTCATTCACAGCTCAAG 660
Db 387 CCTCTGCGGAGAGAGAGCTTACCATCGAGTGTGAGTGTGATTCATTCACAGCTCAAG 328
Qy 661 TATGAAACATAGAAAAAAGATAGACTTGTGCTGGAGCAAGACCTCAGCCAAAGTGTG 720
Db 327 TATGAAACATAGAAAAAAGATAGACTTGTGCTGGAGCAAGACCTCAGCCAAAGTGTG 268
Qy 721 AACCTGAGCTGAAGAGCTTGAATAATCTCGGACAGTGGAGGTGAGGTGGGAATPACCC 780
Db 267 AACCTGAGCTGAAGAGCTTGAATAATCTCGGACAGTGGAGGTGAGGTGGGAATPACCC 208
Qy 781 GACACCTGGAGACACCCCATCTTCTTCTCCCTGACATTTTGCATACAGGCCAGAGGC 840
Db 207 GACACCTGGAGACACCCCATCTTCTTCTCCCTGACATTTTGCATACAGGCCAGAGGC 148
Qy 841 AAGAAACATAGAAAAAAGATAGACTTGTGCTGGAGCAAGACCTCAGCCAAAGTGTG 900
Db 147 AAGAAACATAGAAAAAAGATAGACTTGTGCTGGAGCAAGACCTCAGCCAAAGTGTG 88
Qy 901 TGCCACAAGATGCGCAAGATCCGGGTGCAAGCCGAGACCGCTACTATAGTTCAATCCGTG 960
Db 87 TGCCACAAGATGCGCAAGATCCGGGTGCAAGCCGAGACCGCTACTATAGTTCAATCCGTG 28
Qy 961 AGCGACTGGGCATCTGTGTCATGACGT 987

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Db      27  AGCCACTGGCATCTGTGTATGCAGT 1
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RESULT 3
US-09-917-265-61
: Sequence 61, Application US/09917265
: Patent No. US20020052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: APPLICANT: Boroughs, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
: FILE REFERENCE: IM-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: PRIOR FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 61
: LENGTH: 1599
: TYPE: DNA
: ORGANISM: Canis familiaris
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(1599)
: OTHER INFORMATION:
US-09-917-265-61

Query Match      100.0%; Score 987; DB 10; Length 1599;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 987; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ATGCACCTCAGCGATTGGTCATCTCTGGTTTCCCTCGTTTGGCTGCCTCTCCCTC 60
Db      1  ATGCACCCCTCAGCGATTGGTCATCTCTGGTTTCCCTCGTTTGGCTGCCTCTCCCTC 60
QY      61  ATGCCCATATGGGAACTGGAGAAAGATGTTATGTTAGTGGAGTGGACCTGCCACCTGAT 120
Db      61  ATGGCCCATATGGGAACTGGAGAAAGATGTTATGTTAGTGGAGTGGACCTGCCATGAT 120
QY      121  GCCCCCGGAGAAATGTTGTTCTCCTACCTGCCATACCCCTGAAGAAGATGACATCTTGG 180
Db      121  GCCCCCGGAGAAATGTTGTTCTCCTACCTGCCATACCCCTGAAGAAGATGACATCTTGG 180
QY      181  ACCTCAGCCGAGACAGTGAAGTCTTAGTCTGTCTGTAATACTCTGACCATCCAAAGTCAA 240
Db      181  ACCTCAGCCGAGACAGTGAAGTCTTAGTCTGTCTGTAATACTCTGACCATCCAAAGTCAA 240
QY      241  GAATTTGGAGATGCTGGCCAGTATACCTGGCCATTAAGAGGCAAGGTTCTGAGCGGCTCA 300
Db      241  GAATTTGGAGATGCTGGCCAGTATACCTGGCCATTAAGAGGCAAGGTTCTGAGCGGCTCA 300
QY      301  CTCCTGTTGATTACCAAAAAAGAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
Db      301  CTCCTGTTGATTACCAAAAAAGAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
QY      361  AANAATATCCAAAAATAGATCTTCTGAAATGTAGAGCAAAAGAAATATTCTGAGCGTTTC 420
Db      361  AANAATATCCAAAAATAGATCTTCTGAAATGTAGAGCAAAAGAAATATTCTGAGCGTTTC 420
QY      421  ACATGCTGTGGCTGAGCGCAATCAGTATTGGAATTCAGTGTCAAAAGTAGCAGA 480
Db      421  ACATGCTGTGGCTGAGCGCAATCAGTATTGGAATTCAGTGTCAAAAGTAGCAGA 480
QY      481  GGCCTTCTGACCCCCCAAGGGGTGACATGTGGACAGTACACATTTCAGCAGAGAGGCTC 540
Db      481  GGCCTTCTGACCCCCCAAGGGGTGACATGTGGACAGTACACATTTCAGCAGAGAGGCTC 540
QY      541  AGAGTGACAAACAGGATTAAGAAGTACACAGTGTGAGAGGAGGCGGCGCTGC 600
Db      541  AGAGTGACAAACAGGATTAAGAAGTACACAGTGTGAGAGGAGGCGGCGCTGC 600
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QY      601  CCTCTGCCGAGAGAGCCTACCCATCGAGGTCGTGTGATGCTATTACAAAGCTCAAG 660
Db      601  CCTCTGCCGAGAGAGCCTACCCATCGAGGTCGTGTGATGCTATTACAAAGCTCAAG 660
QY      661  TATGAAAATCTACACGAGCAGCTTCTTCATCAGAGACATCATCAAAACGAGCCACCCACA 720
Db      661  TATGAAAATCTACACGAGCAGCTTCTTCATCAGAGACATCATCAAAACGAGCCACCCACA 720
QY      721  AACCTGCAGCTGAAGCCATTGAAAATTCTGCGACAGTGGAGGTGACTGGGAATACCCC 780
Db      721  AACCTGCAGCTGAAGCCATTGAAAATTCTGCGACAGTGGAGGTGACTGGGAATACCCC 780
QY      781  GACACCTGAGACACCCCATTTCTACTTTCCTCGATTTCCGATTTTGGATCAGGCCAGGGC 840
Db      781  GACACCTGAGACACCCCATTTCTACTTTCCTCGATTTTCCGATTTTGGATCAGGCCAGGGC 840
QY      841  AAGAACATAGAGAAAAGAAAGATAGACTGTGCTGTGACAAGACCTCAGCCAAAGTCTGTG 900
Db      841  AAGAACATAGAGAAAAGAAAGATAGACTGTGCTGTGACAAGACCTCAGCCAAAGTCTGTG 900
QY      901  TGCCACAAGATGCCAGATCCGCGTGTGCAACCCGAGACCCGCTACTATATGTTCAATCCTGG 960
Db      901  TGCCACAAGATGCCAGATCCGCGTGTGCAACCCGAGACCCGCTACTATATGTTCAATCCTGG 960
QY      961  AGCGACTGGCATCTGTGTCAATGCAGT 987
Db      961  AGCGACTGGCATCTGTGTCAATGCAGT 987

RESULT 4
US-09-917-265-63/c
: Sequence 63, Application US/09917265
: Patent No. US20020052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: APPLICANT: Boroughs, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
: FILE REFERENCE: IM-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: PRIOR FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 63
: LENGTH: 1599
: TYPE: DNA
: ORGANISM: Canis familiaris
US-09-917-265-63

Query Match      100.0%; Score 987; DB 10; Length 1599;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 987; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ATGCACCTCAGCGATTGGTCATCTCTGGTTTCCCTCGTTTGGCTGCCTCTCCCTC 60
Db      1599  ATGCACCTCAGCGATTGGTCATCTCTGGTTTCCCTCGTTTGGCTGCCTCTCCCTC 1540
QY      61  ATGCCCATATGGAAGTGGAGAAAGATGTTATGTTAGAGTTGAGTGGACCTGACCTGAT 120
Db      1539  ATGCCCATATGGAAGTGGAGAAAGATGTTATGTTAGAGTTGAGTGGACCTGACCTGAT 1480
QY      121  GCCCCCGGAGAAATGTTGTTCTCCTACCTGCCATACCCCTGAAGAAGATGACATCTTGG 180
Db      1479  GCCCCCGGAGAAATGTTGTTCTCCTACCTGCCATACCCCTGAAGAAGATGACATCTTGG 1420
QY      181  ACCTCAGCGAGACAGTGAAGTCTTAGTCTGTGTAATACTCTGACCATCCAAAGTCAA 240
Db      1419  ACCTCAGCGAGACAGTGAAGTCTTAGTCTGTGTAATACTCTGACCATCCAAAGTCAA 1360
QY      241  GAATTTGGAGATGCTGGCCAGTATACCTGGCCATTAAGAGGCAAGGTTCTGAGCGGCTCA 300
Db      1359  GAATTTGGAGATGCTGGCCAGTATACCTGGCCATTAAGAGGCAAGGTTCTGAGCGGCTCA 1300
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| | | | |
|----|------|---|------|
| Oy | 301 | CTCCGTTGATTCACAAAAAAGAGATGGAAATTTGGTCCACTGATATCTTAAAGAACAG | 360 |
| Db | 1299 | CTCCGTTGATTCACAAAAAAGAGATGGAAATTTGGTCCACTGATATCTTAAAGAACAG | 1240 |
| Oy | 361 | AAAGATCCAAAAATAGATCTTTCTGAAATGTGAGGCCAAGAAATTAATTCAGAGTTTC | 420 |
| Db | 1239 | AAAGATCCAAAAATAGATCTTTCTGAAATGTGAGGCCAAGAAATTAATTCAGAGTTTC | 1180 |
| Oy | 421 | ACATCGTGTGGCTGAGGGCAATCATGCTATTTGAATTCAGTGCATAAAGTAAGCAGA | 480 |
| Db | 1179 | ACATCGTGTGGCTGAGGGCAATCATGCTATTTGAATTCAGTGCATAAAGTAAGCAGA | 1120 |
| Oy | 481 | GACTTCTTGAACCCCAAGGGGTGCATAGTGGAGCAGTGAACACTTTCAGCAGAGAGGCTC | 540 |
| Db | 1119 | GACTTCTTGAACCCCAAGGGGTGCATAGTGGAGCAGTGAACACTTTCAGCAGAGAGGCTC | 1060 |
| Oy | 541 | AGAGTGGCAACACAGGATTTATAGAACATACACATGGAGTGTCAAGAGGCACTGTCC | 600 |
| Db | 1059 | AGAGTGGCAACACAGGATTTATAGAACATACACAGTGGAGTGTCAAGAGGCACTGTCC | 1000 |
| Oy | 601 | CCCTGTGCGCAGAGAGCCTACCCATCAGGTGCGGGTGGATTCATTCACAAGCTCAAG | 660 |
| Db | 999 | CCCTGTGCGCAGAGAGCCTACCCATCAGGTGCGGGTGGATTCATTCACAAGCTCAAG | 940 |
| Oy | 661 | TATGAAAACCTACACCAGACGCTTTCTTATCAAGACATCAATCAACACAGACCACACA | 720 |
| Db | 939 | TATGAAAACCTACACCAGACGCTTTCTTATCAAGACATCAATCAACACAGACCACACA | 880 |
| Oy | 721 | AACCTGCAGCTGAAGCCATTTGAAAAAATCTCGGCGCGTGGAGGTGACGTGGGAATACCC | 780 |
| Db | 879 | AACCTGCAGCTGAAGCCATTTGAAAAAATCTCGGCGCGTGGAGGTGACGTGGGAATACCC | 820 |
| Oy | 781 | GACACCTGAGCACCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCACAGGC | 840 |
| Db | 819 | GACACCTGAGCACCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCACAGGC | 760 |
| Oy | 841 | AAGAACATTAAGAAAAAAGAAAGATTAAGTGTGCGTGGACCAAGACTCCGCAAGGTGCTG | 900 |
| Db | 759 | AAGAACATTAAGAAAAAAGAAAGATTAAGTGTGCGTGGACCAAGACTCCGCAAGGTGCTG | 700 |
| Oy | 901 | TGCCACAAGATGGCCAAAGATCCGGGTGCACACCCGAGACCGCTACTATAGTTCACTCTGG | 960 |
| Db | 699 | TGCCACAAGATGGCCAAAGATCCGGGTGCACACCCGAGACCGCTACTATAGTTCACTCTGG | 640 |
| Oy | 961 | AGCGACTGTGGCATCTGTCTCATGCACT | 987 |
| Db | 639 | AGCGACTGTGGCATCTGTCTCATGCACT | 613 |

RESULT 5

```

US-09-917-265-107
: Sequence 107, Application US/09917265
: Patent No. US20020052030A1
:
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: APPLICANT: Boroughs, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
: FILE REFERENCE: 1W-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: CURRENT FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: PRIOR FILING DATE: 2000-08-04
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 107
: LENGTH: 2267
: TYPE: DNA
: ORGANISM: Canis familiaris
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (154)..(1140)
: OTHER INFORMATION:
:

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US-09-917-265-107

| | | | | |
|-----------------------|-----------------|---------------|-----------|--------------|
| Query Match | 98.7% | Score 974; | DB 10; | Length 2267; |
| Best Local Similarity | 100.0% | Pred. No. 0; | | |
| Matches 974; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |

| | | | |
|----|------|--|------|
| OY | 160 | CCTCAGCAGTGGTGCATCTCCCGTGGTTTCCCGTGGTTTGGTGGGGCTCCGCCCTATGGCC | 66 |
| Db | 160 | CCTCAGCAGTGGTGCATCTCCCGTGGTTTCCCGTGGTTTGGTGGGGCTCCGCCCTATGGCC | 219 |
| OY | 67 | ATATGGGAACTGGGAAAGATGTTATGTGTAGAGTTGGACTGGCACCCCTGATGCCCC | 126 |
| Db | 220 | ATATGGGAACTGGGAAAGATGTTATGTGTAGAGTTGGAGTGGCACCCCTGATGCCCC | 279 |
| OY | 127 | GGAGAAATGGTGGTCTCACCCTGGCATACCCCTGAGAGATGACATCACTTGGACCTCA | 186 |
| Db | 280 | GGAGAAATGGTGGTCTCACCCTGGCATACCCCTGAGAGATGACATCACTTGGACCTCA | 339 |
| OY | 187 | GGCGAGAGCACTGAAGTCTTAGGTTCTGTGTTAAACTCTGACCATTCGAAGTCAAGAAATT | 246 |
| Db | 340 | GGCGAGAGCACTGAAGTCTTAGGTTCTGTGTTAAACTCTGACCATTCGAAGTCAAGAAATT | 399 |
| OY | 247 | GGAGATGGTGGCCAGTATACCTGGCATTAAGAGAGGACAGTGTCTGAGCGGTCACTCTG | 306 |
| Db | 400 | GGAGATGGTGGCCAGTATACCTGGCATTAAGAGAGGACAGTGTCTGAGCGGTCACTCTG | 459 |
| OY | 307 | TTGATTCCAAAAAAAGATGGAATTTGGTCTGCTGATATCTTAAAGAACACAGAAAGA | 366 |
| Db | 460 | TTGATTCCAAAAAAAGATGGAATTTGGTCTGCTGATATCTTAAAGAACACAGAAAGA | 519 |
| OY | 367 | TCCAAAATAGATCTTCTGAAATGTGAGCCAAAGAAATTTCTGACGTTGCATATGC | 426 |
| Db | 520 | TCCAAAATAGATCTTCTGAAATGTGAGCCAAAGAAATTTCTGACGTTGCATATGC | 579 |
| OY | 427 | TGTGTGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGACAGAGCTTC | 486 |
| Db | 580 | TGTGTGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGACAGAGCTTC | 639 |
| OY | 487 | TCTGACCCCCAAGGGGTGACATGTGGAGCACTGACACTTATAGCAGAGAGGGTCAAGATG | 546 |
| Db | 640 | TCTGACCCCCAAGGGGTGACATGTGGAGCACTGACACTTATAGCAGAGAGGGTCAAGATG | 699 |
| OY | 547 | GACAAACAGGATTTATAGAGTATACACAGTGTGATGATGATGAGAGGGCATGTGCCCTCTCT | 606 |
| Db | 700 | GACAAACAGGATTTATAGAGTATACACAGTGTGATGATGATGAGAGGGCATGTGCCCTCTCT | 759 |
| OY | 607 | GCCGAGGAGACCTATACCCTATGAGGTGGTGGATGTATTTCCAACTCAAGTATATA | 666 |
| Db | 760 | GCCGAGGAGACCTATACCCTATGAGGTGGTGGATGTATTTCCAACTCAAGTATATA | 819 |
| OY | 667 | AAGTACACAGACCTTCTTCATCAGACATCATCAACACAGACCCACCCACAACCTG | 726 |
| Db | 820 | AAGTACACAGACCTTCTTCATCAGACATCATCAACACAGACCCACCCACAACCTG | 879 |
| OY | 727 | CAGCTGAAGCAATTTGAAAAATTTCTCGGACGTGGAGGTCACTGTGGAAATTACCCGACAC | 786 |
| Db | 880 | CAGCTGAAGCAATTTGAAAAATTTCTCGGACGTGGAGGTCACTGTGGAAATTACCCGACAC | 939 |
| OY | 787 | TGAGACACCCACATCTCTACTCTCTCCCTGACATTTTGCATACAGAGCCACAGGCAAGAC | 846 |
| Db | 940 | TGAGACACCCACATCTCTACTCTCTCCCTGACATTTTGCATACAGAGCCACAGGCAAGAC | 999 |
| OY | 847 | AATGAGAAAAAAGAAATAGACTGTGGTGGACAAAGCTCAAGCAAGTGTGTGGCAC | 906 |
| Db | 1000 | AATGAGAAAAAAGAAATAGACTGTGGTGGACAAAGCTCAAGCAAGTGTGTGGCAC | 1055 |
| OY | 907 | AAGATGCGCAAGATCCGGCTGCAAGCCCGAAGCCGCTACTATAGTTCACTCTGAGAGCAC | 966 |
| Db | 1060 | AAGATGCGCAAGATCCGGCTGCAAGCCCGAAGCCGCTACTATAGTTCACTCTGAGAGCAC | 1119 |
| OY | 967 | TGGCATCTGTGTC 980 | |
| Db | 1120 | TGGCATCTGTGTC 1133 | |

RESULT 6
US-09-917-265-109/c
: Sequence 109, Application US/09917265
: Patent No. US20020052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Raman S.
: APPLICANT: Boroughs, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
: FILE REFERENCE: IM-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: CURRENT FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: PRIOR FILING DATE: 2000-08-04
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 109
: LENGTH: 2267
: TYPE: DNA
: ORGANISM: Canis familiaris
US-09-917-265-109

Query Match 98.7% Score 974 DB 10 Length 2267:

Best Local Similarity 100.0% Pred. No. 0:

Matches 974: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 CCTGACGAGTGGTCATCTCCTGGTTCCCTCGCTTTGCTGGCGTCCCTCATGCGC 66
DB 2108 CCTGACGAGTGGTCATCTCCTGGTTCCCTCGCTTTGCTGGCGTCCCTCATGCGC 2049
OY 67 ATATGGGAAGTGAAGAAAGATGTTATGTTGTAGAGTTGAGCTGGACCCCTGATCCCCC 126
DB 2048 ATATGGGAAGTGAAGAAAGATGTTATGTTGTAGAGTTGAGCTGGACCCCTGATCCCCC 1989
OY 127 GGAGAAATGTTGGTCTCCTACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 186
DB 1988 GGAGAAATGTTGGTCTCCTACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 1929
OY 187 GCGGAGAGCACTGAAGTCTTCAAGTTCTGTGTAAGTCTGACCATTCAGTCAAGAAATTT 246
DB 1928 GCGGAGAGCACTGAAGTCTTCAAGTTCTGTGTAAGTCTGACCATTCAGTCAAGAAATTT 1869
OY 247 GGAGATGCTGGCCGATATACCTGCCATTAAGGAGCAAGTTCTGAGCCGCTCACTCCTG 306
DB 1868 GGAGATGCTGGCCGATATACCTGCCATTAAGGAGCAAGTTCTGAGCCGCTCACTCCTG 1809
OY 307 TTGATTCACAAAAAAGAAAGATGGAATTTGTCACATGATATCTTAAAGAAACAGAAAGAA 366
DB 1808 TTGATTCACAAAAAAGAAAGATGGAATTTGTCACATGATATCTTAAAGAAACAGAAAGAA 1749
OY 367 TTCCAAAAATAGATCTTTCTGAAATGTGAGCCAAAGATTTATTCGACGTTTCATATGC 426
DB 1748 TTCCAAAAATAGATCTTTCTGAAATGTGAGCCAAAGATTTATTCGACGTTTCATATGC 1689
OY 427 TGGTGGCTGAGCGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAAGTAGCAGAGCTTC 486
DB 1888 TGGTGGCTGAGCGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAAGTAGCAGAGCTTC 1629
OY 487 TCTGACCCCCAAGGGGTGACATGTGAGCAGTGCACATTTTCAGCAGAGAGGGTCAAGCTG 546
DB 1628 TCTGACCCCCAAGGGGTGACATGTGAGCAGTGCACATTTTCAGCAGAGAGGGTCAAGCTG 1569
OY 547 GACAAACGGAATTTAAGCAATACACANTGAGCTGTGAGAGGGCAGTGGCTGCCCTCT 606
DB 1568 GACAAACGGAATTTAAGCAATACACANTGAGCTGTGAGAGGGCAGTGGCTGCCCTCT 1509
OY 607 GCCGAGAGAGCCTACCCATCAGAGTGTGTTGATGATGATTCACAAACCTCAAGTATGAA 666
DB 1508 GCCGAGAGAGCCTACCCATCAGAGTGTGTTGATGATGATTCACAAACCTCAAGTATGAA 1449
OY 667 AACTACACAGCAGCTTCTTCATCAGACATCATCAACAGACCCACCCAAACCTG 726
|||||

DB 1448 AACTACACAGCAGCTTCTTCATCAGACATCATCAACAGACCCACCCAAACCTG 1389
OY 727 CAGCTGAAGCCATTGAAAAAATCTCGGCACCGTAGAGTCACTGGGAAATACCCGACAC 786
DB 1388 CAGCTGAAGCCATTGAAAAAATCTCGGCACCGTAGAGTCACTGGGAAATACCCGACAC 1329
OY 787 TGGAGCACCCACATCTCTACTTCTCCCTGACATTTTGCATACAGAGCCAGGGCAAGAC 846
DB 1328 TGGAGCACCCACATCTCTACTTCTCCCTGACATTTTGCATACAGAGCCAGGGCAAGAC 1269
OY 847 AATAGAGAAAGAAAGATAGACTCTGCTGCAAGAACCTCAGCCAGGTGTGTCCAC 906
DB 1268 AATAGAGAAAGAAAGATAGACTCTGCTGCAAGAACCTCAGCCAGGTGTGTCCAC 1209
OY 907 AAGGATGCCAAGATCCGGGTGCAACCCGAGACCGCTACTATGTTCAATCCGTGGAGCAC 966
DB 1208 AAGGATGCCAAGATCCGGGTGCAACCCGAGACCGCTACTATGTTCAATCCGTGGAGCAC 1149
OY 967 TGGGCACTGCTGTC 980
DB 1148 TGGGCACTGCTGTC 1135

RESULT 7

US-09-917-265-66

: Sequence 66, Application US/09917265

: Patent No. US20020052030A1

: GENERAL INFORMATION:

: APPLICANT: Wonderling, Raman S.

: APPLICANT: Boroughs, Karen L.

: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH

: FILE REFERENCE: IM-5

: CURRENT APPLICATION NUMBER: US/09/917,265

: CURRENT FILING DATE: 2001-07-27

: PRIOR APPLICATION NUMBER: 60/223,016

: PRIOR FILING DATE: 2000-08-04

: NUMBER OF SEQ ID NOS: 109

: SOFTWARE: PatentIn version 3.1

: SEQ ID NO 66

: LENGTH: 1533

: TYPE: DNA

: ORGANISM: Canis familiaris

: FEATURE:

: NAME/KEY: CDS

: LOCATION: (1)..(1533)

: OTHER INFORMATION:

US-09-917-265-66

Query Match 93.3% Score 921 DB 10 Length 1533:

Best Local Similarity 100.0% Pred. No. 0:

Matches 921: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 67 ATATGGGAAGTGAAGAAAGATGTTATGTTGTAGAGTTGAGCTGGACCCCTGATGCCCC 126
DB 1 ATATGGGAAGTGAAGAAAGATGTTATGTTGTAGAGTTGAGCTGGACCCCTGATGCCCC 60
OY 127 GGAGAAATGTTGGTCTCCTACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 186
DB 61 GGAGAAATGTTGGTCTCCTACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
OY 187 GCGGAGAGCAGTGAAGTCTAGTCTGTGTAAACTCTGACCATTCAGTCAAGTCAAGAAATTT 246
DB 121 GCGGAGAGCAGTGAAGTCTAGTCTGTGTAAACTCTGACCATTCAGTCAAGTCAAGAAATTT 180
OY 247 GGAATGCTGGCCGATATACCTGCCATTAAGGAGCAAGTTCTGAGCCGCTCACTCCTG 306
DB 181 GGAATGCTGGCCGATATACCTGCCATTAAGGAGCAAGTTCTGAGCCGCTCACTCCTG 240
OY 307 TTGATTCACAAAAAAGAAAGATGGAATTTGTCACATGATATCTTAAAGAAACAGAAAGAA 366
DB 241 TTGATTCACAAAAAAGAAAGATGGAATTTGTCACATGATATCTTAAAGAAACAGAAAGAA 300
OY 367 TTCCAAAAATAGATCTTTCTGAAATGTGAGCCAAAGATTTATTCGACGTTTCATATGC 426
|||||

Db 301 TCCAAAATTAAGATCTTCTTCTGAAATGTGAGGCAAGAATTAATCTTGACGTTCCACATGC 360

Qy 427 TGTGGCTGACGGCAATCACTAGTGAATTTGAAATTCAGTGTCAAAAGTAGCAGAGCTTC 486

Db 361 TGTGGCTGACGGCAATCACTAGTGAATTTGAAATTCAGTGTCAAAAGTAGCAGAGCTTC 420

Qy 487 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTACACTTTTCAGCGAGAGGGTCCAGAGTG 546

Db 421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTACACTTTTCAGCGAGAGGGTCCAGAGTG 480

Qy 547 GACAAACAGGATTTATTAAGATGACACAGTGTGAGTGTGAGAGGGCAGTCCCTGCCCTCT 606

Db 481 GACAAACAGGATTTATTAAGATGACACAGTGTGAGTGTGAGAGGGCAGTCCCTGCCCTCT 540

Qy 607 GCCGAGGAGAGCCTACCCATGAGAGTGTGGTGATGCTATTTCACAAAGTCAAGTATGAA 666

Db 541 GCCGAGGAGAGCCTACCCATGAGAGTGTGGTGATGCTATTTCACAAAGTCAAGTATGAA 600

Qy 667 AACTACACACACAGCTTTTTCATCAGACATCATCAACCCAGACCCACACAAACCTG 726

Db 601 AACTACACACACAGCTTTTTCATCAGACATCATCAACCCAGACCCACACAAACCTG 660

Qy 727 CAGCTGAAGCCATTGAAAATAATTCGCGAGCTGGAGGTCAAGCTGTGGAAATCCCGACACC 786

Db 661 CAGCTGAAGCCATTGAAAATAATTCGCGAGCTGGAGGTCAAGCTGTGGAAATCCCGACACC 720

Qy 787 TGGAGCACCCCAACATTTCTACTTCTCCCTACATTTTTCATACAGGCCACGGGCAAGAAC 846

Db 721 TGGAGCACCCCAACATTTCTACTTCTCCCTACATTTTTCATACAGGCCACGGGCAAGAAC 780

Qy 847 AATGAGAAAAAAGAAAGATAGACTGTGCTGGACAAGCCCTCAGCCAAAGTCTGTGCCAC 906

Db 781 AATGAGAAAAAAGAAAGATAGACTGTGCTGGACAAGCCCTCAGCCAAAGTCTGTGCCAC 840

Qy 907 AAGGATGCCAAGATCCGCGTGCAGAGCCGAGACCGCTACTATAGTTCATCTGAGACGAC 966

Db 841 AAGGATGCCAAGATCCGCGTGCAGAGCCGAGACCGCTACTATAGTTCATCTGAGACGAC 900

Qy 967 TGGGCAATCTGTGTCAATGACAGT 987

Db 901 TGGGCAATCTGTGTCAATGACAGT 921

RESULT 8

US-09-917-265-68/c

Sequence 68, Application US/09917265

Patent No. US20020052030A1

GENERAL INFORMATION:

APPLICANT: Wonderling, Ramani S.

APPLICANT: Boroughs, Karen L.

TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF

FILE REFERENCE: IM-5

CURRENT APPLICATION NUMBER: US/09/917,265

CURRENT FILING DATE: 2001-07-27

PRIOR APPLICATION NUMBER: 60/223,016

PRIOR FILING DATE: 2000-08-04

NUMBER OF SEQ ID NOS: 109

SOFTWARE: PatentIn version 3.1

SEQ ID NO 68

LENGTH: 1533

TYPE: DNA

ORGANISM: Canis familiaris

US-09-917-265-68

| | | | | |
|-----------------------|----------------|---|----------|-------------|
| Query Match | 93.3% | Score 921 | DB 10 | Length 1533 |
| Best Local Similarity | 100.0% | Pred. No. 0 | | |
| Matches 921 | Conservative 0 | Mismatches 0 | Indels 0 | Gaps 0 |
| QY | 67 | ATTGTGACACTGCAGAAAGATGTTTATGTTGTACAGTTGACGCGCAACCCATGCCCC | 126 | |
| | | | | |
| Db | 1533 | ATTGTGAACTGCAGAAAGATGTTTATGTTGTAGAGTTGACGCGCAACCCATGCCCC | 1474 | |

QY 127 GGAGAAATGCTGCTCTCACCTGCCATACCCCTGAAGAAGATACATCACTTGGACCTCA 186
 Db 1473 GGAGAAATGCTGCTCTCACCTGCCATACCCCTGAAGAAGATACATCACTTGGACCTCA 1414
 QY 187 GCCCAGACAGTAATGTAATCTAGTCTTGTTGTTAACTCTACATCCAACTCAAGAAATTT 246
 Db 1413 GCCCAGACAGTAATGTAATCTAGTCTTGTTGTTAACTCTACATCCAACTCAAGAAATTT 1354
 QY 247 GGAGATGCTGGCCAGTATACCTGCCATTAAGAAGAGCCAAAGTTCTGGCCGCTACTCCG 306
 Db 1353 GGAGATGCTGGCCAGTATACCTGCCATTAAGAAGAGCCAAAGTTCTGGCCGCTACTCCG 1294
 QY 307 TTGATTCAAAAAAAGAGATGGAAATTTGGTCCACTGATATCTTAAAGAACAGAAAGAA 366
 Db 1293 TTGATTCAAAAAAAGAGATGGAAATTTGGTCCACTGATATCTTAAAGAACAGAAAGAA 1234
 QY 367 TCCAAAAATTAAGATCTTCTGAAATGTAGGCAAAAGATTTATCTGGACGTTTCAATGC 426
 Db 1233 TCCAAAAATTAAGATCTTCTGAAATGTAGGCAAAAGATTTATCTGGACGTTTCAATGC 1174
 QY 427 TGTGGCGTAGCGGCATACGATCTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 486
 Db 1173 TGTGGCGTAGCGGCATACGATCTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 1114
 QY 487 TCTGACCCCAAGGGGTGACATGTGAGCAGCTGACACTTTCAGAGAGAGAGGTTCAGAGTG 546
 Db 1113 TCTGACCCCAAGGGGTGACATGTGAGCAGCTGACACTTTCAGAGAGAGAGGTTCAGAGTG 1054
 QY 547 GACAAACGGGATTTAAGAGATACACAGTGTGAGAGGAGGAGCTGCTGCCCTCT 606
 Db 1053 GACAAACGGGATTTAAGAGATACACAGTGTGAGAGGAGGAGCTGCTGCCCTCT 994
 QY 607 GCCGAGAGAGCCTACCCATCGAGTGTGTTGATGCTATTTCACAAAGCTCAAGTATGAA 666
 Db 993 GCCGAGAGAGCCTACCCATCGAGTGTGTTGATGCTATTTCACAAAGCTCAAGTATGAA 934
 QY 667 AACTACGCCAGCAGCTTCTTCATGAGACATCATCAAAACAGACCACCAAACTTG 726
 Db 933 AACTACGCCAGCAGCTTCTTCATGAGACATCATCAAAACAGACCACCAAACTTG 874
 QY 727 CACCTGAAGCATTGAAAAATTCCTGGCAGCTGAGAGTCACTGGGAATTAACCCGACACC 786
 Db 873 CACCTGAAGCATTGAAAAATTCCTGGCAGCTGAGAGTCACTGGGAATTAACCCGACACC 814
 QY 787 TGGAGACCCCACTTCTACTTCTCCCTGACATTTTGCATACAGGCCCCAGGCAAGAAC 846
 Db 813 TGGAGACCCCACTTCTACTTCTCCCTGACATTTTGCATACAGGCCCCAGGCAAGAAC 754
 QY 847 AATAGAGAAAGAGATAGACTGCTGCCGTGGACAGAGCTCAGCCNAAGTGTGTGCCAC 906
 Db 753 AATAGAGAAAGAGATAGACTGCTGCCGTGGACAGAGCTCAGCCNAAGTGTGTGCCAC 694
 QY 907 AAGGATGCCAAGATCCGGGTGCAGGCCGAGACCCGCTACTATAGTTTCACTCGGAGCGAC 966
 Db 693 AAGGATGCCAAGATCCGGGTGCAGGCCGAGACCCGCTACTATAGTTTCACTCGGAGCGAC 634
 QY 967 TGGGATCTGTTCTATGAGT 987
 Db 633 TGGGATCTGTTCTATGAGT 613
 RESULT 9
 US-09-917-265-52
 : Sequence 52, Application US/09917265
 : Patent No. US20020052030A1
 : GENERAL INFORMATION:
 : APPLICANT: Wonderling, Ramani S.
 : APPLICANT: Boroughs, Karen L.
 : TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREIN
 : FILE REFERENCE: IN-5
 : CURRENT APPLICATION NUMBER: US/09/917, 265
 : CURRENT FILING DATE: 2001-07-27
 : PRIORITY APPLICATION NUMBER: 60/223,016

```

: PRIOR FILING DATE:2000-08-04
: NUMBER OF SEQ ID NOS:109
: SOFTWARE: PatentIn version 3.1.1
: SEQ ID NO 52
: LENGTH: 921
: TYPE: DNA
: ORGANISM: Canis familiaris
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(921)
: OTHER INFORMATION:
: IS-09-917-2655-52

```

| Query Match | 92.68; Score 914; DB 10; Length 921; |
|-------------|--------------------------------------|
|-------------|--------------------------------------|

| | | | |
|----|-----|--|-----|
| OY | 67 | ATATGGGAACCTGGAGAAAGATGTTATGTCTAGAGTTGGAGTGGACCTGATATGCCCC | 126 |
| Db | 1 | ATATGGGAACCTGGAGAAAGATGTTATGTCTAGAGTTGGAGTGGACCTGATATGCCCC | 60 |
| OY | 127 | GGAGAAATGGTGTCTCTCACCCTGACCTGACCTACCCCTGAGAAGATGACATCATCTTGGACCTCA | 185 |
| Db | 61 | GGAGAAATGGTGTCTCTCACCCTGACCTGACCTACCCCTGAGAAGATGACATCATCTTGGACCTCA | 120 |
| OY | 187 | GCCGAGAGCAGTGAAGTCTTAGGTTCTGTGTAAGAACTGTGACCATTCAGTCAAGAATTT | 246 |
| Db | 121 | GCCGAGAGCAGTGAAGTCTTAGGTTCTGTGTAAGAACTGTGACCATTCAGTCAAGAATTT | 180 |
| OY | 247 | GGAGATCTGTGGCCCTGATACCTGGCATTAAGAGGCAAGGTTCTGAGCGCTCACTCCGTG | 306 |
| Db | 181 | GGAGATCTGTGGCCCTGATACCTGGCATTAAGAGGCAAGGTTCTGAGCGCGCTCACTCCGTG | 240 |
| OY | 307 | TTGATTCACAAAAAAGAGATGAATTTGCTCACATGATATCTTTAAAGAACAGAAAGAA | 366 |
| Db | 241 | TTGATTCACAAAAAAGAGATGAATTTGCTCACATGATATCTTTAAAGAACAGAAAGAA | 300 |
| OY | 367 | TTCCAAAAATTAAGATCTTTCTGAAATGTGAGGCAAAAGATTTATCTGACGTTTCATGTC | 426 |
| Db | 301 | TTCCAAAAATTAAGATCTTTCTGAAATGTGAGGCAAAAGATTTATCTGACGTTTCATGTC | 360 |
| OY | 427 | TGGTGGCTGAGCGCAATCAGTACGATTTGTAATTCAGTGTCAAAAGTAGCAGAGGCTTC | 486 |
| Db | 361 | TGGTGGCTGAGCGCAATCAGTACGATTTGTAATTCAGTGTCAAAAGTAGCAGAGGCTTC | 420 |
| OY | 487 | TCTGACCCCGCAAGGGGTGACATGTTGGAGCAGTGCACCTTTAGCAGAGAGGTCAGAGTGTG | 546 |
| Db | 421 | TCTGACCCCGCAAGGGGTGACATGTTGGAGCAGTGCACCTTTAGCAGAGAGGTCAGAGTGTG | 480 |
| OY | 547 | GACAAACGGGATTTAAGAAAGTACACAGTGGAGTGTCAAGAGGGCAGTGTGCCCCCTCT | 606 |
| Db | 481 | GACAAACGGGATTTAAGAAAGTACACAGTGGAGTGTCAAGAGGGCAGTGTGCCCCCTCT | 540 |
| OY | 607 | GCCGAGAGAGACCTTACCCATGAGAGTGTGTGTGATGTTATTCACAACTCAAGTATGAA | 666 |
| Db | 541 | GCCGAGAGAGACCTTACCCATGAGAGTGTGTGTGATGTTATTCACAACTCAAGTATGAA | 600 |
| OY | 667 | AACCTACCCAGCAGCTTCTTCATCAGAGACATCATCAACGAGACCCACCCAAACCTGTG | 726 |
| Db | 601 | AACCTACCCAGCAGCTTCTTCATCAGAGACATCATCAACGAGACCCACCCAAACCTGTG | 660 |
| OY | 727 | CAGCTGAAGCATTTGAAAAATTTCTGGCAGCTGGAGGTCACTGTGGAAATACCCCCACAC | 786 |
| Db | 661 | CAGCTGAAGCATTTGAAAAATTTCTGGCAGCTGGAGGTCACTGTGGAAATACCCCCACAC | 720 |
| OY | 787 | TGGAGCAACCCACATTTCTACTTCTCCCTGCAATTTTGCATACAGGCCAGGCAAGAAC | 846 |
| Db | 721 | TGGAGCAACCCACATTTCTACTTCTCCCTGCAATTTTGCATACAGGCCAGGCAAGAAC | 780 |
| OY | 847 | AATAGAGAAAAAGAAATACACTCTGCGTGGACAAGACCTGAGCCCAAGGTCTGTGCCAC | 906 |
| Db | 781 | AATAGAGAAAAAGAAATACACTCTGCGTGGACAAGACCTGAGCCCAAGGTCTGTGCCAC | 840 |

```

RESULT 10
US-09-917-265-54/c
: Sequence 54, Application US/09917265
: Patent No. US20020052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
: FILE REFERENCE: IM-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: CURRENT FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: PRIOR FILING DATE: 2000-08-04
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 54
: LENGTH: 921
: TYPE: DNA
: ORGANISM: Canis familiaris
US-09-917-265-54

```

Query Match 92.68; Score 914; DB 10; Length 921;

| | | | |
|----|-----|--|-----|
| OY | 67 | ATATGGAACTGGAGAAAGATGTTATATGTTAGAGTTGGACTGGACCTGATGCCCC | 126 |
| Db | 921 | ATTGTGGAACTGGAGAAAGATGTTATATGTTAGAGTTGGACTGGACCTGATGCCCC | 862 |
| OY | 127 | GGAGAAATGCTGTCTCTCACTGCCATPACCCCTGAAGAATGACATCACTGTGACCTCA | 186 |
| Db | 861 | GGAGAAATGCTGTCTCTCACTGCCATACCCCTGAAGAATGACATCACTGTGACCTCA | 802 |
| OY | 187 | GGCAGAGCAGTGAAGTCTCTAGTTCTGTAAAACCTGCACATCCAAAGCAAGATTT | 246 |
| Db | 801 | GGCAGAGCAGTGAAGTCTCTAGTTCTGTAAAACCTGCACATCCAAAGCAAGATTT | 742 |
| OY | 247 | GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGCAAGTTCTGAGCCCTCACTCTG | 306 |
| Db | 741 | GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGCAAGTTCTGAGCCCTCACTCTG | 682 |
| OY | 307 | TTGATTCACAAAAGAAAGATGGAATTGTGTCCACTGATACCTTAAGGAAACGAAAGAA | 366 |
| Db | 681 | TTGATTCACAAAAGAAAGATGGAATTGTGTCCACTGATACCTTAAGGAAACGAAAGAA | 622 |
| OY | 367 | TCCAAAATAAATATCTTTCTGAAATGTGAGCCAAAGATTTATCTGAGCTTTCACATGC | 426 |
| Db | 621 | TCCAAAATAAATATCTTTCTGAAATGTGAGCCAAAGATTTATCTGAGCTTTCACATGC | 562 |
| OY | 427 | TGTGTGCTAGCGGCATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGCTTC | 486 |
| Db | 561 | TGTGTGCTAGCGGCATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGCTTC | 502 |
| OY | 487 | TCTGACCCCCAAGGGGTGACATGTGAGACACTTGACACTTTCAGAGAGAGGGTCCAGAGT | 546 |
| Db | 501 | TCTGACCCCCAAGGGGTGACATGTGAGACACTTTCAGAGAGAGGGTCCAGAGT | 442 |
| OY | 547 | GACAAAGAGGATTTATTAAGAGTACACAGTGGAGGTGACAGAGGCACTGGCTCCCTCT | 606 |
| Db | 441 | GACAAAGAGGATTTATTAAGAGTACACAGTGGAGGTGACAGAGGCACTGGCTCCCTCT | 382 |
| OY | 607 | GCCGAGAGAGCCTACCATCGAGCTGTGGTGGATGCTATTTCACAAGCTCAAGTAGAA | 666 |
| Db | 381 | GCCGAGAGAGCCTACCATCGAGCTGTGGTGGATGCTATTTCACAAGCTCAAGTAGAA | 322 |

OY 667 AACTACACAGAGCTTCTTCATCAGACATCATCAACAGACCCACCAACCTG 726
DB 321 AACTACACAGAGCTTCTTCATCAGACATCATCAACAGACCCACCAACCTG 262
OY 727 CAGCTGAAGCCATTAAAAATTTCTGGACGCTGGAGGTCAGCTGGGAATACCCGACACC 786
DB 261 CAGCTGAAGCCATTAAAAATTTCTGGACGCTGGAGGTCAGCTGGGAATACCCGACACC 202
OY 787 TGGACACCCACCATTTCTTACTTCTCCTGACATTTTGCATACAGCCCGAGGCAAGAC 846
DB 201 TGGACACCCACCATTTCTTACTTCTCCTGACATTTTGCATACAGCCCGAGGCAAGAC 142
OY 847 AATAGAGAAAGAAAGATAGACTCTGCGTGGACAGACCTGAGCCAGGTCGTGTGCAC 906
DB 141 AATAGAGAAAGAAAGATAGACTCTGCGTGGACAGACCTGAGCCAGGTCGTGTGCAC 82
OY 907 AAGATGGCCAGATCCGGGTGCAGACCCGAGACCGCTACTATAGTTCATCTCTGGAGCAC 966
DB 81 AAGATGGCCAGATCCGGGTGCAGACCCGAGACCGCTACTATAGTTCATCTCTGGAGCAC 22
OY 967 TGGGCATCTGTGTC 980
DB 21 TGGGCATCTGTGTC 8

RESULT 11
US-09-917-265-26
; Sequence 26, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Borouhgs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(921)
; OTHER INFORMATION:
US-09-917-265-26

Query Match 6.7%; Score 66; DB 10; Length 921;
Best Local Similarity 100.0%; Pred. No. 1.5e-24;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 537 GGTGAGGTGAGCAACAGGATTATAGAGTACACAGTGTCTCAGAGGGCAGTGC 596
DB 471 GGTGAGGTGAGCAACAGGATTATAGAGTACACAGTGTCTCAGAGGGCAGTGC 530
OY 597 CTGCCC 602
DB 531 CTGCCC 536

RESULT 12
US-09-917-265-28/c
; Sequence 28, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Borouhgs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5

; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265-28

Query Match 6.7%; Score 66; DB 10; Length 921;
Best Local Similarity 100.0%; Pred. No. 1.5e-24;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 537 GGTGAGGTGAGCAACAGGATTATAGAGTACACAGTGTCTCAGAGGGCAGTGC 596
DB 451 GGTGAGGTGAGCAACAGGATTATAGAGTACACAGTGTCTCAGAGGGCAGTGC 392
OY 597 CTGCCC 602
DB 391 CTGCCC 386

RESULT 13
US-10-079-616-6
; Sequence 6, Application US/10079616
; Patent No. US20020107366A1
; GENERAL INFORMATION:
; APPLICANT: IMAMURA, Takayuki
; MAEDA, Hiroaki
; FUJIYASU, Takeshi
; IMAGAWA, Yoshitaka
; TOKIYOSHI, Sachio
; TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/079,616
; FILING DATE: 22-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/011,143
; FILING DATE: 04-FEB-1998
; APPLICATION NUMBER: PCT/JP97/01824
; FILING DATE: 29-MAY-1997
; APPLICATION NUMBER: JP 165249/1996
; FILING DATE: 04-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: IMAMURA-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-377-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 921 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-079-616-6

Query Match 6.7%; Score 66; DB 12; Length 921;
Best Local Similarity 100.0%; Pred. No. 1.5e-24;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 537 GGTGAGTGGACACAGGATTTATAGAGTACAGTGGAGTGTCTCAGAGGCGCAGTGC 596
|||||
DB 471 GGTGAGTGGACACAGGATTTATAGAGTACAGTGGAGTGTCTCAGAGGCGCAGTGC 530
OY 597 CTGCCC 602
|||||
DB 531 CTGCCC 536

RESULT 14

US-09-917-265-55
Sequence 55, Application US/09917265
Patent No. US20020052030A1
GENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/09/917,265
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 109
SOFTWARE: PatentIn version 3.1
SEQ ID NO 55
LENGTH: 985
TYPE: DNA
ORGANISM: felis catus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)-(984)
OTHER INFORMATION:
US-09-917-265-55

Query Match 6.7%; Score 66; DB 10; Length 985;
Best Local Similarity 100.0%; Pred. No. 1.5e-24;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 537 GGTGAGTGGACACAGGATTTATAGAGTACAGTGGAGTGTCTCAGAGGCGCAGTGC 596
OY 597 CTGCCC 602
|||||
DB 597 CTGCCC 602

RESULT 15

US-09-917-265-57/c
Sequence 57, Application US/09917265
Patent No. US20020052030A1
GENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/09/917,265
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 109
SOFTWARE: PatentIn version 3.1
SEQ ID NO 57
LENGTH: 985
TYPE: DNA

ORGANISM: felis catus
US-09-917-265-57

Query Match 6.7%; Score 66; DB 10; Length 985;
Best Local Similarity 100.0%; Pred. No. 1.5e-24;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 537 GGTGAGTGGACACAGGATTTATAGAGTACAGTGGAGTGTCTCAGAGGCGCAGTGC 596
|||||
DB 449 GGTGAGTGGACACAGGATTTATAGAGTACAGTGGAGTGTCTCAGAGGCGCAGTGC 390
OY 597 CTGCCC 602
|||||
DB 389 CTGCCC 384

Search completed: July 16, 2003, 19:58:56
Job time : 187.875 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 16, 2003, 15:58:34 ; Search time 2941.09 Seconds

(without alignments)
3255.531 Million cell updates/sec

Title: US-09-917-265-59
Perfect score: 1764
Sequence: 1 MHPOQVISMFSVLVLLASPL.....QARDRYSSSSMSDWASVSCS 329

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=genEmbl -OPMT=fastlap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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-DOCALLIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=plc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=us09917265.qcgn.1.1.11328.@runat.15072003_092106_1601 -NCPU=6 -ICPU=3
-DEV_MMAR -LARGESOURCE -NEG.SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOC
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: gb_hlg:*
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4: gb_om:*
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8: gb_pl:*
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14: gb_vl:*
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16: em_fun:*
17: em_hum:*
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28: em_un:*

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33: em_hlg_mus:*
34: em_hlg_pln:*
35: em_hlg_rod:*
36: em_hlg_mam:*
37: em_hlg_vrt:*
38: em_sy:*
39: em_hlgo_hum:*
40: em_hlgo_mus:*
41: em_hlgo_other:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|--------|-------------|--------|----|------------|--------------------|
| 1 | 1764 | 100.0 | 990 | 6 | AR151071 | AR151071 Sequence |
| 2 | 1764 | 100.0 | 990 | 6 | EI5017 | EI5017 Canine mRNA |
| 3 | 1751 | 99.3 | 1015 | 4 | CFU49100 | U49100 Canis faml |
| 4 | 1731 | 98.1 | 990 | 6 | AR151061 | AR151061 Sequence |
| 5 | 1657 | 93.9 | 990 | 6 | AR076200 | AR076200 Sequence |
| 6 | 1657 | 93.9 | 990 | 6 | AX076482 | AX076482 Sequence |
| 7 | 1657 | 93.9 | 4522 | 6 | AX076209 | AX076209 Sequence |
| 8 | 1657 | 93.9 | 4522 | 6 | AX076476 | AX076476 Sequence |
| 9 | 1655 | 93.8 | 990 | 4 | FCU83184 | U83184 Felis catu |
| 10 | 1643 | 93.1 | 1006 | 4 | FCU112P40 | Y07762 F. catus mB |
| 11 | 1667 | 88.8 | 990 | 6 | AX154603 | AX154603 Sequence |
| 12 | 1557 | 88.3 | 984 | 6 | AX154600 | AX154600 Sequence |
| 13 | 1552 | 88.0 | 1626 | 12 | AF401989 | AF401989 Synthetic |
| 14 | 1551 | 87.9 | 1058 | 4 | ECU112P40 | Y11129 Equus cabal |
| 15 | 1527 | 86.6 | 993 | 4 | CEU57752 | U57752 Cervus elap |
| 16 | 1515 | 85.9 | 1012 | 4 | BTU11815 | U11815 Bos taurus |
| 17 | 1515 | 85.9 | 1019 | 6 | E35794 | E35794 Process for |
| 18 | 1512 | 85.7 | 984 | 6 | AX154599 | AX154599 Sequence |
| 19 | 1511 | 85.7 | 984 | 4 | AF004024 | AF004024 Ovis arie |
| 20 | 1511 | 85.7 | 984 | 4 | AF209435 | AF209435 Ovis arie |
| 21 | 1511 | 85.7 | 1012 | 4 | AF007576 | AF007576 Capra hlr |
| 22 | 1504 | 85.3 | 984 | 6 | AX154598 | AX154598 Sequence |
| 23 | 1502.5 | 85.2 | 1623 | 6 | AR091394 | AR091394 Sequence |
| 24 | 1502.5 | 85.2 | 1870 | 6 | A92079 | A92079 Sequence 3 |
| 25 | 1502.5 | 85.2 | 2318 | 9 | HUMNKSFP40 | M65290 Human natur |
| 26 | 1502.5 | 85.2 | 6139 | 6 | AR091393 | AR091393 Sequence |
| 27 | 1501.5 | 85.1 | 987 | 6 | AR008950 | AR008950 Sequence |
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| 30 | 1501.5 | 85.1 | 987 | 6 | BD007076 | BD007076 Gene expr |
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| 35 | 1501.5 | 85.1 | 1018 | 6 | AR052857 | AR052857 Sequence |
| 36 | 1501.5 | 85.1 | 1389 | 6 | AX084106 | AX084106 Sequence |
| 37 | 1501.5 | 85.1 | 1399 | 6 | AR091391 | AR091391 Sequence |
| 38 | 1501.5 | 85.1 | 1399 | 9 | HUMCLMF40 | M65272 Human cytot |
| 39 | 1501.5 | 85.1 | 2362 | 6 | AR082684 | AR082684 Sequence |
| 40 | 1501.5 | 85.1 | 2362 | 6 | AR122960 | AR122960 Sequence |
| 41 | 1501.5 | 85.1 | 2362 | 6 | I28325 | I28325 Sequence 1 |
| 42 | 1501.5 | 85.1 | 1389 | 6 | I89770 | I89770 Sequence 1 |
| 43 | 1493.5 | 84.7 | 1080 | 9 | MMU19841 | U19841 Macaca mula |
| 44 | 1481.5 | 84.0 | 975 | 6 | AX154597 | AX154597 Sequence |
| 45 | 1480.5 | 83.9 | 969 | 6 | AX154601 | AX154601 Sequence |

RESULT 1

ALIGNMENTS

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 LOCUS AR151071 990 bp DNA Linear PAT 08-AUG-2001
 DEFINITION Sequence 11 from patent US 6231850.
 ACCESSION AR151071
 VERSION AR151071.1 GI:15117121
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 990)
 AUTHORS Okano, F., Satoh, M. and Yamada, K.
 TITLE Canine interleukin 12
 JOURNAL Patent: US 6231850-A 11 15-MAY-2001;
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 source Location/Qualifiers
 1. 990
 /organism="unknown"
 BASE COUNT 279 a 244 c 249 g 218 t
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 Alignment Scores:
 Pred. No.: 2,61e-165 Length: 990
 Score: 1764.00 Matches: 329
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
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 Db 1 ATGCATCTCAGACGTTGGTGCATCTCTGCTTTCCCTGTTGGTGGCGTCTCCCTC 60
 QY 21 MetAlaIleTrpGluLeuGluLysAspValTyrValAlaGluLeuAspTrpHisProasp 40
 Db 61 ATGGCCATATGGAGACCTGGAGAAAGATGTTATGTTGTAGAGTTGGACCTGCCAT 120
 QY 41 AlaproglyluMetValIleuLeuThrCysHisThrProgluLysAspPilleThrTrp 60
 Db 121 GCCCCGCGAAGATGGTGCCTCCACCTGCCATACCCCTGAGAGATGACATCATTGG 180
 QY 61 ThrSerAlaGlnSerSerGluValIleuGlySerGlyThrLeuThrIleGlnValLys 80
 Db 181 ACCTCAGCGAGACGACTGAGTCTGAGTTGCTGTAACCTCTGACCATCCAGATCAA 240
 QY 81 GlupheGlyAspAlaGlyGlnTyrThrCysHisLysGlyLysValLeuSerArgSer 100
 Db 241 GAATTGGAGATGCTGGCCAGTATACCTGCCATAAAGAGGCAAGTTCTGAGCGCTCA 300
 QY 101 LeuLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGln 120
 Db 301 CTCTCTGTGATTCACAAAAGAAAGATGATTGGTCCACTGATATCTTAAAGGAACAG 360
 QY 121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
 Db 361 AAGAGATCCAAAAATTAAGATCTTCTGTAATGTGAGCCAAAGATTAATTTGTGACGTTTC 420
 QY 141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArg 160
 Db 421 ACATGCTGGTGGCTGACGCGCAATCAGTACTGTAATTCAGTGCATAAAGTAGAGAGA 480
 QY 161 GlyPheSerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgVal 180
 Db 481 GGCTTCTGTACCCCAAGGGGTGACATGTGAGACATGACATTTTCAGCAGAGAGGTC 540
 QY 181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluGlyGlnGluLysSerAlaCys 200
 Db 541 AGAGTGACACAAAGGATTTATAGAACTACACAGTGGAGTGAGGCGAGGCGCTGC 600
 QY 201 ProSerAlaGluLysLeuSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
 Db 601 CCTGTGCCGAGAGAGCCCTACCATCGAGCTGCTGTGATGCTATTACAAAGCTAAG 660

QY 221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProThr 240
 Db 661 TATGAAGAACTACACACACACTTCTTCATCAGACATCATCAAAACAGACACACACACA 720
 QY 241 AsnLeuGlnLeuLysProIleLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
 Db 721 AACCTGAGCTGAAGCATTGAAATAATTCGCGACCTGAGGTCAGCTGGAAATACCCC 780
 QY 261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGly 280
 Db 781 GACACCTGGAGACACCCACACTTCTACTTCTCCTGACATTTTGCAATACAGGCCAGGCG 840
 QY 281 LysAsnAsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysVal 300
 Db 841 AAGACAAATAGCAAAAGAAAGATAGACTGTGGTGAGCAAGACCTCAGCAAGGTCGTG 900
 QY 301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
 Db 901 TGGCACAAGGATCCCAAGATCCGCGCAAGCCGAGACCGCTACTATGATTCATCTCTG 960
 QY 321 SerAspTrpAlaSerValSerCysSer 329
 Db 961 AGCGACTGGCGCATCTGTCTCTCAGT 987
 RESULT 2
 E15017
 LOCUS E15017 990 bp DNA Linear PAT 28-JUL-1999
 DEFINITION Canine mRNA for interleukin 12 40kDa subunit, complete cds.
 ACCESSION E15017
 VERSION E15017.1 GI:5709700
 KEYWORDS JP 1998036397-A/1.
 SOURCE Canis sp.
 ORGANISM Canis sp.
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 REFERENCE 1 (bases 1 to 990)
 AUTHORS Okano, F.
 TITLE CANINE INTERLEUKIN 12 AND ITS PRODUCTION
 JOURNAL Patent: JP 1998036397-A 1 10-FEB-1998;
 TORAY IND INC
 COMMENT OS Canis sp. (dog)
 PN JP 1998036397-A/1
 PD 10-FEB-1998
 PF 08-NOV-1996 JP 1996296789
 PR 08-NOV-1995 JP 95P 289729, 23-MAY-1996 JP 96P 128104 PI
 OKANO FUMIYOSHI
 PC C07K14/54, C07H21/04, C12M5/10, C12N15/09, C12P21/02, C12M5/10, PC
 C12R1:911)
 CC (C12P21/02, C12R1:911);
 CC strandedness: Double;
 CC topology: Linear;
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 FT source 1. 990
 FT /organism="Canis sp."
 FT /tissue="liver"
 FT CDS 1. 990
 FT /product="interleukin 12 40kDa subunit".
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 source Location/Qualifiers
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 /db_xref="taxon:9616"
 BASE COUNT 279 a 244 c 249 g 218 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 2,61e-165 Length: 990
 Score: 1764.00 Matches: 329
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-917-265-59 (1-329) x E15017 (1-990)

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Db 1 ATGCATCCTCGACGACATTCGTCATCTCCGCTTTTCCCTCGCTTTCTGCGCTCCCTC 60
Oy 21 MetAla1etPglInleuGluLysAspValTyValValGluLeuAspTrpHisProAsp 40
Db 61 ATGGCATATCGGAAGCTGGAGAAAGATGTTATATGTTAGAGTTGGACTGGACCCCTGAT 120
Oy 41 AlaProGlyGluMetValValleuThrcysHisThrProGluGluAspIleThrTrp 60
Db 121 GCGCCCGGAGAAATCGCTGCTCCCTGACCTCCATCCCTGGAAGAGATGACATCTGCG 180
Oy 61 ThrSerAlaGlnSerSerGluValleuGlySerGlyLysTrpPheThrIleGlnValLys 80
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Oy 81 GluPheGlyAspAlaGlyGlnTyTrpThrcysHisGlyGlyLysValleuSerArgSer 100
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Oy 121 LysGlnSerLysAsnLys11ePheLeuLysGlyGlnAlaLysAsnTyTrpSerGlyArgPhe 140
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Oy 141 ThrCysTrpTrpLeuThrAla11eSerThrAspLeuLysPheSerValLysSerSerArg 160
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RESULT 3
LOCUS CFU49100 1015 bp mRNA linear MAM 13-MAR-1996

DEFINITION Canis familiaris interleukin-12 p40 subunit mRNA, complete cds.
ACCESSION U49100
VERSION 049100.1 GI:1223907
KEYWORDS
SOURCE
ORGANISM Canis familiaris.
Canis familiaris.
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
1 (bases 1 to 1015)
Belke-Louis, G.F. and Buetner, M.
Cloning and sequence analysis of the p35 and p40 subunits of canine interleukin-12
JOURNAL Unpublished
2 (bases 1 to 1015)
Belke-Louis, G.F.
Direct Submission
TITLE Submitted (13-FEB-1996) Georg F. Belke-Louis, Institute of Med.
JOURNAL Microbiology, Veterinaerstr. 13, Muenchen, D-80539, Germany
FEATURES
source
location/Qualifiers
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LKENYTSFPFLRDIIRKPDPTNQLKPLKNSRHYVESMEYEDPTWSTPSPSYSLFPCV
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Gaps: 0
US-09-917-265-59 (1-329) x CFU49100 (1-1015)
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Db 1 ATGCATCCTCGACGACATTCGTCATCTCCGCTTTTCCCTCGCTTTCTGCGCTCCCTC 60
Oy 21 MetAla1etPglInleuGluLysAspValTyValValGluLeuAspTrpHisProAsp 40
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Db 241 GAATTTGGAGATGCGCGCCAGATATACCTGCCATTAAGSAGGCAAGCTTCTGAGCGGCTCA 300
Oy 101 LeuLeuLeu11eHisLysLysGluAspGly11etPseThrAspIleLeuLysGluGln 120
Db 301 CTCCTGTTGATTCACAAAAAGAGATGAAATTTGCTGACATGATATCTTAAAGGAACAG 360
Oy 121 LysGlnSerLysAsnLys11ePheLeuLysGlyGlnAlaLysAsnTyTrpSerGlyArgPhe 140
Db 361 AAAGATCCAAAAATTAAGATCTTCTGAAATGTGAGGCAAGAAATTTATCTTGAGCGTTTC 420

| | | | | | |
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| Qy | 141 | ThrcysrtprrplethrhAl1eserthrspLeuylsPheSerVallysSerSerArg | 160 | | |
| Db | 421 | ACATGCTGGTGGCTGACGGCAATCATCTACTATTGTAATTCAGTGTCAAAAGTACGACA | 480 | | |
| Qy | 161 | GlYPheSerAspProGlnGlyValThrcysGlyAlaValThrLeuSerAlaGluArgVal | 180 | | |
| Db | 481 | GGCTTCTGTGACCCCAAGGGGGTGCACATGTGGAGACAGTGCACACTTTCAGCAGAGGGCTC | 540 | | |
| Qy | 181 | ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGlnGlySerAlaCys | 200 | | |
| Db | 541 | AGAGTGGCAACAGGAGTATTAAAGAATCACAGTACAGTGGAGTGTCAAGGAAGGAGTGCCTGC | 600 | | |
| Qy | 201 | ProSerAlaGlnGluSerLeuProIleGluValValAlaAspAlaIleHisLysLeuLys | 220 | | |
| Db | 601 | CCCTGTGGCCGAGAGAGGCTTACCCATCGAGGTCTGGTGGATTCGATTTCACAGCTCAG | 660 | | |
| Qy | 221 | TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProThr | 240 | | |
| Db | 661 | TATGAAAACTACACCAGCAGCTTCTCTCACTCAGAGCATCATCAACCAAGACCCACCCACA | 720 | | |
| Qy | 241 | AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro | 260 | | |
| Db | 721 | AACCTGCAGCTGAAGCCATTGAAAAATTCTGGCAGCGTGGAGTCACTGGGAATACCC | 780 | | |
| Qy | 261 | AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGly | 280 | | |
| Db | 781 | GACACCTGGACACCCCCACATTCCTCACTTCCCTGACATTTTGGTGTAAGGCCAGGGCC | 840 | | |
| Qy | 281 | LysAsnAsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysVal | 300 | | |
| Db | 841 | AAGAAACATTAAGAAAAAGAAAGATATGACTCTGCGTGGACAAGACCTCAGCCAAAGTCCGTG | 900 | | |
| Qy | 301 | CysHisLysAspAlaLysIleArgValGlnIleArgAspArgTyrTyrSerSerSerTrp | 320 | | |
| Db | 901 | TGCCCAAGAGATGCCAAGATTCGCCCTGCAGACCCGAGACCCGCTACTATATGTTCACTCG | 960 | | |
| Qy | 321 | SerAspTrpAlaSerValSerCysSer | 329 | | |
| Db | 961 | AGCGACTGGCATCTGTCTCCCTGCAGCT | 987 | | |
| RESULT 4 | | | | | |
| AR151061 | AR151061 | 990 bp | DNA | linear | PAT 08-AUG-2001 |
| LOCUS | Sequence 1 from patent US 6231850. | | | | |
| DEFINITION | AR151061 | | | | |
| ACCESSION | AR151061.1 | GI:15117111 | | | |
| VERSION | | | | | |
| KEYWORDS | | | | | |
| SOURCE | Unknown. | | | | |
| ORGANISM | Unclassified. | | | | |
| REFERENCE | 1 (bases 1 to 990) | | | | |
| AUTHORS | Okano, F., Satoh, M. and Yamada, K. | | | | |
| TITLE | Canine interleukin 12 | | | | |
| JOURNAL | Patent: US 6231850-A 1 15-MAY-2001; | | | | |
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| source | 1..990 | | | | |
| | /organism="unknown" | | | | |
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| Score: | 1731.00 | Matches: | 323 | | |
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| Best Local Similarity: | 99.08% | Mismatches: | 1 | | |
| Query Match: | 98.13% | Indels: | 0 | | |
| DB: | 6 | Gaps: | 0 | | |
| US-09-917-265-59 (1-329) x AR151061 (1-990) | | | | | |
| Qy | 4 | GlnGlnLeuValIleSerTrpPheSerLeuValLeuLeuAlaSerProLeuMetaIle | 23 | | |
| | | | | | |

SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.

REFERENCE
AUTHORS Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
TITLE Feline interleukin-12 as an immune stimulant
JOURNAL Patent: WO 0104155-A 1 18-JAN-2001;
Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
CALIFORNIA (US)

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source
1..990
/organism="synthetic construct"
/db.xref="taxon:32630"
/note="feline IL-12 p40"

BASE COUNT 283 a 249 c 248 g 210 t
ORIGIN

Alignment Scores:
Pred. No.: 1.03e-154 Length: 990
Score: 1657.00 Matches: 308
Percent Similarity: 96.66% Conservative: 10
Best Local Similarity: 93.62% Mismatches: 11
Query Match: 93.93% Indels: 0
Gaps: 0

US-09-917-265-59 (1-329) x AX076200 (1-990)

QY 1 MethisProgluInleuValIleSerTrpPheSerLeuValLeuLeuAlaSerProleu 20
Db 1 ATGCATCCTCAGCAGTTGGTCATCGCTGGTTTCCCTGGTTTGGCCACCTCCCTC 60

QY 21 MetAlaIleTrpGluLeuGluLysAspValTyraValGluLeuAspTrpHisProasp 40
Db 61 ATGGCCATATGGAGACTGGCAAAACGTTATGTTAGAGTTGGAGCTGGACCTGGAT 120

QY 41 AlaProgluLumEtValIleLeuThrcysHisThrProgluLysAspPleThrTrp 60
Db 121 GCCCCCGGAGAAATGGTGCTCTTACTGCAATCTCTGAGAAAGATGACATACCTCG 180

QY 61 ThrSerAlaGlnSerSerGluValIleGlySerGlyLysThrLeuThrIleGlnValLys 80
Db 181 ACCCTGTACCAAGACAGCTGAAGTCTAGGCTGTGTAAGTCTGACCATCCAGTCAAA 240

QY 81 GluPheGlyAspAlaGlyIntYrThrcysHisLysGlyLysValLeuSerArgSer 100
Db 241 GAATTTGACATGCTGGCAGATATACCTGATTAAGAGGCGAGTTCTGAGCATTCG 300

QY 101 LeuLeuLeuIleHisLysGluAspGlyIleTrpSerThrAspIleLeuLysGln 120
Db 301 TTCTCTCTCATACCAAAAGGAAGATGGAATTTGGTCCACTGATCTTAAGGGAACAG 360

QY 121 LysGluSerLysAsnLysIlePheLeuLysGlyLysAlaLysAsnTyrSerGlyArgPhe 140
Db 361 AAGCAATCCAAAATAAGATCTTCTAAATGTCAGCAAAAGATTAATTCGACGTTTC 420

QY 141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerArg 160
Db 421 ACCGTGGTGCGTGACGCAATCAGTACCAATTTGAATTCACCTGCAAAAAGCAGCA 480

QY 161 GlyPheSerAspProgluInglyValIleThrcysGlyAlaValIleThrLeuSerAlaArgVal 180
Db 481 GGCTCCTCTACGCCCAAGGGGTGACTGTGTGACACGACGACACTCTCAGCGAGAAGTTC 540

QY 181 ArgValAspAsnArgAspTyrLysLysTyThrValGluCysGlnGluInglySerAlaCys 200
Db 541 AGAGTGCACAACAGCGCATTTAAGAACTACACACTGAGTGTCAGAGCGCAGTGCTGC 600

QY 201 ProSerAlaGluInglySerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
Db 601 CCGGCTCCGAGGAGACCTTACCATTTGAAGTCTGTGGTGGAGCGCTATTTCACAAGCTCAAG 660

QY 221 TyroLysAsnTyThrSerSerPhePheIleArgAspIleIleLysProAspProPthr 240

Db 661 TACGAAACATCACCAGAGCTTCTCATCGAGGACATCATCAACGAGCACCCACAG 720

QY 241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyPro 260
Db 721 AACCTGCAACATGGAAGCCATTAAAAATTCCTGGCATGTGGAGAGTGCAGCTGGAAATACCT 780

QY 261 AspThrTrpSerTrpProHisSerTyThrSerLeuThrPheCysIleGlnAlaGlnGly 280
Db 781 GACACCTGGAGACCCACATCTTCTACTTCTTAAACATTGGCGTACAGCTCCAGGCG 840

QY 281 LysAsnAsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValIle 300
Db 841 AAGAACAAACAGAGAAGAAAGACAGACTCCCTGGCAGACACTCAGCCAAAGTGTGTG 900

QY 301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyThrSerSerTrp 320
Db 901 TGCCCAAGAGATGGCAAGATCCGGTCCAAAGCAGGAGCCGCTACTATAGCTCATCTCG 960

QY 321 SerAspTrpAlaSerValSerCysSer 329
Db 961 AGCAACTGGGATCCGTGCTCGAGT 987

RESULT 6
AX076482 990 bp DNA Linear PAT 06-FEB-2001
LOCUS
DEFINITION Sequence 8 from Patent WO0104280.
ACCESSION AX076482
VERSION AX076482.1 GI:12711034
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequences.

REFERENCE
AUTHORS Lutz,H., Schroff,M., Wittig,B. and Lutz,H.
TITLE Vaccine against lentiviral infections, such as the feline immune
deficiency virus of the cat
JOURNAL Patent: WO 0104280-A 8 18-JAN-2001;
Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
Universitaet Zuerich (CH)

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/organism="synthetic construct"
/db.xref="taxon:32630"
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BASE COUNT 283 a 249 c 248 g 210 t
ORIGIN

Alignment Scores:
Pred. No.: 1.03e-154 Length: 990
Score: 1657.00 Matches: 308
Percent Similarity: 96.66% Conservative: 10
Best Local Similarity: 93.62% Mismatches: 11
Query Match: 93.93% Indels: 0
Gaps: 0

US-09-917-265-59 (1-329) x AX076482 (1-990)

QY 1 MethisProgluInleuValIleSerTrpPheSerLeuValLeuLeuAlaSerProleu 20
Db 1 ATGCATCCTCAGCAGTTGGTCATCGCTGGTTTCCCTGGTTTGGCCACCTCCCTC 60

QY 21 MetAlaIleTrpGluLeuGluLysAspValTyraValGluLeuAspTrpHisProasp 40
Db 61 ATGGCCATATGGAGACTGGCAAAACGTTATGTTAGAGTTGGAGCTGGACCTGGAT 120

QY 41 AlaProgluLumEtValIleLeuThrcysHisThrProgluLysAspPleThrTrp 60
Db 121 GCCCCCGGAGAAATGGTGCTCTTACTGCAATCTCTGAGAAAGATGACATACCTCG 180

QY 61 ThrSerAlaGlnSerSerGluValIleGlySerGlyLysThrLeuThrIleGlnValLys 80
Db 181 ACCCTGTACCAAGACAGTGAAGTCTTAGGCTGTGTAAGTCTGACCATCCAGTCAAA 240

| | | | |
|------------|--|--|----------------------------|
| OY | 81 | GlupheglyAspAlaGlyGlnIrrThrCysHisLysGlyGlyLysValLeuSerArg | 100 |
| Db | 241 | GAATTTCGAGATGCTGGCCAGATATACCTGTCTATAAAGAGGCGAAGTTTCGACCATTCG | 300 |
| OY | 101 | LeuLeuLeuLeuHisLysLysGlnAspGlyIleTrrPserThrAspIleLeuLysGln | 120 |
| Db | 301 | TTCCCTCCGATGCACAAAAAGGAAGATGGAATTTGGTCCACATCATCTTAAGGGAACAG | 360 |
| OY | 121 | LysGlnSerLysAsnLysLlePheLeuLysCysGlnAlaLysAsnTyrSerLyrPhe | 140 |
| Db | 361 | AAAGATCCAAAAATTAAGATCTTCTTAATAATGTGAGCAAAATAATTTATTCGAGCTTC | 420 |
| OY | 141 | ThrCysTrpTrpLeuThrAlaIleSerThrAspLysLysPheSerValLysSerArg | 160 |
| Db | 421 | ACCTCGCTGGCTGACGGCATTCAGTACCGATTTTGAATTCACGTCAAAAGCAGCA | 480 |
| OY | 161 | GlyPheSerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGlnArgVal | 180 |
| Db | 481 | GGCTCTCTGACCCCCAAGGGGTGACTGTGGAGCAGGACACTCTCAGCAGAGAAGTC | 540 |
| OY | 181 | ArgValAspAsnArgAspTyrLysLysTrrPheValGlnCysGlnGlnGlySerLacys | 200 |
| Db | 541 | AGAGTCGACACACAGGATTTATAGAAATACACAGTCGAGGTGCAGAGGAGGCGTCCGC | 600 |
| OY | 201 | ProSerAlaGlnGluSerLeuProIleGluValValAspAlaIleHisLysLeuLys | 220 |
| Db | 601 | CCGGCTGCCGAGAGACAGCTTACCATTGTAAGTCGTGGTGAGCGATTATCACAAAGCTCAAG | 660 |
| OY | 221 | TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProThr | 240 |
| Db | 661 | TACGAAACTACACCAGACGCTTCTTCATCAGGACATCATCAAAACCGAGCCACCAAG | 720 |
| OY | 241 | AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGlnValSerTrpGluTrrPro | 260 |
| Db | 721 | AACCTGCACATCGAAGCCATTAATAAATCTCGGCATGTGGAGTAGCTGAGGAAATACCT | 780 |
| OY | 261 | AspTrpTrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGly | 280 |
| Db | 781 | GACACCTGGAGACCCCACTTCCTACTCTCTTAACATTTGGGTGAGGTCCAGGGGC | 840 |
| OY | 281 | LysAsnAsnArgGlnLysLysAspArgLeuCysValAspLysThrSerAlaLysVal | 300 |
| Db | 841 | AAGAACACACAGAAAGAAAGACAGACTCTCCGTGGACAGACCTCAGCCAGGTCTG | 900 |
| OY | 301 | CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTrrSerSerSerTrp | 320 |
| Db | 901 | TGCCCAAGAGATGCCAAGATCCGCGTCGCAAGCAGGAGCAGCCCTACTATAGCATCATCTG | 960 |
| OY | 321 | SerAspTrpAlaSerValSerCysSer 329 | |
| Db | 961 | AGCAACTGGGATCCGTCTCTGCAGT 987 | |
| RESULT 7 | | | |
| LOCUS | AX076209 | 4522 bp | DNA linear PAT 06-FEB-2001 |
| DEFINITION | Sequence 10 from Patent WO0104155. | | |
| ACCESSION | AX076209 | | |
| VERSION | AX076209.1 | GI:12710834 | |
| KEYWORDS | | | |
| ORGANISM | | | |
| REFERENCE | | | |
| AUTHORS | Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wiltig,B. | | |
| TITLE | Feline interleukin-12 as an immune stimulant | | |
| JOURNAL | Patent: WO 0104155-A 10 18-JAN-2001; Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ; Universitaet Zuerich (CH) ; THE REAGENTS OF THE UNIVERSITY OF CALIFORNIA (US) | | |
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| Source | Location/Qualifiers | | |
| | 1..4522 | | |
| | /organism="synthetic construct" | | |

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| | | /db_xref="taxon:32630" | |
| | | /note="Plasmid pmol-fil12p40" | |
| BASE COUNT | 1180 a 1126 c 1106 g 1110 t | | |
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| Alignment Scores: | | | |
| Pred. No.: | 6,856-154 | Length: | 4,522 |
| Score: | 1657.00 | Matches: | 308 |
| Percent Similarity: | 96.66% | Conservative: | 10 |
| Best Local Similarity: | 93.62% | Mismatches: | 11 |
| Query Match: | 93.93% | Indels: | 0 |
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| QY | 1 | MethisrProginleuValIleSertrrPheSerleuValleuLeuAlaSerProleu | 20 |
| DB | 3047 | ATGCAATCCCGACAGCAATGTCATCCCGGTTTTTCCTGGTTTGCTGGCACTCCCTC | 3106 |
| QY | 21 | MetaIaIetrpgJleuGlulysAspAlaYrValValIgluLeuAspTrpHisProas | 40 |
| DB | 3107 | ATGGCGCATGGGAAGCACTGGAGAAAAACGTTATGTTAGAGTTGAGCTGGCACCCCTAT | 3166 |
| QY | 41 | AlaProgluJleuMetValleuThrCysHisThrProgluJluAspPleThrTrp | 60 |
| DB | 3167 | GCCCCCGAGAAATGCTGCTCTACCGCAATACTCCTGGAAGAAGATGCATCACTCG | 3226 |
| QY | 61 | ThSerAlaGlnSerSerGluValleuGlySerGlyLysTrpIleuThrIleGluValLys | 80 |
| DB | 3227 | ACCTTGACCCAGAGCATGAAGTCTTACGCTCTGGTAAACTCTGACCATCCAACTCAA | 3286 |
| QY | 81 | GluPheGlyAspAlaGlyGlnTrpThrCysHisLysGlyGlyLysValleuSerArgSer | 100 |
| DB | 3287 | GAATTTCGAGATGCTGGCCAGCATATACCTGATAAAGAGGCGAGGCTTCTGACCATTCG | 3346 |
| QY | 101 | LeuLeuLeuIleHisLysLysGluAspGlyIleTrpSerTrpAspIleLeuLysGluIn | 120 |
| DB | 3347 | TTCTCTCGATACAAAAAGAAAGCAATGTGCTCACGATATCTTAAAGGACACAG | 3406 |
| QY | 121 | LysGlnSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTrpSerGlyArgPhe | 140 |
| DB | 3407 | AAAGATCCAAAAATTAAGATCTTCTTAATAGTGAGGCAAAAGATATTCTGGACGTTTC | 3466 |
| QY | 141 | ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArg | 160 |
| DB | 3467 | ACCTGCTGGTGGCTGACGGCAATCATGCCATTTGAAATTGCATGCTCAAAAAGCGCAGA | 3526 |
| QY | 161 | GlyPheSerAspProGlnGlyValThrCysGlyAlaValTrpLeuSerAlaGluArgVal | 180 |
| DB | 3527 | GGCTCTCTGACCCCAAGGGGTGACTTGTGGAGCAGGACACTCTCAGCAGAGAAGGTC | 3586 |
| QY | 181 | ArgValAspAsnArgAspTrpLysLysTrpThrValGluCysGlnGlySerAlaCys | 200 |
| DB | 3587 | AGAGCGCAACACAGGATTAATACGAATACACAGCTGAGTGCAGAGGACGAGTGCCTGC | 3646 |
| QY | 201 | ProSerAlaGlnGluSerLeuProIleGluValValYalaAspAlaIleHisLysLeuLys | 220 |
| DB | 3647 | CCGGGTGCGGAGGAGGCTACCCATTGAAGTCGGGGAGCGCATTCACAAAGCTCAG | 3706 |
| QY | 221 | TyrGluAsnTrpThrSerSerPhePheIleArgAspIleIleLysProAspProProThr | 240 |
| DB | 3707 | TACGAAACACTACACAGACGCTTCTTCATCAGGACATCATCAAAACCGACCCACCCAAAG | 3766 |
| QY | 241 | AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTrpPro | 260 |
| DB | 3767 | AACTGCAACATGAAGCCATTAAAAAATTCCTGGCATGGAAGAGAGCTGGGAATTACCT | 3826 |
| QY | 261 | AspThrTrpSerTrpProHisSerTrpPheSerLeuThrPheCysIleGluAlaGlnGly | 280 |
| DB | 3827 | GACACCTTGAGACCCCACTTCTACTTCTTCCTTAACATTGGCGTACAGGTCACAGGCG | 3886 |
| QY | 281 | LysAsnAsnArgGluLysLysAspArgLeuCysValAspLysTrpSerAlaLysValVal | 300 |

Db 3887 AAGAACACAGAAAAAGAACACAGACTCTCCGTGACACAGACTCAGCCAGAGTCGTG 3946
QY 301 CYSHTLSASPALALysLleArGValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
Db 3947 TGCACCAAGAGATGCCAGATCCGCGTGCAGCCAGGACCGCTACTATAGCTCATCTCG 4006
QY 321 SerAspTrpAlaSerValSerCysSer 329
Db 4007 ACCAACTGGGATCCGTCCTGCTGCACT 4033

RESULT 8
AX076476 4522 bp DNA linear PAT 06-FEB-2001
LOCUS Sequence 2 from patent WO0104280.
DEFINITION AX076476
ACCESSION AX076476
VERSION AX076476.1 GI:12711028
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 4522)
AUTHORS Leutenegger, C., Schroff, M., Wiltig, B. and Lutz, H.
TITLE Vaccine against lentiviral infections, such as the feline immune
JOURNAL deficiency virus of the cat
Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
Universitaet Zuerich (CH)
FEATURES
source location/Qualifiers
1..4522
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="IL-12p40"

BASE COUNT 1180 a 1126 c 1106 g 1110 t
ORIGIN

Alignment Scores:
Pred. No.: 6,85e-154 Length: 4522
Score: 1657.00 Matches: 308
Percent Similarity: 96.66% Conservative: 10
Best Local Similarity: 93.62% Mismatches: 11
Query Match: 93.93% Indels: 0
DB: Gaps: 0

US-09-917-265-59 (1-329) x AX076476 (1-4522)

QY 1 MethHSProGInGlnLeuValIleSerTrpPheSerLeuValLeuLeuAlaSerProLeu 20
Db 3047 ATGCATCCCTCACAGCTGGTCATCGCTGGTTTCCCTGGTTTGGCTGCACCTCCCTC 3106
QY 21 MetaIaIeTrpGluLeuGluLysAspValTyrValIValGluLeuAspTrpHisProAsp 40
Db 3107 ATGGCATATGTGGAACTGGAGAAAAAGCTTTATGTTGTAGACTTGGAGTGGACCTCGAT 3166
QY 41 AlaProGlyGluMetValValLeuThrCysHisThrProGluGluAspAspIleThrTrp 60
Db 3167 GCCCCCGAGAAATGGTGCTCTTACTGTCATACCTCGAAGAAGATCACATCACCTCG 3226
QY 61 ThrSerAlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
Db 3227 ACCCTTGACCAAGAGAGTGAAGTCTAGAGCTGTGTAATAAAGCTGTGCATCCAGTCAAA 3286
QY 81 GluPheGlyAspAlaGlyGlnTyrThrCysHisLysGlyGlyLysValLeuSerArgSer 100
Db 3287 GAATTTGCAGATGCTGCCAGATATACCTGTCAATAAGAGGCGGAGGTTGTGAGCCATTGC 3346
QY 101 LeuLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGln 120
Db 3347 TTCCTCTGATACACAAAAGCAAGATGGAATTTGGTCCATGATATCTTAAGGACACAG 3406
QY 121 LysGluSerLysAsnLysLlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
Db 3407 AAGAAATCCAAAATAAGATTTCTTAATAATGTGAGGCAAAAGAAATTAATTCGACGTTTC 3466

QY 141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArg 160
Db 3467 ACCTGCTGGTGGTGGCGGCAATCACTACCGATTTGAAATTCACCTCAAAAGCACAGAGA 3526
QY 161 GlyPheSerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgVal 180
Db 3527 GGGTCTCTGACCCCAAGGGGTGACTTGGGAGCGACACACTCTCAGACAGAAAGGTC 3586
QY 181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
Db 3587 AGAGTGACAAACAGGGATTATGAAGAGTACACAGTGGAGTGGCAGAGGCGAGTGCCTCC 3646
QY 201 ProSerAlaGluGlnSerLeuProIleGluValValAspAlaIleHisLysLeuLys 220
Db 3647 CCGGCTGCCGAGAGAGCGCTACCCATTGAAGTGTGGAGGCTATTTCACAAAGCTCAAG 3706
QY 221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProThr 240
Db 3707 TACGAAAACTACACACGACGACTTCTTCATCAGGACATCATCAACCGACCCACAG 3766
QY 241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
Db 3767 AACCTGCAACTGAAGCATTTAAAAAATCTCGGCATGTGAGTGGAGTGGCAATACCT 3826
QY 261 AspTrpTrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGly 280
Db 3827 GACACCTGAGACACCCACATTCCTACTCTCTCTTACACTTTGGCTACAGGTCCAGGGC 3886
QY 281 LysAsnAsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysVal 300
Db 3887 AAGAACACAGAAAAAGAAAGACAGCAGCTCCGTGGACAAAGACCTCAGCCAAAGTCGTG 3946
QY 301 CysHisLysASPALALysLleArGValGlnAlaArgAspArgTyrTyrSerSerTrp 320
Db 3947 TGCACCAAGAGATGCCAGATCCGCGTGCAGCCAGGACCGCTACTATAGCTCATCTCG 4006
QY 321 SerAspTrpAlaSerValSerCysSer 329
Db 4007 ACCAACTGGGATCCGTCCTGCTGCACT 4033

RESULT 9
FCU83184
LOCUS FcU83184 990 bp mRNA linear MAM 16-JUL-1999
DEFINITION FcU83184 Interleukin-12 p40 subunit (IL-12) mRNA, complete cds.
ACCESSION U83184
VERSION U83184.1 GI:2735050
KEYWORDS
SOURCE FcU83184.1
ORGANISM FcU83184.1
Felis catus.
Felis catus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
1 (bases 1 to 990)
Fehr, D., Dean, G.A., Huder, J., Fan, Z., Huettner, S., Higgins, J.W.,
Pedersen, N.C. and Lutz, H.
Nucleotide and predicted peptide sequence of feline interleukin-12
(IL-12)
JOURNAL DNA Seq. 8 (1-2), 77-82 (1997)
MEDLINE 98182592
PUBMED 9522125
REFERENCE 2 (bases 1 to 990)
AUTHORS Fehr, D., Dean, G.A., Huder, J., Fan, Z., Huettner, S., Higgins, J.W.,
Pedersen, N.C. and Lutz, H.
TITLE Direct Submission
JOURNAL Submitted (24-DEC-1996) Clinical Laboratory, Department of Internal
Veterinary Medicine, University of Zurich, Winterthurerstrasse 260,
Zurich, ZH 8057, Switzerland
FEATURES
source location/Qualifiers
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| Db | 61 | ATGCCCATATGGGAACCTGGAGAAAAACGTTTATGTGTGATGAGCTGGACCTGCACCTGAT | 120 |
| QY | 41 | AlaProGluGluMeValValLeuThrCysHisThrProGluGluAspAspIleThrTrp | 60 |
| Db | 121 | GCCCCGGAGAAATGTGTGCTCTCACCTGTGACAGCCCTGGAAGAAAGATGACATCACTGG | 180 |
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| Db | 181 | ACCTGTGACCAAGAGAGTAGAGTCTTACGCTGTGGTAAACCTGACCATCAAGTCAAA | 240 |
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| QY | 101 | LeuLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGln | 120 |
| Db | 301 | TTCTCTCCGTGATACAAAAAGAGAAATGGAATGTGTCACATGATATCTTAAAGGAGACG | 360 |
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| QY | 161 | GlyPheSerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgVal | 180 |
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| Db | 541 | AGAGTGCACAAACAGGATTAATAGACAGTACACAGTGGATGTCAGAGAGGCGATCTGTC | 600 |
| QY | 201 | ProSerAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys | 220 |
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| QY | 221 | TyrGluAsnTyThrSerSerPhePheIleArgAspIleIleLysProAspProThr | 240 |
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| QY | 241 | AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyPro | 260 |
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| QY | 261 | ASPIRTPSPSTRHPRONHSSETPYRPhseerleuthrPhcysILGLaIaagIngly | 280 |
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| QY | 281 | LysaSnAsnArGjLuLysAspArgLeuCySValAspLysTrhSerAlaLysVal | 300 |
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| QY | 301 | CysHsLysAspAlaLysILearGValGlnaIaargAspaTgTYTrSerSerSerTrp | 320 |
| DB | 901 | TGCACACAAGATGCGCAACATCCGGTGCACGCCAGAGACCGCTACTATAGCTACATCCGTGG | 960 |
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| ACCESSION | Y07762 | | |
| VERSION | Y07762.1 | GI:2102664 | |
| KEYWORDS | interleukin-12 p40. | | |
| SOURCE | cat. | | |
| ORGANISM | Felis catus | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis. | | |
| AUTHORS | 1 (bases 1 to 1006) | | |
| TITLE | Schijns,V.E., Wierda,C.M., Vahlenkamp,T.W. and Horzinek,M.C. | | |
| JOURNAL | Molecular cloning of cat interleukin-12 | | |
| MEDLINE | Immunogenetics 45 (6), 462-463 (1997) | | |
| PUBMED | 97246745 | | |
| REFERENCE | 2 (bases 1 to 1006) | | |
| AUTHORS | Schijns,V.E.C.J. | | |
| TITLE | Direct Submission | | |
| JOURNAL | Submitted (03-SEP-1996) V.E.C.J. Schijns, Virology Division, Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL Utrecht, NETHERLANDS | | |
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US-09-917-265-59 (1-329) x FCIL12P40 (1-1006)

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| Db | 1 | ATGCATCCTCAGCAGTTGCTCATCGCGGCTTTCCTCCGTCTTCTCGACCTCCCTCC | 60 |
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| Db | 181 | ACCTCTACCCAGACAGCTGAGACTCTAGGCTGTGGTAAACTCTACCTACCTCCAAAGCAAA | 240 |
| QY | 81 | GluPheGluYsPalagIyGlnTyrThrCysHisLysGluYsValLeuSerAsp | 100 |
| Db | 241 | GAATTTGCACATGCTGGCCACTATACTGCATAAAGAGCGCAGAGCTTCTGACCATTCG | 300 |
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| Db | 301 | TTCTCTCTGATACCAAAAAGAGATGCAATTTGCTGCACGATATCTTAAGGGAACAG | 360 |
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| Db | 361 | AAGATATCCAAAATTAAGATCTTTCTAAATGTCAGCGCAAAAGATATTATTCGACCTTTC | 420 |
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| VERSION | AX154603.1 GI:14536186 | | | | |
| KEYWORDS | synthetic construct. | | | | |
| SOURCE | synthetic construct. | | | | |
| ORGANISM | artificial sequences. | | | | |
| REFERENCE | 1 (bases 1 to 990) | | | | |
| AUTHORS | Leon, S.R. and Punnonen, J. | | | | |
| TITLE | Cytokine polypeptides and nucleic acids | | | | |
| JOURNAL | Patent: WO 0140257-A 7 07-JUN-2001; | | | | |
| FEATURES | Maxygen, Inc. (US) | | | | |
| source | Location/Qualifiers | | | | |
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| Oy | 24 | TrpGluLeuGluLysAspValYrValValGluLeuAspTrpHisProAspAlaProGly | 43 | | |
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| Oy | 44 | GluMetValValLeuThrCysHisIsthrProGluGluAspAspIleThrTrpThrSerAla | 63 | | |
| Db | 130 | GAATGGTGGTCTCTGCCCTGCACACCTCTGTAAGAAGATGGCATCAGCTGAC | 189 | | |
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REFERENCE 2 (bases 1 to 1626)
AUTHORS McMonagle, L.J., Taylor, S., Keanie, L.J., Hopkins, C.A., Logan, N.A.,
Argyle, D.J., Orlons, D.E. and Nicolson, L.
TITLE Direct Submission
JOURNAL Submitted (24-Jul-2001) Veterinary Pathology, Glasgow Veterinary
School, Bearsden Rd, Glasgow G61 1QH, UK
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VERSION Y11129.1 GI:5441622
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SOURCE Equus caballus.
ORGANISM Equus caballus
REFERENCE 1 (bases 1 to 1058)
AUTHORS Argyle, D.J., and Orlons, D.E.
TITLE Mammalia: Eutheria: Perissodactyla: Equidae: Equus.
Nicolson, L., Penna-Gonzales, M.N., Keanie, J.L., Logan, N.A.,
Cloning and sequencing of horse interleukin-12 and interleukin-18
CDNAs
JOURNAL Immunogenetics 50 (1-2), 94-97 (1999)
MEDLINE 20009534
PUBMED 10541814
REFERENCE 2 (bases 1 to 1058)
AUTHORS Nicolson, L.
TITLE Direct Submission
JOURNAL Submitted (04-FEB-1997) L. Nicolson, Dept. of Vet. Pathology,
University of Glasgow Vet. School, Bearsden Rd., Glasgow G61 1QH,
UK
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GenCore version 5.1.6
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-LIST=45 -LOCALICN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USR=US09917265.@CGN_1_1_876.@runat_15072003_092106_1592 -NCPU=6 -ICPU=3
-NO_MMAR -LARGEOUTRT -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
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11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
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23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|--------|-------------|--------|----|----------|--------------------|
| 1 | 1764 | 100.0 | 990 | 19 | AAV13817 | Canine IL-12 p40 s |
| 2 | 1764 | 100.0 | 990 | 20 | AAV35625 | Nucleic acid encod |
| 3 | 1764 | 100.0 | 990 | 20 | AAV03162 | Nucleic acid encod |
| 4 | 1764 | 100.0 | 990 | 22 | AAI64388 | Canine coding sequ |
| 5 | 1735 | 98.4 | 990 | 19 | AAV13816 | Canine IL-12 p40 s |
| 6 | 1735 | 98.4 | 990 | 20 | AAV35615 | Nucleic acid encod |
| 7 | 1735 | 98.4 | 990 | 20 | AAV03152 | Nucleic acid encod |
| 8 | 1735 | 98.4 | 990 | 22 | AAV64378 | Canine coding sequ |
| 9 | 1729.5 | 98.0 | 2154 | 20 | AAV18176 | Canine full length |
| 10 | 1657 | 93.9 | 990 | 22 | AAV26082 | Feline IL-12p40 en |
| 11 | 1657 | 93.9 | 990 | 22 | AAV26085 | Feline IL-12p40 en |
| 12 | 1657 | 93.9 | 4522 | 22 | AAV26076 | Feline IL-12p40 en |
| 13 | 1657 | 93.9 | 4522 | 22 | AAV26094 | Plasmid pMOJ-fil12 |
| 14 | 1651 | 93.6 | 2193 | 19 | AAV56625 | Feline FLAPp40 cDN |
| 15 | 1618.5 | 91.8 | 924 | 20 | AAV18177 | Canine mature CLAF |
| 16 | 1567 | 88.8 | 990 | 22 | AAV15209 | Modified human cyt |
| 17 | 1557 | 88.3 | 984 | 22 | AAV15206 | Modified human cyt |
| 18 | 1554 | 88.1 | 921 | 19 | AAV56626 | Feline FLAPp40 cDN |
| 19 | 1554 | 88.1 | 921 | 19 | AAV56627 | Feline FLAPp40 cDN |
| 20 | 1515 | 85.9 | 1019 | 21 | AAV70709 | Bovine interleukin |
| 21 | 1512 | 85.7 | 984 | 22 | AAV15205 | Modified human cyt |
| 22 | 1504 | 85.3 | 984 | 22 | AAV15204 | Modified human cyt |
| 23 | 1502.5 | 85.2 | 987 | 20 | AAV83199 | Interleukin (IL)-1 |
| 24 | 1502.5 | 85.2 | 5686 | 20 | AAZ40415 | Plasmid pIN143 co |
| 25 | 1502.5 | 85.2 | 6139 | 21 | AAZ40023 | Interleukin-12 fus |
| 26 | 1502.5 | 85.2 | 6538 | 24 | AAZ31545 | PIRES-hb7-1-IL12.1 |
| 27 | 1502.5 | 85.2 | 8578 | 24 | AAZ31546 | PIRES-hb7-1-IL12.0 |
| 28 | 1502.5 | 85.2 | 8608 | 24 | AAZ31547 | PIRES-hb7-1-IL12.2 |
| 29 | 1502.5 | 85.2 | 8623 | 24 | AAZ31548 | PIRES-hb7-1-IL12.3 |
| 30 | 1502.5 | 85.2 | 8629 | 24 | AAZ31552 | PIRES-IL12.2-hb7.1 |
| 31 | 1502.5 | 85.2 | 8638 | 24 | AAZ31549 | PIRES-IL12.2-hb7.1 |
| 32 | 1502.5 | 85.2 | 8644 | 24 | AAZ31550 | PIRES-IL12.3-hb7-1 |
| 33 | 1502.5 | 85.2 | 8659 | 24 | AAZ31551 | PIRES-IL12.3-hb7-1 |
| 34 | 1501.5 | 85.1 | 987 | 16 | AAO97484 | Human interleukin- |
| 35 | 1501.5 | 85.1 | 987 | 19 | AAV07273 | Human interleukin- |
| 36 | 1501.5 | 85.1 | 987 | 19 | AAV07217 | DNA encoding human |
| 37 | 1501.5 | 85.1 | 987 | 20 | AAZ40404 | Human interleukin |
| 38 | 1501.5 | 85.1 | 987 | 20 | AAZ40405 | Human interleukin |
| 39 | 1501.5 | 85.1 | 987 | 20 | AAZ40406 | Human interleukin |
| 40 | 1501.5 | 85.1 | 987 | 22 | AAZ15210 | Human cytokine p40 |
| 41 | 1501.5 | 85.1 | 1007 | 22 | AAZ18585 | Human interleukin- |
| 42 | 1501.5 | 85.1 | 1018 | 15 | AAO67879 | EPV 42 kd promoter |
| 43 | 1501.5 | 85.1 | 1018 | 20 | AAZ08510 | EPV 42 kDa/human I |
| 44 | 1501.5 | 85.1 | 1389 | 22 | AAV76880 | Human p40-IL-2 cod |
| 45 | 1501.5 | 85.1 | 1397 | 18 | AAV00401 | 40 kDa subunit of |

ALIGNMENTS

RESULT 1

ID AAV13817 standard: cDNA to mRNA: 990 BP.

AAV13817

AAV13817: 14-MAY-1998 (first entry)

Canine IL-12 p40 subunit cDNA.

Canine: interleukin-12 p40 subunit: IL-12 p40 subunit: antitumour;

antiviral: vaccine adjuvant; ds.

Canis sp.

Location/Qualifiers

1..990

/*tag= a

FT /product= interleukin-12_p40_subunit
 XX JPI0036397-A.
 PN 10-FEB-1998.
 XX 08-NOV-1996; 96JP-0296789.
 XX 23-MAY-1996; 96JP-0128104.
 PR 08-NOV-1995; 95JP-0289729.
 XX (TORA) TORAY IND INC.
 PA WPI: 1998-174914/16.
 DR P-PSDB: AAM41791.
 XX
 XX Canine interleukin 12 - comprises p40 and p35 subunits; useful in
 PT veterinary medicine, e.g. antitumour, antiviral and vaccine adjuvant
 PT activities are expected
 XX
 XX Claim 10: Pages 10-11; 12pp; Japanese.
 PS
 XX
 CC The present sequence encodes a canine interleukin-12 (IL-12) p40
 CC subunit. A canine IL-12 comprising a p40 and p35 subunit is capable
 CC of inducing an antiviral activating factor and the expression of
 CC class II MHC molecules in canine tumour cells, stimulating
 CC proliferation of canine blastogenic lymphocytes and activating
 CC canine leukocytes to inhibit canine tumour cells. The canine IL-12
 CC can be used in veterinary medicines, e.g. antitumour, antiviral and
 CC vaccine adjuvant activities are expected.
 XX
 SO Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 other;

Alignment Scores:
 Pred. No.: 3.07e-170 Length: 990
 Score: 1764.00 Matches: 329
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 19 Gaps: 0

US-09-917-265-59 (1-329) x AAV13817 (1-990)

QY 1 MethisProGlnGluLeuValIleSerThrPheSerLeuValLeuLeuAlaSerProLeu 20
 DB 1 ATGCATCCTCAGCAGATTGGTCATCTGCTGTTCCCTGTTGGCTGGCGTCCCTC 60
 QY 21 MetAlaIleTrpGluLeuGluLysAspValTyrValValGluLeuAspTrpPheSerProAsp 40
 DB 61 ATGGCATATGGGAACTGGAGAAAGATGTTATGTTGTAGAGTTGGACCTGGACCTGAT 120
 QY 41 AlaProGlyGluMetValValLeuThrCysHisThrProGluGluAspIleThrTrp 60
 DB 121 GCCCCGGGAAATGGTGTCTCCACCTGCATACCCCTGAAAGAAATGATCATCTGG 180
 QY 61 ThrSerAlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
 DB 181 ACCTGAGCCGAGAGCAGTGAAGTCCCTGCTGTAAGCTCTGACCATCCAAATGCAAA 240
 QY 81 GluPheGlyAspAlaGlyLysIleThrCysHisLysGlyGlyLysValLeuSerArgSer 100
 DB 241 GAATTTGGAGATGCTGGCAGATATACCTCCATAAAGAGGAGGAGTTCTGAGCCGCTCA 300
 QY 101 LeuLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGln 120
 DB 301 CTCCTGTTGATTCACAAAAGAAAGATGGAAATTTGCTCCACGATATCTTAAAGCAAC 360
 QY 121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTrpSerGlyArgPhe 140
 DB 361 AAGAGATCAAAAATATAGATCTTTCTGAAATGTGAAGCAAAAGATATATCTGAGACGTTTC 420
 QY 141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArg 160

DB 421 ACATGCTGTGTGCTGACGGCAATCATGACTGATTGAAATTCAGTGTCAAAAGTAGCAGA 480
 QY 161 GlyPheSerAspProGlnGlyValThrCysGlyValAlaThrLeuSerAlaGluArgVal 180
 DB 481 GGCTTCTGTGACCCCAAGGGGTGACATGTGAGACAGTGCACACTTTCAGCAGAGAGGTC 540
 QY 181 ArgValAspAsnArgAspTyrLysLysThrValGluGlyGlnGlnGlnLysSerAlaCys 200
 DB 541 AGAGTGGACAAACAGAGGATTTATAGAACTACACACTGGAGTGTCAAGAGGAGGAGTCTGC 600
 QY 201 ProSerAlaGluGlnSerLeuProIleGluValValAlaAspAlaIleHisLysLeuLys 220
 DB 601 CCTCTGCGCAGAGAGACCTACCATGAGAGTGTGCTGATGCTATTACAAAGCTCAAG 660
 QY 221 TyrGluAsnTrpTrpSerSerPhePheIleArgAspIleIleLysProAspProProThr 240
 DB 661 TATGAAGATACACACACCTCTTTCATGAGACATCATCAAAACCAACCAACCCACCA 720
 QY 241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
 DB 721 AACCTGAGCTGAAGCCATTGAAAAATTCCTCGGCACCTGAGAGCTGGGAATACCCC 780
 QY 261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGly 280
 DB 781 GACACCTGGAGCACCCCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
 QY 281 LysAsnAsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValVal 300
 DB 841 AAGACATATGAGAAAGAAAGATAGACTGTGCTGGACAAAGCTCAGCCAAAGGTGGT 900
 QY 301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTrpSerSerSerTrp 320
 DB 901 TGCCACAGCATGCCAAAGATCCGCTGCAGAGCCGAGACCGCTACTATAGTTGATCTGTG 960
 QY 321 SerAspTrpAlaSerValSerCysSer 329
 DB 961 AGCGACTGGGCACTGTGTCTGCACT 987

RESULT 2
 ID AAX35625
 AAX35625 standard; cdna to mRNA; 990 BP.
 XX
 AC AAX35625;
 XX
 XX 09-JUL-1999 (first entry)
 DT
 XX
 DE Nucleic acid encoding canine Interleukin-12 (IL-12).
 KW Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
 KW tumour; skin disease; infectious disease; allergic disease; ds.
 XX
 OS Canis sp.
 OS
 XX
 FH Key Location/Qualifiers
 FT CDS 1..990
 FT /-tag a
 PN JPI1106350-A.
 XX
 PD 20-APR-1999.
 XX
 PF 15-MAY-1998; 98JP-0133345.
 XX
 XX 07-AUG-1997; 97JP-0213755.
 PR 16-MAY-1997; 97JP-0127690.
 XX
 PA (TORA) TORAY IND INC.
 XX
 XX WPI: 1999-308068/26.
 DR P-PSDB: AAY02342.
 XX
 PT A prevention and treating agent containing interleukin 12 (CaIL12) -
 PT for prevention and treatment of dog and cat immune diseases

XX Claim 1: Page 14-15; 16pp: Japanese.
PS
XX The present sequence encodes canine interleukin-12 (IL-12). The
CC specification describes a method for the prevention and treatment
CC of dog and cat immune diseases. The treatment used an agent comprising
CC dog IL-12 (pail12) proteins to form a heterodimer. The agent is
CC useful for preventing and treating dog and cat immune diseases.
CC including tumours, skin diseases, infectious diseases and allergic
CC diseases.
XX
SQ Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 other:

Alignment Scores:
Pred. No.: 3 07e-170 Length: 990
Score: 1764.00 Matches: 329
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 20 Caps: 0

US-09-917-265-59 (1-329) x AAX35625 (1-990)

QY 1 MethisProGlnGlnLeuValIleSerTrpPheSerLeuValLeuLeuAlaSerProLeu 20
DB 1 ATGCATTCCTCAGCAGTTCATCTCCTGCTTCCCTGTTTGGTGGCCTCTCCCTC 60
QY 21 MetAlaIleTrpPheLeuGluLysAspValTyrValAlaGluLeuAspTrpHisProAsp 40
DB 61 ATGGCCATATGGAGAACTGAGAAAGATTATGTTTAAAGTTGAGTGCACCTGCACCCGAT 120
QY 41 AlaProGlyGluMetValValLeuThrCysHisThrProGluGluAspAlaIleThrTrp 60
DB 121 GCCCGCGAATAATGGTGGTCTCCTCCTGATACCTGCAAGAGATGACATCTCTGG 180
QY 61 ThrSerAlaGlnSerSerGluValLeuGlySerGlyThrLeuThrIleGlnValLys 80
DB 181 ACCTCAGCCGACGACGTGAGTCTAGTTCGTGTAACCTGACCATCCAGTCACAA 240
QY 81 GluPheGlyAspAlaGlyInTyrThrCysHisLysGlyGlyLysValLeuSerArgSer 100
DB 241 GAATTTGGAGATCTGGCCAGTATACCTGCCATTAAGACGCAAGTTCTGACCGCTCA 300
QY 101 LeuLeuLeuIleHisLysGlyAspGlyIleTrpSerThrAspIleLeuLysGluGln 120
DB 301 CTCCTCTGTGATTACCAAAAAGAAAGATGGAATTTGGTCCACTGATCTTAAGAGAAC 360
QY 121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
DB 361 AAGGATCCAAAATTAAGATCTTTCTGAATGTCAGCAAAAGATTATTCTGGACGTTTC 420
QY 141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArg 160
DB 421 ACATGCTGTGGTGGAGGCAATCAGTACGATTTGAATTTCACTGCAAAAAGTAGCAGA 480
QY 161 GlyPheSerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgVal 180
DB 481 GCGTTCTCTACCCCAAGGGGTGACATGTGGACAGTGCACCTTTAGCAGAGAGGGTC 540
QY 181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
DB 541 AGAGTGGACACACGCGATTAAGAGATACACAGTGGAGTGCAGAGGCGACGCTCC 600
QY 201 ProSerAlaGluGluSerLeuProIleGluValValAlaValAlaIleHisLysLeuLys 220
DB 601 CCTCTGCCGAGGAGAGCTTACCCATCGAGGTGCTGGTGAATGCTATTCAACCTCAAG 660
QY 221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleLeuLysProAspProProThr 240
DB 661 TAGGAAACTACACACGACCTTCTCATAGACACTCATCAACACGACCCACCCACA 720
QY 241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
|||||

DB 721 AACCTGCAGCTGAAGCCATTGAAAATTCTCGGACGCTGAGTGCAGCTGGCAATACCCC 780
QY 261 AspThrTrpSerTrpProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGly 280
DB 781 GACACCTGGACACCCCAACATCTTCTCCTGATTTTCCATATACAGCCCAAGGCG 840
QY 281 LysAsnAsnArgGlyLysLysAspArgLeuLysValAspLysThrSerAlaLysValAl 300
DB 841 AAGAACCAATAGAGAAAGAAAGATAGACTCTGCTGTCAGCAAGACCTCAGCCAAAGTCTG 900
QY 301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTrpSerSerTrp 320
DB 901 TGCCACAAGATGCGCAAGATCCGCTGCAACCCGAGACCGCTACTATAGTTCAATCTCGG 960
QY 321 SerAspTrpAlaSerValSerCysSer 329
DB 961 AGCGACTGGGCACTGTGTCTGCACT 987

RESULT 3
AAX03162
ID AAX03162 standard; cDNA to mRNA; 990 BP.
XX
XX AAX03162:
AC
XX 30-MAR-1999 (first entry)
DT
XX
DE Nucleic acid encoding canine interleukin 12.
XX
XX Canine: interleukin 12; IL-12; feline; immunological disease; tumour;
KW skin disease; viral infection; allergic disease; breast tumour;
KW eosinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW othematoma; pneumoedema; skin soft pedicled soft tumour; anal tumour;
KW otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW feline leukaemia; allergy; pollinosis; ds.
XX
XX Canis sp.
OS
XX
FH Key Location/Qualifiers
FT CDS 1..990
FT /*tag= a
FT /product= interleukin_12
XX
XX W09851327-A1.
XX
XX 19-NOV-1998.
PD
XX 07-MAY-1998; 98WO-JP02031.
XX
XX 16-MAY-1997; 97JP-0127690.
PR
XX (TORA) TORAY IND INC.
PA
XX
P1 Okano F, Satoh M, Yamada K:
XX
XX WPI: 1999-070100/06.
DR P-PSDB: AAMW4373.
XX
XX New therapeutic and prophylactic agents - comprise
PT genetically-engineered canine interleukin 12, used to treat, e.g.
PT canine and feline immunological diseases
XX
PS Claim 1: Page 30-32; 45pp: Japanese.
XX
XX The present sequence encodes a canine interleukin 12 (IL-12) protein.
CC The IL-12 protein can be used in therapeutic or prophylactic agents.
CC The agents can be used to prevent and treat canine and feline
CC immunological diseases including dog and cat tumours, skin diseases,
CC viral infections and allergic diseases, especially tumours, breast
CC tumour, eosinophilic granuloma, epidermoid tumour, skin tumour, lipoma,
CC othematoma, pneumoedema, skin soft pedicled soft tumour and anal
CC tumour; skin diseases, otitis externa, dermatitis, eczema, fungal

CC diseases of the skin, pyoderma, allergic dermatitis, nettle rash,
 CC traumatic dermatitis and hair loss; infections: dog parvovirus infection
 CC and distemper virus, cat plaque virus infection and feline leukaemia, and
 CC allergic diseases, e.g. pollinosis.

XX Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 other:

Alignment Scores:

| Pred. No.: | Length: | 990 |
|------------------------|---------|-----------------|
| Score: | 1764.00 | 329 |
| Percent Similarity: | 100.00% | Conservative: 0 |
| Best Local Similarity: | 100.00% | Mismatches: 0 |
| Query Match: | 100.00% | Indels: 0 |
| DB: | 20 | Gaps: 0 |

US-09-917-265-59 (1-329) x AA03162 (1-990)

QY 1 MethisProGlnGlnLeuValIleSerTrpSerLeuValLeuLeuAlaSerProLeu 20
 DB 1 ATGCATCTCAGCAGTTGGTCATCTCTGTTTCCTGTTTGGCTGGCTCTCCCTC 60
 QY 21 MetAlaIleTrpGluLeuGluLysAspValTyrValValGluLeuAspTrpHisProAsp 40
 DB 61 ATGGCCATATGGCACTGGAGAAAGATGTTATGTTTAAAGTTGGACCTGGAT 120
 QY 41 AlaProGlnLysMetValValLeuThrCysHisThrProGlnLysAspIleThrTrp 60
 DB 121 GCCCCGAGAAATGGTGGTCCTCACCCTGCAATCCCTGAGAAAGATGATCATTGG 180
 QY 61 ThrSerIaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
 DB 181 ACCCTGAGGAGACGACTGAGGATCTTCTGTTGTAACCTGACCATCCAAAGTCAAA 240
 QY 81 GluPheGlyAspAlaGlnTyrThrCysHisLysGlyLysValLeuSerArgSer 100
 DB 241 GAATTGGATGCTGGCCAGTACCTGCCATTAAGAGCAAGTTCTGAGCCGCTCA 300
 QY 101 LeuLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGln 120
 DB 301 CTCTGTTGATTCACAAAAGAAAGATGATTTGCTCCACTGATATCTTAAAGAAACAG 360
 QY 121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
 DB 361 AAGAAATCCAAAATTAAGATCTTCTGAAATGTGAGCAAAAGATTAATCTGGACGTTTC 420
 QY 141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArg 160
 DB 421 ACATGCTGGTGGCTGAGCGCAATCAGTATTTGAATTCAGTCCAAAGTAGAGAGA 480
 QY 161 GlyPheSerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgVal 180
 DB 481 GGCTTCTCTACCCCAAGGGGTGACATGTGAGCACTGACACTTTCAGAGAGAGGTC 540
 QY 181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluLysGlnGluLysSerAlaCys 200
 DB 541 AGATGGACACACAGGATTTAAGAAATACACAGTGAAGTCCGAGGGGCAAGGCTTGC 600
 QY 201 ProSerAlaGluLysLeuSerProIleGluValValValAspAlaIleHisLysLeuLys 220
 DB 601 CCCCTGCCGAGGAGACCTACCATGAGGTGCTGTGATGATTCACAAAGCTAAG 660
 QY 221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProThr 240
 DB 661 TATGAAAACCTACACACACACTCTTCTCATAGACATCATCAAAACAGACCCACACACA 720
 QY 241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValLeuSerTrpGluTyrPro 260
 DB 721 AACCTGAGCTGAAGCCATTGAAAATTTCTGGCACTGAGAGGCTGAGATATACCCC 780
 QY 261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGly 280
 DB 781 GACACCTGAGAGACCCCAATCTCTACTCTCCCTGACATTTTGCAATACAGGCCAGGCGC 840

QY 281 LysAsnAsnArgGlnLysLysAspArgLeuCysValAspLysThrSerAlaLysVal 300
 DB 841 AAGAAATTAAGAAAAAGATAGACTCTGGCTGAGACAGACCTCACCAAGGTCGTG 900
 QY 301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTrpSerSerTrp 320
 DB 901 TGGCACAGAGATCCAGATCCGCTGCAAGCCCGAGACCGCTACTATGATTCATCTGG 960
 QY 321 SerAspTrpAlaSerValSerCysSer 329
 DB 961 AGGACTGGGCACTCTGTCTCTCACT 987
 RESULT 4
 ID AA164388 standard; DNA: 990 BP.
 AA164388;
 AC AA164388;
 XX
 XX 23-NOV-2001 (first entry)
 XX
 DE Canine coding sequence #3.
 XX
 KW Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
 XX
 OS Canis familiaris.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..990
 FT sig-peptide 1..66 /product= "Canine protein #1"
 FT mat-peptide 67..987 /tag- b
 FT /tag- c
 XX JP2001161378-A.
 XX
 PD 19-JUN-2001.
 XX
 PF 26-SEP-2000; 2000JP-0292946.
 XX
 PR 01-OCT-1999; 99JP-0281234.
 XX
 PA (TORA) TORAY IND INC.
 XX
 DR WPI: 2001-592466/67.
 DR P-PSDB: AAG66482.
 XX
 PT Preparation of a highly pure protein, interleukin 12, a protein
 PT inhibiting the activity of interleukin 12, and a treating agent and a
 PT treating method for immunopathy of mammalian
 XX
 PS Claim 6; Page 16-17; 21pp; Japanese.
 XX
 CC The present invention relates to a method for the preparation of a highly
 CC pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
 CC the activity of IL12 is contacted to an ion exchanging carrier and/or a
 CC pigment carrier to get IL12 and/or a protein inhibiting the activity of
 CC IL12. The protein is used as a preventive agent for dog immunopathy. The
 CC present sequence was used in the method of the present invention.
 XX
 SQ Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 other:
 Alignment Scores:

| Pred. No.: | Length: | 990 |
|------------------------|---------|-----------------|
| Score: | 1764.00 | Matches: 329 |
| Percent Similarity: | 100.00% | Conservative: 0 |
| Best Local Similarity: | 100.00% | Mismatches: 0 |
| Query Match: | 100.00% | Indels: 0 |
| DB: | 22 | Gaps: 0 |

US-09-917-265-59 (1-329) x AA164388 (1-990)


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Qy 1 MethisProGInGInLeuValIleSerTrpPheSerLeuValIleuLeuAlaSerProLeu 20
Db 1 ATGCATCTCTCAGACATGGTCATCTCGGTTTCCCTGGTTTCTGCGCTCCCTCC 60
Qy 21 MetAlaIleTrpGluLeuGluLysAspValTyrValValGluLeuAspTrpHisProAsp 40
Db 61 ATGGCCATATGGAGACTGGAGAAAGATGTTTATGTTTGAGAGTTGGACAGCCCTGAT 120
Qy 41 AlaProGluGluMetValValLeuThrCysHisTrpProGluGluLysAspIleThrTrp 60
Db 121 GCCCCCGAGAAATGGTGGCTCTCAGCTGCCATACCCCTGAGAGAGATGACATCACTGG 180
Qy 61 ThrSerAlaGlnSerSerGluValLeuGluSerGlyLysThrLeuThrIleGlnValLys 80
Db 181 ACCTCAGCGGACAGACAGTGAAGTCTAGTTCTGGTAAACCTGACCATCCAAAGTCAA 240
Qy 81 GluPheGluAspAlaGlyGlnTyrThrCysHisLysGlyGlyLysValLeuSerArgSer 100
Db 241 GAATTTGGAGATGCTGGCCAGTATACCTCCATAAGAGAGCCAGCGTTCTGAGCCGCTCA 300
Qy 101 LeuLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGln 120
Db 301 CTCTCTGTTGATTCACAAAAAGAGATGGAATTTGGTCCACTGATATCTTAAAGAGACAG 360
Qy 121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
Db 361 AAAGATTCCAAAATATAGATCTTCTGAAATGTGAGCAAAAGATTTATCTTGAGACTTTC 420
Qy 141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerArg 160
Db 421 ACATGCTGGTGGTCACGCGCAATCAGTACTGATTTGAATTCAGCTCAAAAGTAGACA 480
Qy 161 GlyPheSerAspProGluGlnValThrCysGlyAlaValThrLeuSerAlaGluArgVal 180
Db 481 GGCTTCTCTGACCCCAAGGGGTGACATGTGGAGAGACACTTTCAGCAGAGAGGGTC 540
Qy 181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerLacys 200
Db 541 AGAGTGGACACAGAGGATTTAAGAGATACACAGTGGAGTGTACAGAGGGCGCTCCCTGC 600
Qy 201 ProSerAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
Db 601 CCCCTGCTGCCGAGGAGCCCTACCCATCGAGGTCGTGATGCTATTCACAACTCAAG 660
Qy 221 TyrGluAsnTyrTrpSerSerPhePheIleArgAspIleIleLysProAspProProThr 240
Db 661 TATGAAAGCTACACCAGCAGCTTCTTCATCAGAGACATCATCAACCCAGACCACACA 720
Qy 241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
Db 721 AACCTGCAGCTGAAGGCATTTGAAAAATTTCTGGCACGTGGAGGTCACTCGGCAATACCCC 780
Qy 261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGly 280
Db 781 GACACCTGGACACCCCAATCTCTACCTTCCTCCGACATTTTGCATCAGAGCCACAGGC 840
Qy 281 LysAsnAsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValVal 300
Db 841 AAGAACATATAGAGAAAGAAAGATAGACTTGGCTGGACAAAGACCTCGACCAAGTCGG 900
Qy 301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
Db 901 TGGCACAAGATGCGCAAGATCCCGCTGCAAGCCGAGACCGCTACTACTAGTTCAATCCGG 960
Qy 321 SerAspTrpAlaSerValSerCysSer 329
Db 961 AGCGACTGGGCATCTGTGCTCTGCACT 987

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RESULT 5
 AAV13816
 ID AAV13816 standard: cDNA to mRNA: 990 BP.
 XX
 AC AAV13816:

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XX 14-MAY-1998 (first entry)
DT Canine IL-12 P40 subunit cDNA.
XX
DE Canine; interleukin-12 P40 subunit; IL-12 P40 subunit; antitumour;
XX antiviral; vaccine adjuvant; ds.
XX
OS Canis sp.
XX
FH Key
FT Location/Qualifiers
FT 1..990
FT CDS /tag= a
FT /product= Interleukin-12_P40_subunit
XX
PN JP10036397-A.
XX
XX 10-FEB-1998.
XX
XX 08-NOV-1996; 96JP-0296789.
XX
XX 23-MAY-1996; 96JP-0128104.
XX
XX 08-NOV-1995; 95JP-0289729.
XX
XX (TORA ) TORAY IND INC.
XX
XX WPI: 1998-174914/16.
XX
XX P-PSDB: AAM41790.
XX
XX Canine interleukin 12 - comprises P40 and P35 subunits; useful in
XX veterinary medicine, e.g. antitumour, antiviral and vaccine adjuvant
XX activities are expected
XX
XX Claim 8: Page 8; 12pp: Japanese.
XX
XX
XX The present sequence encodes a canine interleukin-12 (IL-12) P40
XX subunit. A canine IL-12 comprising a P40 and P35 subunit is capable
XX of inducing an antiviral activating factor and the expression of
XX class II MHC molecules in canine tumour cells, stimulating
XX proliferation of canine blastogenic lymphocytes and activating
XX canine leukocytes to inhibit canine tumour cells. The canine IL-12
XX can be used in veterinary medicines, e.g. antitumour, antiviral and
XX vaccine adjuvant activities are expected.
XX
SQ Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 other;

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Alignment Scores:
 Pred. No.: 2,78e-167 Length: 990
 Score: 1735.00 Matches: 324
 Percent Similarity: 99.69% Conservative: 1
 Best Local Similarity: 99.39% Mismatches: 1
 Query Match: 98,368 Indels: 0
 DB: 19 Gaps: 0

US-09-917-265-59 (1-329) x AAV13816 (1-990)

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Qy 4 GInGInLeuValIleSerTrpPheSerLeuValIleuLeuAlaSerProLeuMetAlaIle 23
Db 10 CAGCGATGGTCATCTCTTGTTGTTCCCTGCTTGGCGCTCCCTCATGGGCCATA 69
Qy 24 TrpGluLeuGluLysAspValTyrValValGluLeuAspTrpHisProAspAlaProGly 43
Db 70 TGGGAAGTGGAAAGATGTTTATGTTGTAAGAGTTGAGTGGACCCCTGATGCCCGCGA 129
Qy 44 GluMetValValLeuThrCysHisThrProGluGluAspAspIleThrTrpThrSerAla 63
Db 130 GAAATGGTGGTCTCAGCCATCACTGCAAGAAAGATGACATCACTTGACACTCAGCG 189
Qy 64 GlnSerSerGluValLeuGluSerGlyLysThrLeuThrIleGlnValLysGluPheGly 83
Db 190 CAGACAGAGTGAAGTCTTAGCTTGTGTAAGACTGTGACCATCAAGTCAAAAGAAATTTGGA 249
Qy 84 AspAlaGlyGlnTyrThrCysHisLysGlyLysValLeuSerArgSerLeuLeu 103

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Db      250 GATGCTGGCAGATATACCTCCATAAAGGAGCAGGTTGTGAGCCGCTACCTCGTTTG
OY      104 ILEHISLYSLYSGIUSPGLYILETRPSETRHPSELEULYSGIUSGLUSER 123
Db      310 ATTCACAAAAAAGAGATGGAATTTGGTCACGATATCTTAAAGACAGAAAGAAATCC 369
OY      124 LYSASNLYSLIEPHELEULYSCYGIUALALYASNTYRSEGLYARGPHERHCYSTRP 143
Db      370 AAAAATTAAGATCTTTCTGAAATGTGAGCCAAAGAAATTAATCTTGAGCGTTTCACATCTCG 429
OY      144 TRPLEUTHRALALESETRHPSELEULYSPHESEVALLYSSERARGLYPHESER 163
Db      430 TGGCTGACGGCAATCATGACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGCTTCTCT 489
OY      164 ASPPROGLINGLYVALTHRCYSGIYALVALTHRLSESERALGLUARGLARGLVALASP 183
Db      490 GACCCCAAGGGGTGACATGTGAGCAGTGTGACACTTTCAGCAGAGAGGTCCAGAGTGAC 549
OY      184 ASNARGSPTRYLYSLYSTRYTRHVALGLUCYSGINGLYSERALACYSERARALA 203
Db      550 AACAGGATTAATAGACAGTACACAGTGTGAGTGTGAGGAGGCGAGTGCCTGCCCTCTGCC 609
OY      204 GLUGLUSERLEUPROILEGLVALVALALASPALALEHISLYSLEULYSTYRGLUSN 223
Db      610 GAGGAGAGCCTACCATCGAGGTGCTGTGGATGCTATTTCACAGCTCAAGTAGAAGAAC 669
OY      224 TYRTHRSETRPHEPHELEARGSPLEILELYSPROASPPROTHRASNLEULIN 243
Db      670 TACACACAGACTTCTTCATCAGACATCATCAAAACCAACCCACCAAAACCTGCGAG 729
OY      244 LEULYSPROLEULYASNSERARGLHISVALGLUALSERTPGLUTYRPROASPPHTRIP 263
Db      730 CTGAAGCCATTGGAATAATTTCGGCAGCTGAGAGTGGACCTGGCAATACCCGACACCTGG 789
OY      264 SESTRHPHSHSESTRYPHSETRLEUTHRPHESCYLEGLUALGLINGLYLYSASN 283
Db      790 AGCACCCACATCTCTCTCTCTCTCTCTGACATTTTGACATACAGCCGAGGACAGACAT 849
OY      284 ARGGLULYSLYSPARGLEUCYVALASPYSRHSERIALYVALVALCYSHISLYS 303
Db      850 AGAGAAAAAAGATAGACTCTGCTGACACAGACCTGACCAAGTGTGCTGCCACAG 909
OY      304 ASPALALYSLIEARGVALGLUALARGSPARGTYRYSERSESTRIPSEARASPTIP 323
Db      910 GATGCCAAGATCCCGCTGCAAGCCGAGACCGCTACTATATGTTTCATCTCTGAGCGACTCG 969
OY      324 ALASERVALSERCYSSER 329
Db      970 GCATCTGTGCCCTGCACT 987

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RESULT 6
ID AAX35615 standard; cDNA to mRNA; 990 BP.
XX AAX35615;
AC AAX35615;
DT 09-JUL-1999 (first entry)
XX Nucleic acid encoding canine Interleukin-12 (IL-12).
KW Interleukin-12; IL-12; dog; cat; immune disease; CALL12; heterodimer;
XX tumour; skin disease; infectious disease; allergic disease; ds.
OS Canis sp.
XX
XX
FH key Location/Qualifiers
FT CDS 1..990 /tag= a
XX
XX JP11106350-A.
XX
PD 20-APR-1999.

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XX      15-MAY-1998; 98JP-0133345.
XX      07-AUG-1997; 97JP-0213755.
XX      16-MAY-1997; 97JP-0127690.
XX
PA      (TORA ) TORAY IND INC.
XX      WPI: 1999-308068/26.
XX      P-PSDB: AAY02339.
XX
DR      A prevention and treating agent containing interleukin 12 (CALL12)
XX      for prevention and treatment of dog and cat immune diseases
XX
PS      Claim 1: Page 12; 16pp; Japanese.
XX
CC      The present sequence encodes canine interleukin-12 (IL-12). The
CC      specification describes a method for the prevention and treatment
CC      of dog and cat immune diseases. The treatment used an agent comprising
CC      dog IL-12 (CALL12) proteins to form a heterodimer. The agent is
CC      useful for preventing and treating dog and cat immune diseases,
CC      including tumours, skin diseases, infectious diseases and allergic
CC      diseases.
XX
SQ      Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 other.
XX
Alignment Scores:
Pred. No.: 2,78e-167 Length: 990
Score: 1735.00 Matches: 324
Percent Similarity: 99.69% Conservative: 1
Best Local Similarity: 99.39% Mismatches: 1
Query Match: 98.36% Indels: 0
DB: Gaps: 0

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US-09-917-265-59 (1-329) x AAX35615 (1-990)

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OY      4 GLUGLNUVALILSESTRPHESETRLEUTHRALALASERPROLEUMETALALE 23
Db      10 CACACAGTGTGATCTCTGTGGTTTCCGCTTTCTGCGTCCCTCATGGCCATA 69
OY      24 TRGGLUENGLUUSPVALTYRVALVALGLULEUASPTRPHISPROASPALPROGLY 43
Db      70 TGGGAACGTGAGAAACATTTATGTTGATGAGATTGAGCTGACCTGATGCCCGGA 129
OY      44 GLUMETVALVLEUTHRCYSHISHTRPROGLUGIUSPASPILLETHTRPHSERALA 63
Db      130 GAAATGTGCTCCTCACCTGCCATACCCCTGANAAGATGACATCTGGACCTGACCG 189
OY      64 GINSESERGLUVALLEUGLYSERGLYSTRHLEUTHRILEGLVALLYSGIUPHEGLY 83
Db      190 CAGAGCAGTGAAGTCTCTAGCTTCTGTAAACTCTGACCAATCCCAAGTCAAGAAATTGGA 249
OY      84 ASPALAGLYGINTYRTHRCYSHISLYSGIYLYSVALLEUSERARGSERLEULEU 103
Db      250 GATGCTGGCAGATATACCTGCCATTAAGAGAGCAAGTGTGAGCCGCTCACTCTCTTG 309
OY      104 ILEHISLYSLYSGIUSPGLYILETRPSETRHPSELEULYSGIUSGLUSER 123
Db      310 ATTCACAAAAAAGAGATGGAATTTGGTCACGATATCTTAAAGAACAGAAAGAAATCC 369
OY      124 LYSASNLYSLIEPHELEULYSCYGIUALALYASNTYRSEGLYARGPHERHCYSTRP 143
Db      370 AAAAATTAAGATCTTTCTGAAATGTGAGCCAAAGAAATTAATCTTGAGCGTTTCACATCTCG 429
OY      144 TRPLEUTHRALALESETRHPSELEULYSPHESEVALLYSSERARGLYPHESER 163
Db      430 TGGCTGACGGCAATCATGACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGCTTCTCT 489
OY      164 ASPPROGLINGLYVALTHRCYSGIYALVALTHRLSESERALGLUARGLARGLVALASP 183
Db      490 GACCCCAAGGGGTGACATGTGAGCAGTGTGACACTTTCACACAGAGAGGTCCAGAGTGAC 549
OY      184 ASNARGSPTRYLYSLYSTRYTRHVALGLUCYSGINGLYSERALACYSERARALA 203

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Db AACAGGATTTAAGAACTACACAGTGAGTGTGAGGAGGAGTGCCTGCCCTCTGCC 609
OY 204 GluGluSerLeuProIleGluValValAlaSpAlaIleHisLysLeuLysTyrGluAsn 223
Db 610 GAGAGAGCCCTAACCCATCGAGGTCTCGTGTGATGCTATTTCACAACTCAAGTATGAAAC 669
OY 224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProPheAsnLeuGln 243
Db 670 TACACGACGACCTTCTCATCAGACATCATCAACCAACCAACCAACCAACCAACCTGCAG 729
OY 244 LeuLysProLeuLysAsnSerArgHisValGluValSerTyrGluTyrProAspThrTrp 263
Db 730 CTGAAGCATTGGAATAATTCCTGCGCAGCTGAGCGTGCACCTGGAAATACCCGACACCTGG 789
OY 264 SerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsnAsn 283
Db 790 AGCACCCACATCTCTACTCTCTCCCTGACATTTTGCAATACAGGCCAGGCAAGAACAT 849
OY 284 ArgGluLysLysAspArgLeuCysValAlaSpLysThrSerAlaLysValValCysHisLys 303
Db 850 AGAAGAAAGAAAGATAGACTCTGCGTGACAAAGCTCTAGCCAAAGTGTGTGCCAAG 909
OY 304 AspaLalysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTyrPheSerPTrp 323
Db 910 GATGCCAAGATCCGCGTCCAGACCCGAGACCCGCTACTACTACTACTCTCTGAGGAGCTGG 969
OY 324 AlaSerValSerCysSer 329
Db 970 GCATCTGTGCCCTGCAGT 987

RESULT 7
AA03152
AA03152 standard; cDNA to mRNA; 990 BP.
AC AAX03152:
DT 30-MAR-1999 (first entry)
XX Nucleic acid encoding canine interleukin 12.
DE
XX Canine: interleukin 12; IL-12; feline: immunological disease; tumour;
KW skin disease; viral infection; allergic disease; breast tumour;
KW eosinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW othematoma; pneumoedema; skin soft pedicled soft tumour; anal tumour;
KW otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW dog parvovirus infection; distemper virus; cat plaque virus infection;
KW feline leukaemia; allergy; pollinosis; ds.
XX
OS Canis sp.
FH
FH Key Location/Qualifiers
FT CDS 1..990
FT /tag= a
FT /product= interleukin_12
PN W09851327-A1.
XX
XX 19-NOV-1998.
PD
XX
XX 07-MAY-1998; 98WO-JP02031.
PF
XX 16-MAY-1997; 97JP-0127690.
PR
XX
XX (TORA ) TORAY IND INC.
PA
XX Okano F, Satoh M, Yamada K:
PI
XX WPI: 1999-070100/06.
DR P-PSDB: AAMW84371.
XX
XX New therapeutic and prophylactic agents - comprise
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PT genetically-engineered canine interleukin 12, used to treat, e.g.
PT canine and feline immunological diseases
XX
PS Claim 1; Page 23-25; 45pp; Japanese.
XX
XX The present sequence encodes a canine interleukin 12 (IL-12) protein.
CC The IL-12 protein can be used in therapeutic or prophylactic agents.
CC The agents can be used to prevent and treat canine and feline
CC immunological diseases including dog and cat tumours, skin diseases,
CC viral infections and allergic diseases, especially tumours, breast
CC tumour, eosinophilic granuloma, epidermoid tumour, skin tumour, lipoma,
CC othematoma, pneumoedema, skin soft pedicled soft tumour and anal
CC tumour; skin diseases, otitis externa, dermatitis, eczema, fungal
CC diseases of the skin, pyoderma, allergic dermatitis, nettle rash,
CC traumatic dermatitis and hair loss; infections; dog parvovirus infection
CC and distemper virus, cat plaque virus infection and feline leukaemia, and
CC allergic diseases, e.g. pollinosis.
XX
SO Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 other:

Alignment Scores:
Pred. No.: 2.78e-167 Length: 990
Score: 1735.00 Matches: 324
Percent Similarity: 99.69% Conservative: 1
Best Local Similarity: 99.39% Mismatches: 1
Query Match: 98.36% Indels: 0
DB: 20 Gaps: 0

US-09-917-265-59 (1-329) x AAX03152 (1-990)
OY 4 GlnGluLeuValIleSerTrpPheSerLeuValLeuAlaSerProLeuMetAlaIle 23
Db 10 CAGCAGTGTGTCATCTCTGTTGTTTCCCTGTTTGTGCGGCTCCCTCATGCGCATTA 69
OY 24 TrpGluLeuGluLysAspValTyrValValGluLeuAspTrpHisProAspAlaProGly 43
Db 70 TGGGAAGTGGAGAAAGATGTTATGTGTAGAGTTGGAGCTGCACCTGATGGCCCGGA 129
OY 44 GluMetValIleLeuThrCysHisThrProGluGluAspAspIleThrTrpThrSerAla 63
Db 130 GAAATGGTGTCTCCTACCTGCCATACCCCTGAAGAAAGATGACATCTTGACCTCAGCG 189
OY 64 GlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPheGly 83
Db 190 CAGACCACTGAAGTCTAGTGTCTGTAACCTGACACCATCCAAAGTAAAGAAATTGGA 249
OY 84 AspaLaglGlnTyrThrCysHisLysGlyGlyLysValLeuSerArgSerLeuLeuLeu 103
Db 250 GATCGTGCAGTATACCTGCCATPAAAGAGCAAGTTTCAGACCGCTCCTGTTG 309
OY 104 IleHisLysLysGluAspGlyIleTyrPheThrAspIleLeuLysGluGlnLysGluSer 123
Db 310 ATTTCACAAAAAGAAAGATGAAATTGGTCCACTGATTACTTAAAGAAACAGAAATATCC 369
OY 124 LysAsnLysIlePheLeuLysCysGlnAlaLysAsnTyrSerGlyArgPheThrCysTrp 143
Db 370 AAAAATTAAGATCTTTCTCAAAATGTAGGCCAAAGAAATTTTCTGGACGTTTCAATGCTGG 429
OY 144 TrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPheSer 163
Db 430 TGGCTGACGGCAATCAGTACGATGTTGAATTTCACTGTCACAAAGTACGAGAGGCTTCT 489
OY 164 AspProGlnGlyValThrCysGlyValAlaValThrLeuSerAlaGluArgValArgValAsp 183
Db 490 GACCCCAAGGCGGTACATGTGACACACTTTCAGCAGAGAGGCTCAGAGGTGAC 549
OY 184 AsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlnLysSerAlaCysProSerAla 203
Db 550 AACAGGATTTAAGCACTACACACTGAGAGTGTACAGGAGGCGAGTGCCTGCTCTGCC 609
OY 204 GluGluSerLeuProIleGluValValAlaSpAlaIleHisLysLeuLysTyrGluAsn 223
Db 610 GAGAGAGCCCTAACCCATCGAGGTCTCGTGTGATGCTATTTCACAACTCAAGTATGAAAC 669
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OY 224 TyrThrSerSerPhePheIleArgAspIleIleIleuysProAspProProThrAsnLeuGln 243
 DB 670 TACACCACAGCAGCTTCTTCATCAGACATCATCAACCAAGCCAGCCACCAACCTGCAG 729
 OY 244 LeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTrpProAspThrTrp 263
 DB 730 CTGAAGCCATTGGAAATTTCTCGCAGCTGGAGCTGACCTGGGAATACCCGACACCTGG 789
 OY 264 SerThrProHisSerTyrPheSerLeuThrPheCysIleGlnIleGlnGlyLysAsnAsn 283
 DB 790 AGCACCCACATCTCTTCTACTTCTCTCCCTGACATTTTGACATACAGGCCAGGCAAGAACAT 849
 OY 284 ArgGluLysLysAspArgLeuGlyValAspLysThrSerAlaLysValIleCysHisLys 303
 DB 850 AGAGAAAGAAAGATAGACTCTGCGGTGACAAAGACCTAGCAAGTCGTGTCACACAG 909
 OY 304 AspAlaLysIleLeuValGlnAlaArgAspArgTyrTrpSerSerSerTrpSerAspTrp 323
 DB 910 GATGCCAAGATCCCGCTGCAGACCCGAGACCGCTACTATAGTTCATCTGGAGCGACTGG 969
 OY 324 AlaSerValSerCysSer 329
 DB 970 GCATCTGTGCTCCACT 987
 RESULT 8
 AA164378
 ID AA164378 standard; DNA; 990 BP.
 AC AA164378;
 XX 23-NOV-2001 (first entry)
 DT
 XX Canine coding sequence #1.
 DE
 XX Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
 KM
 XX Canis familiaris.
 OS
 XX
 PH Key Location/Qualifiers
 FT CDS 1..990
 FT sig-peptide /product= "Canine protein #1"
 FT mat-peptide /tag= b
 FT 67..987
 FT /tag= c
 PN JP2001161378-A.
 XX 19-JUN-2001.
 PD 26-SEP-2000; 2000JP-0292946.
 XX 01-OCT-1999; 99JP-0281234.
 PR (TORA) TORAY IND INC.
 XX
 PA WPI; 2001-592466/67.
 DR P-PSDB; AAG66480.
 XX
 PT Preparation of a highly pure protein, interleukin 12, a protein
 PT inhibiting the activity of interleukin 12, and a treating agent and a
 PT treating method for immunopathy of mammalian
 XX
 PS Claim 6; Page 14; 21pp; Japanese.
 CC The present invention relates to a method for the preparation of a highly
 CC pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
 CC the activity of IL12 is contacted to an ion exchanging carrier and/or a
 CC pigment carrier to get IL12 and/or a protein inhibiting the activity of
 CC IL12. The protein is used as a preventive agent for dog immunopathy. The
 CC present sequence was used in the method of the present invention.

XX
 SO Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 other.
 Alignment Scores:
 Pred. No.: 2,78e-167 Length: 990
 Score: 1735.00 Matches: 324
 Percent Similarity: 99.69% Conservative: 1
 Best local Similarity: 99.39% Mismatches: 1
 Query Match: 98.36% Indels: 0
 DB: 22 Gaps: 0
 US-09-917-265-59 (1-329) x AA164378 (1-990)
 OY 4 GlnGlnLeuValIleSerTrpPheSerLeuValLeuLeuAlaSerProLeuMetAlaIle 23
 DB 10 CAGAGTTGGTCACTCTCTGGTTTCCCTGGTTTCTGGCTCTCCCTCATGGGCANA 69
 OY 24 TrpGluLeuLysAspValTyrValIleGluLeuAspTrpHisProAspAlaProGly 43
 DB 70 TGGGAACGTGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTCATGCCGGA 129
 OY 44 GluMetValValLeuThrCysHisThrProGluGluAspPilleThrTrpThrSerAla 63
 DB 130 GAATGTGTGCTCCTCACTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCAGCG 189
 OY 64 GlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPheGly 83
 DB 190 CAGAGCAGTGAATCTCTAGGTTCTGTAAACCTGACATCAACCTCAAAAGATTTGGA 249
 OY 84 AspAlaGlyGlnTyrThrCysHisLysGlyGlyLysValLeuSerArgSerLeuLeu 103
 DB 250 GATGCTGGCCAGATACCTGCTGCCATTAAGAGAGGACGTTCTAGCGCTCCTCTGTTG 309
 OY 104 IleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluLysGluSer 123
 DB 310 ATTCACAAAAAAGAAAGATGGAAATTTGGTCCACTGATCTTAAGAGAAACAGAAATCC 369
 OY 124 LysAsnLysIlePheLeuLysCysGluAlaLysAsnTrpSerGlyYrPheThrCysTrp 143
 DB 370 AAAAATTAAGATCTTTTGTGAATGTGAGCAAGAAATTAATTTGTGAGTTTGCATGTGG 429
 OY 144 TrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerArgGlyPheSer 163
 DB 430 TGGCTGACGGCAATCAGTACTGATTTGAATTCAGTGCATAAAGTAGACAGAGCTTCCT 489
 OY 164 AspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgLysP 183
 DB 490 GACCCCAAGGGGTGACATGTGACAGCAGTTCAGCAGAGAGGTCAGACTGGAC 549
 OY 184 AsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProSerAla 203
 DB 550 AACAGGAGATTATAAGAGTACACAGTGGAGTGTGAGAGGAGTGTGCTGCCCTCTGTCC 609
 OY 204 GluGluSerLeuProIleGluValValValAlaIleHisLysLeuLysTyrGluAsn 223
 DB 610 GAGGAGAGCCCTACCATCGAGGTCTGTCGATCTATTACCAAGCTCAAGATGAAAAAC 669
 OY 224 TyrThrSerSerPhePheIleArgAspIleIleIleuysProAspProProThrAsnLeuGln 243
 DB 670 TACACGAGCCTCTTCTATCAGACATCAATCAACCAAGCCAGCCACCAAACTGTGAG 729
 OY 244 LeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTrpProAspThrTrp 263
 DB 730 CTGAAGCCATTGGAAATTTCTCGCAGCTGGAGCTGACCTGGGAATACCCGACACCTGG 789
 OY 264 SerThrProHisSerTyrPheSerLeuThrPheCysIleGlnIleGlnGlyLysAsnAsn 283
 DB 790 AGCACCCACATCTCTTCTACTTCTCTCCCTGACATTTTGACATACAGGCCAGGCAAGAACAT 849
 OY 284 ArgGluLysLysAspArgLeuGlyValAspLysThrSerAlaLysValIleCysHisLys 303
 DB 850 AGAGAAAGAAAGATAGACTCTGCGGTGACAAAGACCTGACCAAGGTCGTGTCACACAG 909

| | | | | |
|------------------------|---|---------------|---|-----|
| Oy | | 30 | ASPAALysLIeArGValGIInAlAArgAsPaRgTrYrTyrSerSerSerTriPserAspTriP | 325 |
| Dd | | 910 | GAATGGCCAAAGATCGCGCTGCACGCCGAGACCCTACTACTACTGTTCATTCTTGAGGCGACTGG | 965 |
| Oy | | 324 | AlAserValserCysSer 329 | |
| Dd | | 970 | GCAATCTGTGCTCCCTGCAGT 987 | |
| RESULT 9 | | | | |
| ID | AAx18176 | | | |
| XX | AAx18176 standard; cDNA: 2154 BP. | | | |
| AC | | | | |
| XX | AAx18176: | | | |
| DT | 07-MAY-1999 (first entry) | | | |
| DE | | | | |
| XX | Canine full length CLAF p40 subunit coding sequence. | | | |
| KW | CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog; | | | |
| KW | viral disease; canine distemper; canine parvovirus; autoimmune disease; | | | |
| XX | canine infectious hepatitis; ds. | | | |
| XX | | | | |
| OS | Canis sp. | | | |
| PN | MO9855511-Al. | | | |
| XX | | | | |
| PD | 10-DEC-1998. | | | |
| XX | | | | |
| PF | 26-MAY-1998: 98MO-JP02295. | | | |
| XX | | | | |
| PR | 03-JUN-1997: 97JP-OI61936. | | | |
| XX | | | | |
| PA | (KAGA) CHEMA-SERO-THERAPEUTIC RES INST. | | | |
| PI | Eda Y, Imamura T, Maeda H, Tokiyoshi S; | | | |
| DR | WPI: 1999-070260/06. | | | |
| XX | P-PDOB: AAW74322. | | | |
| PT | Canine cytokine protein which activates canine cytotoxic T | | | |
| PT | lymphocytes - is useful for treatment of viral and autoimmune | | | |
| XX | diseases in dogs | | | |
| PS | Claim 8; Page 30-31; 51pp; Japanese. | | | |
| XX | | | | |
| CC | This sequence encodes the canine lymphocyte activation factor (CLAF) of | | | |
| CC | the invention. CLAF activates lymphocytes, especially canine cytotoxic | | | |
| CC | T cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies | | | |
| CC | recognizing it may be used in the treatment of viral diseases in dogs | | | |
| CC | (such as canine distemper, canine parvovirus and canine infectious | | | |
| CC | hepatitis). The antibodies may also be used in isolation of CLAF from | | | |
| CC | culture of the transformant host cells by affinity chromatography. The | | | |
| CC | p40 homodimer can be used for the treatment of autoimmune diseases in | | | |
| XX | dogs. | | | |
| SQ | Sequence 2154 BP; 663 A; 448 G; 477 G; 566 T; 0 other: | | | |
| Alignment Scores: | | | | |
| Preed. No.: | 2,94e-166 | length: | 2154 | |
| Score: | 1729.50 | Matches: | 325 | |
| Percent Similarity: | 98.79% | Conservative: | 1 | |
| Best Local Similarity: | 98.48% | Mismatches: | 3 | |
| Query Match: | 98.04% | Indels: | 1 | |
| DB: | 20 | Gaps: | 1 | |
| OY | US-09-917-265-59 (1-329) x AAx18176 (1-2154) | | | |
| OY | 1 MetHisProGlnGluValIleSerTrpHeserLeuValLeuLeuAlaserProLeu 20 | | | |
| Dd | 52 ATGACATCTCACAGAGTTGCTATCTCCGTTTCCCGTTTGCGGCTCCGCCCTC 111 | | | |
| OY | 21 MetAlaIletrPGluLeuGluLysAspValTyraValGluLeuAspTrpHisProasp 40 | | | |

| | | | |
|-----------|--|--|------|
| Db | 112 | ATGGCCCATATGGGCAACTGGAGAAAGATGTTATGTTATGAGGTGGACATGGCACCCGAT | 171 |
| Oy | 41 | AlaProGlyGluMetValValLeuThrCysHisThrProGluGluAspPheIleThrTrp | 60 |
| Db | 172 | GGCCCCGGAGAAATGGTGTCCTCACCCTGCATACCCCTGAAGAAGATGACATCATTGG | 231 |
| Oy | 61 | ThrsSerAlaGlnSerSerGluValLeuGlySerGlyIysThrLeuThrIleGlnValLys | 80 |
| Db | 232 | ACCCACAGCGCAGACAGACAGTGCCTAGGTCTGTGTAAACCTCGACCATCCAAAGTCAA | 291 |
| Oy | 81 | GluPheGlyAspAlaGlyGlnIleThrCysHisLysGlyGlyLysValLleSerArgSer | 100 |
| Db | 292 | GAATTTGGAGATGCTGGCCCACTATACCTGCCATTAAGAGAGCAAGGTTCTGAGCGCTCA | 351 |
| Oy | 101 | LeuLeuLeu---IleHisLysLysGluAspGlyIleThrPheSerThrAspIleLeuLysGlu | 119 |
| Db | 352 | CTCCTGTTGATGATCCACAAAAAAGAAGATGGAAATTTGGTCCACTGATATCTTAAAGAA | 411 |
| Oy | 120 | GlnLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTrpSerGlyArg | 139 |
| Db | 412 | CAGAAAGAAATCCAAAAAATAAGATCTTCTGAAATGTAAGGCAAAAGAAATTAATTCGGACGT | 471 |
| Oy | 140 | PheThrCysTrpTrpIleuThrAlaIleSerThrAspLeuLysPheSerValLysSerSer | 159 |
| Db | 472 | TTCCATATGCTGGTGGCTGACGGCAGATCAGTACTATTGAAATTCAGTGTCAAAAGTAGC | 531 |
| Oy | 160 | ArgGlyPheSerAspProGlnGlyValIleThrCysGlyLysAlaValThrLeuSerAlaGluArg | 179 |
| Db | 532 | AGAGCGTCTCTGACCCCAAGGGGTGACATGTGACAGCAGTACACTTTTCAGCGAAGAG | 591 |
| Oy | 180 | ValArgValAspAsnArgAspTrpLysLysTrpThrValGluCysGlnGluGlySerAla | 199 |
| Db | 592 | GTCAGAGTGGCAGCAACAGGATTTAATAAGATACACAGTGGAGTGTGAGGAGGCGATGGCC | 651 |
| Oy | 200 | CysProSerIleAsnGluGluSerLeuProIleGluValValAlaLysAlaIleHisLysLeu | 219 |
| Db | 652 | TGCCCCCTCGCCGAGGAGAGCCATCCATCGAGGTGTGGTGATGCTATTCCACAAAGCTC | 711 |
| Oy | 220 | LysTrpGluAsnTrpThrPheSerPhePheIleArgAspIleIleLysProAspProPro | 239 |
| Db | 712 | AAGTATGAGAAACTACACCAGAGCTTCTTCATCGACACATCATCAAAACGACCAACC | 771 |
| Oy | 240 | ThrAsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTrp | 259 |
| Db | 772 | ACAAACTGCGAGCTGAGGACCATTTGAAAAATTTCTGGCCAGCGAGGTCAGCTGGGAATAC | 831 |
| Oy | 260 | ProAspThrTrpSerThrProHisSerTrpPheSerLeuThrPheCysIleGlnAlaGln | 279 |
| Db | 832 | CCCCACACCTGGACACCCCACTTCTACTTCTCCCTGACATTTTCCATACACAGCCAG | 891 |
| Oy | 280 | GlyLysAsnAsnArgGluLysLysAspArgLeuGlyValAspLysThrSerAlaLysVal | 299 |
| Db | 892 | GGCAAGAAACATACAGAAAAAGATATAGACTCTGGCTGCACAAGACTTCAGCCAAAGCTC | 951 |
| Oy | 300 | ValCysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTrpTrpSerSerSer | 319 |
| Db | 952 | GTCGGCCCAAGAGATGCCAGATCCGGGTGCAGACCCGAGACCCGCTACTATAGTTCATCC | 1011 |
| Oy | 320 | TrpSerAspTrpAlaSerValSerCysSer 329 | |
| Db | 1012 | TGGAGCGACGTGGCATCTGTGTCTCTGCAGT 1041 | |
| RESULT 10 | | | |
| AAAF26082 | | | |
| ID | AAAF26082 standard; DNA; 990 BP. | | |
| XX | AAAF26082; | | |
| XX | 24-APR-2001 (first entry) | | |
| XX | Feline IL-12p40 encoding DNA SEQ ID 8. | | |
| XX | Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection; | | |

KM interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
 XX
 OS Felis sp.
 XX MO200104280-A2.
 XX
 PD 18-JAN-2001.
 XX
 PF 08-JUL-2000; 2000WO-DE02262.
 XX
 PR 08-JUL-1999; 99CH-0001258.
 XX
 PA (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
 PA (UYZU-) UNIV ZUERICH.
 XX
 PI Leutenegger C, Schroff M, Miltig B, Lutz H;
 DR WPI: 2001-147190/15.
 XX
 PT Vaccine for treating or preventing lentivirus infection in cats,
 PT contains nucleic acid sequence encoding viral protein under control of
 XX eukaryotic promoter -
 PS Claim 14; Page 36; 37pp; German.
 CC This invention describes a novel vaccine (A) for prevention or treatment
 CC of lentivirus infection in felines which comprises an immunizing nucleic
 CC acid sequence (I) that contains, or comprises, at least part of a gene
 CC encoding a protein (II) of the virus, under control of a eukaryotic
 CC promoter functional in the relevant animal. (II) is especially the
 CC envelope (env) protein. The invention also describes (1) vaccine (A)
 CC containing an immunizing protein, or fragment, from a lentivirus plus at
 CC least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
 CC lentivirus protein, or fragment, especially derived from feline immune
 CC deficiency virus (FIV), by expressing the corresponding nucleic acid
 CC sequence in a host cell. The products of the invention have antiviral
 CC activity. The vaccine (A) and related protein-based vaccines, are
 CC particularly used to treat or prevent lentivirus infections in domestic
 CC cats, especially feline immune deficiency virus (FIV). Vaccination with
 CC (A) allows differentiation between vaccinated and infected animals, with
 CC the antibody status. The vaccines may be formulated with an adjuvant
 CC (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
 CC immune response, particularly a Th1 response.
 XX
 SQ Sequence 990 BP; 283 A; 249 C; 248 G; 210 T; 0 other;
 Alignment Scores:
 Pred. No.: 2,49e-159 Length: 990
 Score: 1657.00 Matches: 308
 Percent Similarity: 96.66% Conservative: 10
 Best Local Similarity: 93.62% Mismatches: 11
 Query Match: 93.93% Indels: 0
 DB: 22 Gaps: 0
 US-09-917-265-59 (1-329) x AAF26082 (1-990)
 QY 1 MethisProGInGInLeuValIleSerTrpPheSerLeuValLeuLeuAlaSerProLeu 20
 DB 1 ATGCATCCTCAGAGATTGTCATCGCTTTCCTGCTTTCCTGCGACCTCCCTC 60
 QY 21 MetAlaIleTPGInLeuGInLysAspAlaTyValValGInLeuAspTrpHisProAsp 40
 DB 61 ATGGCCATATGGGAAGTGGAGAAAAACGTTATATGTTGTAAGTTGGAGCTGGCACCTTAT 120
 QY 41 AlaProGInGInMetValValLeuThrCysHisTrpProGInGInLysAspAlaIleThrTrp 60
 DB 121 GCCCCGAGAAATGTCCTTACCTGCAATACCTCTGTAAGAAAGATGACATCACTGG 180
 QY 61 ThrSerAlaGInSerSerGInValLeuGInLysGInLysTrpLeuThrIleGInValLys 80
 DB 181 ACCTCTGACGAGAGAGTGAAGTCTCTAGCTGTAAACTGACCATCTCAAGTCAA 240
 QY 81 GluPheGInAspAlaGInLysTrpThrCysHisLysGInLysValLeuSerArgSer 100

DB 241 GAATTGGAGATGCTGGCCATATACCTGTATTAAGAGCGGAGTTCGAGCCATTCG 300
 QY 101 LeuLeuLeuIleHisLysLysGInAspGlyIleTrpSerThrAspIleLeuLysGInGIn 120
 DB 301 TTCCTCTGATACCAAAAGAGAGATGGAATTTGGTCCATGTATATCTTAAGGAAACAG 360
 QY 121 LysGInSerLysAsnLysIlePheLeuLysCysGInLysAlaLysAsnTrpSerGlyArgPhe 140
 DB 361 AAAGATCCAAAATAAGATCTTCTAAATGTGAGCAAAAGATTTCTGGACGTTTC 420
 QY 141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArg 160
 DB 421 ACCTGCTGTGGTGGTACGAGCGCAATCGATTTGAAATTCACCTGCAAAAGACGACGA 480
 QY 161 GlyPheSerAspProGInGInValThrCysGlyValValThrLeuSerAlaGInArgVal 180
 DB 481 GGCTCTCTGACCCCAAGGGGTGACTTGTGGACACCGACACTCTGAGAGAGAGGTC 540
 QY 181 ArgValAspAsnArgAspTrpLysLysTyThrValGInLysGInGInLysSerAlaCys 200
 DB 541 AGAGTGGACAAACAGGATTTAAGACATGACACTGGAGTGTGAGAGGCGAGCTTCG 600
 QY 201 ProSerAlaGInGInSerLeuProIleGInValValLysAlaIleHisLysLeuLys 220
 DB 601 CCGGCTCCGAGAGAGACCTTACCATTTGAAGTCTGCTGGACGCTATTCAACAGCTCAAG 660
 QY 221 TyrGInAsnTrpTrpSerSerPhePheIleArgAspIleIleLysProAspProProThr 240
 DB 661 TACCAAAACATACACACAGCTTCTTTCATCAGGACATCATCAACCCGAGCCACCAAG 720
 QY 241 AsnLeuGInLeuLysProLeuLysAsnSerArgHisValGInValSerTrpGluTyPro 260
 DB 721 AACCTGCAACGAGAGCCATTAAAAAATTTCGCGCATGTGGAAGTGAAGCTGGAAATACCT 780
 QY 261 AspThrTrpSerTrpProHisSerTrpPheSerLeuThrPheCysIleGInAlaGInGly 280
 DB 781 GACACCTGGACACCCACATCTTCTTCTTAACTTTGGCGTACAGGTCACAGGCG 840
 QY 281 LysAsnAsnArgGInLysLysAspArgLeuLysAspLysTrpSerAlaLysValVal 300
 DB 841 AAGAACAAACAGAGAAAGAAAGACAGACTCTCCGTGGAACAAAGCTGACCAAGTGTGTG 900
 QY 301 CysHisLysAspAlaLysIleArgValGInAlaArgAspArgTyTrpSerSerTrp 320
 DB 901 TGCACCAAGAGATGCCAAGATCCGCGTCAAGCCGAGGAGCGCTATATACATCATCTCG 960
 QY 321 SerAspTrpAlaSerValSerCysSer 329
 DB 961 AGCAACTGGGATCTCGTCTGTGAGT 987
 RESULT 11
 AAF26085
 ID AAF26085 standard; DNA; 990 BP.
 XX
 AC AAF26085;
 XX
 DT 24-APR-2001 (first entry)
 XX
 DE Feline IL-12p40 encoding DNA.
 XX
 KW Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
 KW immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
 KW Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
 XX
 OS Felis sp.
 XX
 PD WO200104155-A2.
 XX
 PD 18-JAN-2001.
 XX
 PF 08-JUL-2000; 2000WO-DE02263.
 XX

PR 08-JUL-1999; 99CH-0001259.
XX (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA (UYZU-) UNIT ZUERICH.
XX (RECC) UNIV CALIFORNIA.
PI Lutz H, Leutenegger C, Pedersen N, Schrott M, Wittig B;
XX WPI: 2001-147178/15.
DR
XX
XX Recombinant feline interleukin-12, useful as immunostimulant and for
PT treating e.g. viral infections in cats, and related nucleic acid
PT constructs
PS
XX
PS Claim 3: Page 30; 35pp: German.
XX
XX This invention describes a novel feline interleukin-12 (fIL-12)
CC polypeptide (f) that is expressed, by recombinant gene expression in
CC eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC of subunits p35 and p40. These proteins are formed so that, in equimolar
CC concentrations and in presence of an immunizing antigen, they can be
CC administered to carnivores, particularly domestic cats. The invention
CC also describes a nucleic acid construct (f1) encoding fIL-12 containing
CC sequences at least 95% identical with the p40- and p35-encoding sequences
CC (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC as immunostimulants for immunization against infectious diseases and/or
CC for treating infections or tumors in felines, especially domestic cats.
CC The products of the invention have immunostimulatory, antiviral and
CC antitumor activity. Nucleic acid constructs that encode (f1) are useful
CC as adjuvants for prophylactic immunization against viral diseases and for
CC treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC is useful for carnivores, and particularly domestic cats in the
CC following: (i) as immunostimulant, for preventative or therapeutic use;
CC and (ii) treating tumors and autoimmune diseases, or diseases associated
CC with a Th1 defect, especially pre-existing infections by feline immune
CC deficiency virus (FIV), feline leukemia virus and corona virus.
XX
SQ Sequence 990 BP; 283 A; 249 C; 248 G; 210 T; 0 other:
Alignment Scores:
Pred. No.: 2,496-159 Length: 990
Score: 1657.00 Matches: 308
Percent Similarity: 96.66% Conservative: 10
Best Local Similarity: 93.62% Mismatches: 11
Query Match: 93.93% Indels: 0
DB: 22 Gaps: 0
US-09-917-265-59 (1-329) x AAF26085 (1-990)
QY 1 MethisProGInGInLeuValIleSerTrpPheSerLeuValLeuLeuAlaSerProLeu 20
DB 1 ATGCATCCTCAGCACTTGTCATCGCTGTTTCCCTGGTTTCTGCGACCTCCCTCC 60
QY 21 MetAlaIleTrpGluLeuGluLysAspValTyrValValGluLeuAspTrpHisProAsp 40
DB 61 ATGGCCATATGGAACTGCAGCAAAACGTTTATGTTGAGACTTGGACTGCGACCTGAT 120
QY 41 AlaProGluGluMetValValLeuThrCysHisThrProGluGluAspAspIleThrTrp 60
DB 121 GCCCCCGGAAATGGTGGCTCTTACTGCACTACTCCGGAAGAGATGACATCCACTG 180
QY 61 ThrSerAlaGlnSerSerGluValLeuGluSerGlyLysThrLeuThrIleGlnValLys 80
DB 181 ACCCTTGACCAAGAGAGTGAAGTCCTAGGCTCTGTTAAACCTTGACCATCCAAAGTCAA 240
QY 81 GluPheGluAspAlaGluGlnTyrThrCysHisLysGluGlyLysValLeuSerArgSer 100
DB 241 GAATTTCGACATGCTGGCGCAGATATACCTGTCATAAAGAGGAGGAGCTTGAGCCATTGC 300
QY 101 LeuLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGln 120
DB 301 TTCCTCTGTATACACAAAAGAGAGATGGAATTTGCTCAGCATATCTTAAGCGAAGAG 360

QY 121 LysGluSerLysAsnLysIlePheLeuLysCysGluValAlaLysAsnTyrSerClyArgPhe 140
DB 361 AAGAAATCCAAATAAAGATCTTCTTAAAGTGGGCAAAAGATTTATTTGGAGCTTTC 420
QY 141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArg 160
DB 421 ACCCTGCTGGTGGCTGACCGCAATTCAGTACCGATTGCAATTTCACGTCAAAAGCAGAGA 480
QY 161 GlyPheSerAspProGluGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgVal 180
DB 481 GCCTCTGTGACCCCAAGGAGGCGGTGACTGTGGAGCAGCAGACCTCTCAGCAGAGAAGTTC 540
QY 181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerLys 200
DB 541 AGAGTGGACAAACAGGAGATTATAGAGTACACAGTGGAGTGCAGAGAGGAGGAGTCCCTGC 600
QY 201 ProSerAlaGluGluSerLeuProIleGluValValAspAlaIleHisLysLeuLys 220
DB 601 CCGGCTGGCGAGAGAGAGCTTACCCTTGAAGTCGTGGTGGAGCGCTATTACAGCTCAAG 660
QY 221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProThr 240
DB 661 TAGCAAAACTACACACAGAGCTTCTTCATCAGGACATCATCAACCGGACCCCAAG 720
QY 241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
DB 721 AACCTGCACATGACACCATTTAAATAATCTCGGCTGTGGAGTACGCTGGCAATATCCT 780
QY 261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGly 280
DB 781 GACACCTGGAGACACCCACATTCCTTACCTTCCCTTAACATTTGGCGTACAGGTCAGGGC 840
QY 281 LysAsnAsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValVal 300
DB 841 AAGAACACACAGAGAAAGAAAGACAGACTCTCCGTGGACAAAGCTCAGCCAAAGTCTCG 900
QY 301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
DB 901 TCCCAACAGATGCCCAAGATCCGCTGCAAGGCAAGGACCGCTACTATATGCTCATCTCG 960
QY 321 SerAspTrpAlaSerValSerCysSer 329
DB 961 AGCACTGGGCGCATCCGTCGTGCTGCAGT 987
RESULT 12
AAF26076
ID AAF26076 standard; DNA: 4522 BP.
AC AAF26076;
XX
DT 24-APR-2001 (first entry)
XX
DE Feline IL-12p40 encoding DNA SEQ ID 2.
XX
KW Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
XX
OS Felis sp.
XX
PN W0200104280-A2.
XX
PD 18-JAN-2001.
XX
PF 08-JUL-2000; 2000WO-DE02262.
XX
PR 08-JUL-1999; 99CH-0001258.
XX
PA (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA (UYZU-) UNIT ZUERICH.
PI Leutenegger C, Schrott M, Wittig B, Lutz H;
XX

DR WPI: 2001-147190/15.

XX Vaccine for treating or preventing lentivirus infection in cats.
PT contains nucleic acid sequence encoding viral protein under control of
PT eukaryotic promoter -

PS Disclosure: Page 29-31; 37pp; German.

CC This invention describes a novel vaccine (A) for prevention or treatment
CC of lentivirus infection in felines which comprises an immunizing nucleic
CC acid sequence (I) that contains, or comprises, at least part of a gene
CC encoding a protein (II) of the virus, under control of a eukaryotic
CC promoter functional in the relevant animal. (II) is especially the
CC envelope (env) protein. The invention also describes (1) vaccine (A)
CC containing an immunizing protein, or fragment, from a lentivirus plus at
CC least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC lentivirus protein, or fragment, especially derived from feline immune
CC deficiency virus (FIV), by expressing the corresponding nucleic acid
CC sequence in a host cell. The products of the invention have antiviral
CC activity. The vaccine (A) and related protein-based vaccines, are
CC particularly used to treat or prevent lentivirus infections in domestic
CC cats, especially feline immune deficiency virus (FIV). Vaccination with
CC (A) allows differentiation between vaccinated and infected animals, from
CC the antibody status. The vaccines may be formulated with an adjuvant
CC (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC immune response, particularly a Th1 response.

XX Sequence 4522 BP; 1180 A; 1126 C; 1106 G; 1110 T; 0 other;

Alignment Scores:

Pred. No.: 2,01e-158 Length: 4522
Score: 1657.00 Matches: 308
Percent Similarity: 96.66% Conservative: 10
Best Local Similarity: 93.62% Mismatches: 11
Query Match: 93.93% Indels: 0
DB: Gaps: 0

US-09-917-265-59 (1-329) x AAF26076 (1-4522)

QY 1 MethisProGlnGlnLeuValIleSerTrpPheSerLeuValLeuLeuAAserProLeu 20
DB 3047 ATGCATCTCAGACGATGGTCATCGCTGGTTTCCCTGGTTGGTGCACCTCCCTC 3106
QY 21 MetAlaIleTrpGluLeuGluLysAspValTrpValValGluLeuLeuSPTPhisProAsp 40
DB 3107 ATGGCCATATGACGACGACGAGAAAGGTTTATGTTTAAAGTTGGACCTGCACCTGAT 3166
QY 41 AlaProGlyGluMetValValLeuThrCysHisThrProGlnGluAspAspIleThrTrp 60
DB 3167 GCCCCGAGAAATGGTGTCTTACCTGCATATCTCTGAAGAAGTGCATCACCCTGG 3226
QY 61 ThrSerAlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
DB 3227 ACCTCTGACGAGCAGTGAAGTCCTAAGCTCTGTGAAGAACTCTGCACATCCAAAGTCAA 3286
QY 81 GluPheGlyAspAlaGlyGlnTrpThrCysHisLysGlyLysValLeuLeuSerArgSer 100
DB 3287 GAATTTGCCAATGCTGCGCCAGTATACCTGTCATTAAGGAGGCGAGGTTCTGAGCCATTCG 3346
QY 101 LeuLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGlnGln 120
DB 3347 TTCTCTCTGATACCAAAAAGAAAGATGGAATTTGGTCCACGTATCTTAAGGGAACG 3406
QY 121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTrpSerGlyArgPhe 140
DB 3407 AAAGAAATCCAAAATAGATCTTTAAATATGAGGCAAAAGAAATATCTGAGACGTTTC 3466
QY 141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArg 160
DB 3467 ACCTGCTGGTGGTGCAGGCAATACCTACCGATTTGATAATTCATCTCAAAAGCAGCA 3526
QY 161 GlyPheSerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgVal 180
DB 161 GlyPheSerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgVal 180

DB 3527 GGCTCTCTGTGACCCCAAGGGGTGACTTGTGAGCAGCAGCAGCTCTCAGCAGAAAGTGC 3586
QY 181 ArgValAlaAspAsnArgAspTrpLysLysTrpThrValGluCysGlnGlnGlySerAlaCys 200
DB 3587 AGAGTGGACAACACAGCATTAATAGAACTACACAGTGGAGTGCAGGAGGCGACCTGC 3646
QY 201 ProSerAlaGlnGlnSerLeuProIleGluValValAlaAspAlaIleHisLysLysLys 220
DB 3647 CCGGCTCCGAGGAGACCTTACCATTTGAAGTGTGTGGACGCTATTTCACAAAGTCAAG 3706
QY 221 TyrGluAsnTrpThrSerSerPhePheIleArgAspIleIleLysProAspProThr 240
DB 3707 TACCAAAACATACACACAGCAGCTTCTCATCAGGAGCATCATCAACCGGACCCCAAG 3766
QY 241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTrpPro 260
DB 3767 AACCTGAACTGAAAGCCATTAAATAATTCCTGGCATGTGGAACTGAGCTGGGAATACCT 3826
QY 261 AspThrTrpSerThrProHisSerTrpPheSerLeuThrPheCysIleGlnAlaGlnGly 280
DB 3827 GACACCTGGAGCAGCCACCATCTCTACTTCTCTTAACTTTGGCTTACAGGTCCAGGGC 3886
QY 281 LysAsnAsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysVal 300
DB 3887 AAGAACACAGCAGAAAGAAAGACAGACTCTCCGTGGACAAAGACCTCAGCCAAAGTCTG 3946
QY 301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTrpTrpSerSerTrp 320
DB 3947 TGCACACAGGATCCCAAGATCCCGCTGCAGAGCCAGGACCGCTACTATAGTCTATCTCG 4006
QY 321 SerAspTrpAlaSerValSerCysSer 329
DB 4007 AGCAACTGGGACATCCGTCTCTCAGT 4033
RESULT 13
ID AAF26094 standard; DNA: 4522 BP.
AC AAF26094:
XX 24-APR-2001 (first entry)
DT XX
DE Plasmid pmol-fill12p40 DNA SEQ ID 10.
XX
KW Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS Synthetic.
PN WO200104155-A2.
PD 18-JAN-2001.
XX
PE 08-JUL-2000; 2000WO-DE02263.
XX
PR 08-JUL-1999; 99CH-0001259.
XX
PA (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA (UYZU-) UNIV ZUERICH.
PA (REGC) UNIV CALIFORNIA.
XX
PI Lutz H, Leutenegger C, Pedersen N, Schrott M, Wittig B;
DR WPI: 2001-147178/15.
XX
PT Recombinant feline interleukin-12, useful as immunostimulant and for
PT treating e.g. viral infections in cats, and related nucleic acid
PT constructs -
XX
PS Example 1c; Page 33-35; 35pp; German.
CC This invention describes a novel feline interleukin-12 (fIL-12)

CC polypeptide (1) that is expressed, by recombinant gene expression in
CC eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC of subunits p35 and p40. These proteins are formed so that, in equimolar
CC concentrations and in presence of an immunizing antigen, they can be
CC administered to carnivores, particularly domestic cats. The invention
CC also describes a nucleic acid construct (11) encoding fli-12 containing
CC sequences at least 95% identical with the p40- and p35-encoding sequences
CC (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC as immunostimulants for immunization against infectious diseases and/or
CC for treating infections or tumors in felines, especially domestic cats.
CC The products of the invention have immunostimulatory, antiviral and
CC antitumor activity. Nucleic acid constructs that encode (11) are useful
CC as adjuvants for prophylactic immunization against viral diseases and for
CC treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC is useful for carnivores, and particularly domestic cats in the
CC following: (1) as immunostimulant, for preventative or therapeutic use;
CC and (11) treating tumors and autoimmune diseases, or diseases associated
CC with a Th1 defect, especially pre-existing infections by feline immune
CC deficiency virus (FIV), feline leukemia virus and corona virus.

XX Sequence 4522 BP; 1180 A; 1126 C; 1106 G; 1110 T; 0 other:

Alignment Scores:
Pred. No.: 2,01e-158 Length: 4522
Score: 1657.00 Matches: 308
Percent Similarity: 96.66% Conservative: 10
Best local Similarity: 93.62% Mismatches: 11
Query Match: 93.93% Indels: 0
DB: 22 Gaps: 0

US-09-917-265-59 (1-329) x AAF26094 (1-4522)

QY 1 MethisProGInGInLeuValIleSerTrpPheSerLeuValLeuLeuAlaSerProLeu 20
Db 3047 ATGCATCCTCAGCAGTTGGTCATGCGCTTTCCCTGGTTCGCGACCCCTC 3106
QY 21 MetaIleTrpGluLeuGluLysAspValTyValValGluLeuAspTrpHisProAsp 40
Db 3107 ATGGCCATATCGAAGCTGAGAAACCTTTATGTTGAGAGTTGCACTGCACCTGAT 3166
QY 41 AlaProGluGluMetValIleLeuThrCysHisThrProGluGluAspPheThrTrp 60
Db 3167 GCCCCCGAGAAATGGTCTCTTACCTGCAATACTCCTGAAGAATGACATCACCCTGG 3226
QY 61 ThrSerAlaGlnSerSerGluValLeuGlySerGlyThrLeuThrIleGlnValLys 80
Db 3227 ACCCTGACCAAGACAGCTGAGCTCTGAGCTCTGTAACCTCGACCATCAAGTCAA 3286
QY 81 GluPheGlyAspAlaGlyGlnTrpThrCysHisLysGlyGlyValLeuSerArgSer 100
Db 3287 GAATTCGACATGCTGGCCATATACCTGATCAAAAGAGCGAGCTTCTAGCCATTGG 3346
QY 101 LeuLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGln 120
Db 3347 TTCTCTCTGTATACCAAAAGCAAGATGGAATTGGTCCACTGATATCTTAAGGAACAG 3406
QY 121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTrpSerGlyArgPhe 140
Db 3407 AAGAAATCCAAAATAAGATCTTTCTAAAATGTAGAGCAAAAGAAATTAATCTGGACGTTTC 3466
QY 141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArg 160
Db 3467 ACCGTGCTGGTGGCGACGGCAATCAGTACCGATTGGAATTCACCTGTAAGAGCAGCA 3526
QY 161 GlyPheSerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgVal 180
Db 3527 GCGTCCCTCAGCAACCCCAAGGCTGACTTGTGACAGCAGCACTCTCAGCAGAGAAGTTC 3586
QY 181 ArgValAspAsnArgAspTrpLysLysTrpThrValGluCysGlnGluGlySerAlaCys 200
Db 3587 AGAGTGACACAGGAGATTAAGAAGTACACAGTGGAGTGTCTCAGAGCGCAGTCCCTGC 3646

QY 201 ProSerAlaGluGluSerLeuProIleGluValValAlaAspAlaIleHisLysLeuLys 220
Db 3647 CCGCGTCCGAGGAGAGCGCTTACCATTTGAGTCCGTGGTGAACCGTATTCACAGCTCAAG 3706
QY 221 TyrGluAsnTrpThrSerSerPhePheIleArgAspIleIleLysProAspProThr 240
Db 3707 TACGAAACCTACACAGCAGCTTCTTCATCAGGACATCAATCAAAACCGACCCACCAAG 3766
QY 241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTrpPro 260
Db 3767 AACCTGCAAGTGAAGCCATTAAATAATCTCGGCATGTGGAAAGTAGCTGGGAATATCCT 3826
QY 261 AspThrTrpSerThrProHisSerTrpPheSerLeuThrPheCysIleGlnAlaGlnGly 280
Db 3827 GACACCTGAGACACCCCACTTCCACTTCTCCTTAACATTTGGCGTACAGTCCAGGCG 3886
QY 281 LysAsnAsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysVal 300
Db 3887 AAGAACAACAGAGAAAGAAAGACAGACTCTCCGTGACAAAGACCTCAGCCAAAGTCTGTG 3946
QY 301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTrpTrpSerSerTrp 320
Db 3947 TGCACAAAGAGATGCCAAGATCCGCTGCAAGCCAGGACCGCTACTATATGATTCATCTGG 4006
QY 321 SerAspTrpAlaSerValSerCysSer 329
Db 4007 AGCAACTGGGATCCGTCTCTCTCGAGT 4033
RESULT 14
AAV56625
ID AAV56625 standard; cDNA; 2193 BP.
AC AAV56625;
XX 23-NOV-1998 (first entry)
DT
XX
DE Feline FLAfp40 cDNA.
XX
KM Cytokine; feline; FLAfp40; FLAfp35; heterodimer; cytotoxic; treatment;
KM T lymphocyte cell; autoimmune disease; ds.
XX
OS Felis catus.
XX
XX
FH Key Location/Qualifiers
FT CDS 64..1053
FT sig_peptide 64..129
FT mat_peptide 130..1050
FT /*tag= c
FT /*product= "FLAfp40"
FT /*note= "feline cytokine"
XX
XX
PN WO9746583-A1.
XX
PD 11-DEC-1997.
XX
XX
PE 29-MAY-1997; 97WO-JP01824.
PR 04-JUN-1996; 96JP-0165249.
XX
XX
PA (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.
PI Fujiyasu T, Imagawa Y, Imamura T, Maeda H, Tokiyoshi S;
XX
XX WPI: 1998-042118/04.
XX P-PSDB: AAW76173.
XX
XX Novel feline cytokine protein - useful for treating feline
XX auto-immune diseases, e.g. those caused by feline herpes virus or
XX feline calicivirus
XX
PS Claim 19; Page 52-54; 94pp; Japanese.

XX This sequence encodes a novel feline cytokine protein, FLAP40. This
 CC protein can be used in the production of a FLAP35/FLAP40 heterodimer
 CC which can potentiate the cytotoxic activity of feline cytotoxic T
 CC lymphocyte cells. Such proteins are used for treatment of feline
 CC autoimmune diseases e.g. as caused by feline herpes virus or feline
 CC calicivirus.

XX Sequence 2193 BP; 680 A; 451 C; 493 G; 569 T; 0 other;

Alignment Scores:

Pred. No.: 3 04e-158 Length: 2193
 Score: 1651.00 Matches: 307
 Percent Similarity: 96.35% Conservative: 10
 Best Local Similarity: 93.31% Mismatches: 12
 Query Match: 93.59% Indels: 0
 DB: 19 Gaps: 0

US-09-917-265-59 (1-329) x AAV56625 (1-2193)

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QY 1 MethisProGInGInLeuVal11SerTrpPheSerLeuValLeuLeuAlaSerProleu 20
DB 64 ATGCATCCTGACGACGCTGCTCATCGCCGTTTACCGTGTTCCTGGCAGCTCTCTC 123
QY 21 MetAlaIleTPGluLeuGluLysAspAlaValValGluLeuAspTrpHisProasp 40
DB 124 ATGGCCATATGGGAAGTGGAGAAAACCTTTATGTGTAGAGTTGGCTGGCACCCTGAT 183
QY 41 AlaProGluGluMetValValLeuThrCysHisThrProGluGluAspAlaIleThrTrp 60
DB 184 GCCCCCGGAAATGGTGGTCCCTCAGCAATCTCTGAGAGAGATGACATACCTGG 243
QY 61 ThrSerAlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
DB 244 ACCCTGTGACGACGACGAGTGAAGTCTAGGCTCTGTAACCTGACCATCAAGTCAAA 303
QY 81 GluPheGlyAspAlaGlyInTyThrCysHisLysGlyGlyLysValLeuSerArgSer 100
DB 304 GAATTTCAGATGCTGGCCAGTATACCTGCTCATTAAGAGAGCGGTTCTGAGCCATTGG 363
QY 101 LeuLeuLeuIleHisLysLysGluAspGly11eTrpSerThrAspIleLeuLysGluGln 120
DB 364 TTCCTCCTGATACCAAAAAGAAAGATGATTTGGCCACTGATATCTTAAGGGAACAG 423
QY 121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyTrpSerGlyArgPhe 140
DB 424 AAGGAATCCAAAAATTAAGATCTTCTTAAATGTGAGGCAAAAGATTAATCTTGACGCTTC 483
QY 141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerArg 160
DB 484 ACCTGGCTGGTGGTGAAGCAATCAGTACGATTTGAATTCACCTGTCMAAACACACAGCA 543
QY 161 GlyPheSerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgVal 180
DB 544 GGCCTCCCTGACCCCAAGGGGTGACTTGTGAGCAGCCGACCTCTCAGCAGAGAGTTC 603
QY 181 ArgValAspAsnArgAspTyTrpLysTyTrpValGluCysGlnGluLysSerAlaGly 200
DB 604 AGAGTGGACAAACAGGATTTAAGACGACAGTGAAGTGAAGGAGGAGGAGTGGCTGC 663
QY 201 ProSerAlaGluGluSerLeuProIleGluValValAlaAspAlaIleHisLysLeuLys 220
DB 664 CCGGCTGCCGAGAGAGCTACCATTTGAAGTCGTGGTGGAGCGCTTTTCAACAGCTCAAG 723
QY 221 TyrGluAsnTyTrpSerSerPhePheIleArgAspIleIleLysProAspProThr 240
DB 724 TACGAAATCTACCCGACAGCTTCTTCATCAGGGACATCATCAAAACCGACCCACCAAG 783
QY 241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTrpPro 260
DB 784 AACCTGCAACGTAGAGCATTAATAAAATTCCTGGCATGTGGAAGTGAAGTGGGGAATACCT 843
QY 261 AspThrTrpSerThrProHisSerTyPheSerLeuThrPheCysIleGlnAlaGlnGly 280

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DB 844 GACACCTGGACACCCACCATTTCTCTTAACTTGGCTACAGGTCCAGGC 903
QY 281 LysAsnAsnArgGluLysLysAspArgLeuCysValAspLysTrpSerAlaLysVal 300
DB 904 AAGAAACAAACAGAGAAAAGAAAGACAGACTCTCCCTGGACAAAGACTGAGCAAGTCTG 963
QY 301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyTrpSerSerTrp 320
DB 964 TGCCCAAGATGCCAGATCCGCTCAAGCCGAGACCCGCTACTTACTCTATCTCTG 1023
QY 321 SerAspTrpLysSerValSerCysSer 329
DB 1024 AGCAACTGGGATCGTGTCTCTGAGT 1050

```

RESULT 15

AAAX18177 standard; cDNA; 924 BP.

```

ID AAX18177
AC AAX18177:
DT 07-MAY-1999 (first entry)
DE Canine mature CIAF p40 subunit coding sequence.
KW CIAF: canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
  viral disease; canine distemper; canine parvovirus; autoimmune disease;
  canine infectious hepatitis; ds.
OS Canis sp.
PN WO9855511-A1.
PD 10-DEC-1998.
PF 26-MAY-1998; 98WO-JP02295.
PR 03-JUN-1997; 97JP-0161936.
PA (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
PI Eda Y, Imanura T, Maeda H, Tokiyoshi S;
DR WPI: 1999-070260/06.
DR P-PsDB; AAW74323.
PT Canine cytokine protein which activates canine cytotoxic T
  lymphocytes - is useful for treatment of viral and autoimmune
  diseases in dogs
PS Claim 8; Page 32; 51pp; Japanese.
XX
XX This sequence encodes the canine lymphocyte activation factor (CIAF) of
  the invention. CIAF activates lymphocytes, especially canine cytotoxic
  T cells. The protein contains a p35 and a p40 subunit. CIAF or antibodies
  recognising it may be used in the treatment of viral diseases in dogs
  (such as canine distemper, canine parvovirus and canine infectious
  hepatitis). The antibodies may also be used in isolation of CIAF from
  CC culture of the transformant host cells by affinity chromatography. The
  CC p40 homodimer can be used for the treatment of autoimmune diseases in
  CC dogs.
SQ Sequence 924 BP; 273 A; 222 C; 234 G; 195 T; 0 other;

```

Alignment Scores:

Pred. No.: 1 91e-155 Length: 924
 Score: 1618.50 Matches: 303
 Percent Similarity: 98.70% Conservative: 1
 Best Local Similarity: 98.38% Mismatches: 3
 Query Match: 91.75% Indels: 1
 DB: 20 Gaps: 1

US-09-917-265-59 (1-329) x AAX18177 (1-924)

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OY 23 ILeTPGIuLeuGIuLysAspValTyrValValIGluLeuAspTrpHisProaspAlaPro 42
    |||||||
Db 1 ATATGGAACTGGAGAAAGATGTTATATGTTAGAGTTGGACTGGCACCCTGATGCCCCC 60
OY 43 GlyIuMetValValLeuThrCysHisThrProGIuGIuAspAsp1LeThrTrpThrSer 62
    |||||||
Db 61 GGAGAAATGTGCTGCTCCTGACCTGACCTGACCCCTGAAGAAGATGACATGCACTTGGACCTCA 120
OY 63 AlaGIuSerSerGIuValLeuGIuSerGIuLysThrLeuThrIleGIuValLysGIuPhe 82
    |||||||
Db 121 GCGCAGACGACGTAAGTCTGAGTCTGTAACCTGACCTGACCATCCAGCTCAAGAAATTT 180
OY 83 GlyAspAlaIGluGIuTyrThrCysHisLysGIuLysValLeuSerArgSerLeuLeu 102
    |||||||
Db 181 GGAGATGCTGGCCATATACCTGCTCCATTAAGAGAGGAGGATTCAGCCGCTCAGCTCTG 240
OY 103 Leu---IleHisLysLysGIuAspGIuLeuTrpSerThrAsp1LeuLysGIuLys 121
    |||||||
Db 241 TTTGATTCACAAAAAGAAAGATGGAATTTGCTCCAGTATCTTAAGAGACAGAAA 300
OY 122 GluSerLysAsnLysIlePheLeuLysCysGIuAlaLysAsnTyrSerGIuArgPheThr 141
    |||||||
Db 301 GAATCCAAAAATTAAGATCTTCTGAAATGTGAGCCAAAGAAATTAATTCGACGTTTCACA 360
OY 142 CysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGly 161
    |||||||
Db 361 TGCTGTGCTGCTGACGGCATTGACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGC 420
OY 162 PheSerAspProGIuGIuValThrCysGIuAlaValThrLeuSerAlaGIuArgValArg 181
    |||||||
Db 421 TTCTCTGACCCCAAGGGGTGACATGTGAGCAGTGCACCTTTCAGCAGAGAGGTGACA 480
OY 182 ValAspAsnArgAspTyrLysLysTyrThrValGIuCysGIuLysGIuLysSerAlaCysPro 201
    |||||||
Db 481 GTGCACAACAGGATTAATAGCAAGTACACAGTGTGAGTGTGACAGCGCAGTGCCTGCCCC 540
OY 202 SerAlaIGluGIuSerLeuProIleGIuValValAlaAspAlaIleHisLysLeuLysTyr 221
    |||||||
Db 541 TCTGCCGAGAGAGAGCTTACCCATCGAGGTGCTGTGTGATGCTATTTCACAGCTCAAGTAT 600
OY 222 GluAsnTyrThrSerSerPhePheIleArgAsp1LeIleLysProAspProProThrAsn 241
    |||||||
Db 601 GAAACTACACCACGAGCTTTTCATCAGAGCATCATCAAACCAAGACCACCCCAAAAC 660
OY 242 LeuGIuLeuLysProLeuLysAsnSerArgHisValGIuValSerTrpGIuTyrProAsp 261
    |||||||
Db 661 CTGCAGCTCAAGCCATGTGAAAAATTCGCGCACGTGAGTGTGAGTGTGAGTGTGAGTGTG 720
OY 262 ThrTrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGIuAlaGIuLysLys 281
    |||||||
Db 721 ACCTGGACACCCCACTTCTCTACTTCTCCTGACATTTTGCATACAGGCCCCAGGCAAG 780
OY 282 AsnAsnArgGIuLysLysAspArgLeuCysValAspLysThrSerAlaLysValCys 301
    |||||||
Db 781 AACCAATAGCAAAAGAAAGATAGACTGTGCTGACCAAGACCTCAAGCCAGTCTGTGTC 840
OY 302 HisLysAspAlaLysIleArgValIleAlaArgAspArgTyrTyrSerSerSerTrpSer 321
    |||||||
Db 841 CACAAGGATGCCAAAGATCCCGCTGCAAGCCGAGACCCGCTACTATATGTTTCATCTGAGC 900
OY 322 AspTrpAlaSerValSerCysSer 329
    |||||||
Db 901 GACTGGCATCTGTGTCTGTCAGT 924
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Search completed: July 16, 2003, 20:24:09
Job time : 239.604 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: July 16, 2003, 19:41:51 ; Search time 1564.91 Seconds

(without alignments)
3404.880 Million cell updates/sec

Title: US-09-917-265-59

Perfect score: 1764

Sequence: 1 MHPOQLVISMFLVLLASPL.....QARDRYSSSSWDVASVSCS 325

Scoring table:

BIOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+.p2n.model -DEV=xlh
-O=/cgn2_1/USPRO.spool/US09917265/runat_15072003_092107_1610/app.query.fasta_1.3114
-DB=EST -QMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST: *
1: em_estba: *
2: em_esthum: *
3: em_estlin: *
4: em_estlmq: *
5: em_estlov: *
6: em_estlpl: *
7: em_estro: *
8: em_hic: *
9: gb_est1: *
10: gb_est2: *
11: gb_hic: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estlom: *
17: gb_gss: *
18: em_gss_hum: *
19: em_gss_inv: *
20: em_gss_pln: *
21: em_gss_vtc: *
22: em_gss_fun: *
23: em_gss_man: *
24: em_gss_mus: *
25: em_gss_other: *
26: em_gss_pro: *
27: em_gss_rtd: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | DB ID | Description |
|------------|-------|---------|--------------|-------|-----------------------------|
| 1 | 566.5 | 32.1 | 475 | 12 | BF704417 MT-P-E6-a |
| 2 | 354 | 20.1 | 535 | 17 | A2441303 1M0232M24 |
| 3 | 324 | 18.4 | 569 | 17 | A2853726 A2853726 2M0157M01 |
| 4 | 170 | 9.6 | 668 | 17 | AG079702 Pan trogl |
| 5 | 156 | 8.8 | 509 | 12 | BG554242 dab70a07 |
| 6 | 153.5 | 8.7 | 875 | 9 | AL537375 AL537375 |
| 7 | 152.5 | 8.6 | 882 | 14 | BQ223533 AGENCOURT |
| 8 | 150.5 | 8.5 | 997 | 9 | AL528607 AL528607 |
| 9 | 144.5 | 8.2 | 873 | 9 | AL518132 AL518132 |
| 10 | 138.5 | 7.9 | 511 | 12 | BG359887 dab88405 |
| 11 | 134.5 | 7.6 | 591 | 14 | BM685621 UI-E-C10 |
| 12 | 134 | 7.6 | 324 | 17 | AO981401 RPI1-23-3 |
| 13 | 133.5 | 7.6 | 481 | 14 | BM710190 UI-E-CQ1 |
| 14 | 133.5 | 7.6 | 769 | 14 | BM719097 UI-E-ED1 |
| 15 | 129.5 | 7.3 | 683 | 10 | AW950312 EST362382 |
| 16 | 129.5 | 7.3 | 938 | 12 | BE901933 601676878 |
| 17 | 127.5 | 7.2 | 912 | 13 | B1760931 603043131 |
| 18 | 127 | 7.2 | 1082 | 14 | BM919605 AGENCOURT |
| 19 | 126 | 7.1 | 700 | 14 | BO749057 UI-M-FB0 |
| 20 | 123.5 | 7.0 | 502 | 10 | BE650170 UI-M-BH3 |
| 21 | 123.5 | 7.0 | 624 | 12 | BG713383 p911n.PK0 |
| 22 | 123 | 7.0 | 846 | 9 | AL525319 AL525319 |
| 23 | 122.5 | 6.9 | 412 | 9 | A1629081 fc09d01.Y |
| 24 | 120.5 | 6.8 | 361 | 14 | T28073 EST26562 Hu |
| 25 | 119.5 | 6.8 | 666 | 14 | BM935910 UI-M-G0P |
| 26 | 119.5 | 6.8 | 859 | 12 | BG434397 602506409 |
| 27 | 119 | 6.7 | 675 | 12 | BG621100 602616982 |
| 28 | 118 | 6.7 | 742 | 9 | AL549396 AL549396 |
| 29 | 118 | 6.7 | 906 | 12 | BG54874 602714263 |
| 30 | 118 | 6.7 | 918 | 9 | AL550798 AL550798 |
| 31 | 118 | 6.7 | 927 | 9 | AL553060 AL553060 |
| 32 | 118 | 6.7 | 948 | 9 | AL545121 AL545121 |
| 33 | 118 | 6.7 | 950 | 9 | AL551603 AL551603 |
| 34 | 118 | 6.7 | 973 | 9 | AL548148 AL548148 |
| 35 | 117 | 6.6 | 707 | 14 | BM718865 UI-E-ED1 |
| 36 | 117 | 6.6 | 793 | 13 | B1834803 603090245 |
| 37 | 116.5 | 6.6 | 916 | 9 | AL576559 AL576559 |
| 38 | 115.5 | 6.5 | 488 | 12 | BF997791 MR2-GN012 |
| 39 | 115 | 6.5 | 877 | 14 | BQ230610 AGENCOURT |
| 40 | 114.5 | 6.5 | 890 | 12 | BG620398 602617523 |
| 41 | 114.5 | 6.5 | 1642 | 14 | BM919170 AGENCOURT |
| 42 | 114 | 6.5 | 856 | 9 | AL546165 AL546165 |
| 43 | 114 | 6.5 | 1022 | 9 | AL554313 AL554313 |
| 44 | 113.5 | 6.4 | 779 | 13 | B133959 60297231 |
| 45 | 113.5 | 6.4 | 866 | 13 | B1520198 603071446 |

ALIGNMENTS

RESULT 1
LOCUS BF704417 475 bp mRNA linear EST 22-DEC-2000
DEFINITION MI-P-E6-acc-g-09-1-UM.s1 MT-P-E6 Sus scrofa cDNA clone
ACCESSION BF704417
VERSION BF704417.1 GI:11989825
KEYWORDS EST.
SOURCE Sus scrofa
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
REFERENCE 1 (bases 1 to 475)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene

Best Local Similarity: 71.00% Mismatches: 21
 Query Match: 20.07% Indels: 1
 DB: 17 Gaps: 0
 US-09-917-265-59 (1-329) x AZ441303 (1-535)

QY 30 ValTrValValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThr 49
 |||||
 DB 86 GTTATGTTGTAGAGGTGAGTGGACTGCCATGCCCTGGAGAAACAGTACACTCAC 145
 QY 50 CysHisThr-ProGluGluAspAspIleThrTrpHisSerAlaGlnSerSerGluValle 69
 |||||
 DB 146 TGTGACACGCTCTCAGAGATGACATCCTGGACCTGAGACGACAGACATGAGCAT 205
 QY 69 uGlySerGlyLysThrLeuThrIleGlnValIysGluPheGlyAspAlaGlyGlnTrpTh 89
 |||||
 DB 206 AGGCTCTGCAAGACCTGACCATCCTGCTCAAGAGTTTCTAGATGCTGGCCAGTACAC 265
 QY 89 rCysHisLysGlyLysValLeuSerArgSerLeuLeuLeuIleHisLysGluAs 109
 |||||
 DB 266 CTGCCACAAAGAGGAGGAGACTGTGAGCCACTGCATCTGCTGCCACAGAGAGAAA 325
 QY 109 pGlyIleTrpSerThrAspIleLeuLysGluGlnLysGlnSerLysAsnLysIlePhe 128
 |||||
 DB 326 TGGAAATTGTGTCACATGAAATTTAAAGTAATTCATCCCTGTCGACATATCTT 383

RESULT 3
 AZ853726/c 569 bp DNA linear GSS 21-FEB-2001
 LOCUS 2M0157M01F Mouse 10kb plasmid UUCGM library Mus musculus genomic
 DEFINITION clone UUCG2M0157M01 F, DNA sequence.
 ACCESSION AZ853726
 VERSION AZ853726.1 GI:13042136
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 569)
 Dnnn.D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamll,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
 and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center
 University of Utah
 Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0157 row: M column: 01
 Seq primer: CGGTGTAACAGCAGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 569.
 Location/Qualifiers
 1..569
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCG2M0157M01"
 /clone_lib="Mouse 10kb plasmid UUCGM library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: pWD42nv: Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (91473211419b1a129072.1), a copy-number
 inducible derivative of plasmid RI. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 143 a 137 c 153 g 136 t
 ORIGIN

Alignment Scores:
 Pred. No.: 1.07e-26 Length: 569
 Score: 324.00 Matches: 66
 Percent Similarity: 82.56% Conservative: 5
 Best Local Similarity: 76.74% Mismatches: 15
 Query Match: 18.37% Indels: 2
 DB: 17 Gaps: 0

US-09-917-265-59 (1-329) x AZ853726 (1-569)

QY 30 ValTrValValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThr 49
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 DB 283 GTTATGTTGTAGAGGTGAGTGGACTGCCATGCCCTGGAGAAACAGTGAACCTCAC 224
 QY 50 CysHisThrProGluGluAspAspIleThrTrpHisSerAlaGlnSerSerGluValle 69
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 DB 223 TGTGACACGCTCTCAGAGATGACATCCTGGACCTGAGACGACAGACATGAGTACAT 164
 QY 70 GlySerGlyLysThrLeuThrIleGlnValIysGluPheGlyAspAlaGlyGlnTrpTh 89
 |||||
 DB 163 GCCTGTGAAAGAGACCTGACCATCCTGCAAGAGTTTCTAGATGCTGGCCAGTACACC 104
 QY 90 CysHisLysGlyGlyValLeuSerArgSerLeuLeuLeuIleHisLysGluLysp 109
 |||||
 DB 103 TGCCCAAGAGGAGGAGACACTGTGAGCCACTGATCTGCTGCTCCCAAGAGAAAAA- 45
 QY 110 GlyIleTrpSerThrAsp 115
 |||||
 DB 44 GGAAT-TGCTCAGCGAT 28

RESULT 4
 AG079702/c 668 bp DNA linear GSS 03-NOV-2001
 LOCUS Pan troglodytes DNA, clone: PTB-075107.R, genomic survey sequence.
 DEFINITION AG079702
 ACCESSION AG079702.1 GI:16631504
 VERSION AG079702.1 GI:16631504
 KEYWORDS GSS.
 SOURCE Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
 BAC Library clone:PTB-075107.R.
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
 1
 Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
 Totokli,Y., Watanabe,H. and Sakaki,Y.
 BAC end sequences of Library PTB
 2 (bases 1 to 668)
 Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
 Totokli,Y., Watanabe,H. and Sakaki,Y.
 Direct Submision
 Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
 1-7-22 Suenho-chou,Tsukumi-Ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail:chimbases@sc.riken.go.jp, URL:http://hnp.gsc.riken.go.jp/,
 Tel:81-45-503-9111, Fax:81-45-503-9170)

COMMENT Clones are derived from the chimpanzee BAC library PIB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.

| FEATURES | SOURCE | Location/Qualifiers |
|------------|--------|-----------------------------|
| | | 1. 668 |
| | | /organism="Pan troglodytes" |
| | | /db_xref="taxon:9598" |
| | | /clone="PTB-075107.R" |
| | | /sex="male" |
| | | /cell_type="lymphoblast" |
| | | /clone.lib="PTB chimpanzee |
| BASE COUNT | | 180 a 138 c 137 g 213 t |
| ORIGIN | | |


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Oy 216 11eHstLysLeuLysTyrGlu-----AsnTyr 224
      :::::
Db 665 CTCACAC--ATCACTACAGAGCTTCACATCACTCAGCAATGCCCTGGGCCACATGGC 722
Oy 225 ThrSerSerPhePheLeuArg---AspIleIleLysProAspProProThrAsnLeuGln 243
      :::::
Db 723 ACAGCTATCACCCTTGGACGAGCTTCACCATTTGAGAGCTGACCTCCACAGAAATGCGTA 782
Oy 244 LeuLysProLeu---LysAsnSerArghisValGluValSerTrpGluTyrProAspThr 262
      :::::
Db 783 GCCCGGCGAGTCCAGCAGACCTCGCGGCTGGAGGTGACGTGGACAGACCCCTCGACC 842
Oy 263 TrpSerThrProHis--SerTyrPheSerLeuThrPheCys 275
      :::::
Db 843 TGGCCTGACCCCTGAGCTTTTTCCTCTCAAGTCTTCTTC 882

RESULT 9
AL518132
LOCUS AL518132 LTI_NFL011.NBC1 Homo sapiens cDNA clone CS0DA010YM20 5
DEFINITION prime, mRNA sequence.
ACCESSION AL518132.1 GI:12781625
VERSION AL518132.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 873)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
          Genoscope Centre National de Sequencage
          BP 191 91006 Evry cedex - France
          Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr.
FEATURES
      source
          1..873
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="CS0DA010YM20"
            /clone_lib="LTI_NFL011_NBC1"
            /sex="male"
            /tissue_type="neuroblastoma cells"
            /lab_host="DH10B"
            /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
          was primed with a NotI-Oligo(dT) primer. Five prime end
          enriched, double-stranded cDNA was digested with Not I and
          cloned into the Not I and Eco RV sites of the pCMVSPORT 6
          vector. Library is not normalized, but is the control for
          the normalized libraries. Library was constructed by Life
          Technologies. Contact : Feng Liang Life Technologies, a
          division of Invitrogen 9800 Medical Center Drive Rockville
          , Maryland 20850, USA fax : (1) 301 610 8371 Email :
          fliang@life.com URL :
          http://fulllength.invitrogen.com"
BASE COUNT 148 a 298 c 251 g 165 t 11 others
ORIGIN

```

Alignment Scores:

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Pred. No.:      8.47e-06      Length:      873
Percent:        144.50       Matches:      62
Best Local Similarity: 36.63%  Conservatve: 27
                        25.51%  Mismatches:   96
Query Match:     8.19%      Indels:      60
                        Gaps:      11

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US-09-917-265-59 (1-329) x AL518132 (1-873)

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Oy 43 G1yglumetValleuThrCysHisThrProGluGluAsp---AspIleThrTrp--- 60
      :::::
Db 264 GCGCTCTGACGTCACACTGCTGCGACAGCAAACTCGATGCTCGCTGACGTCGCG 323

```

```

Oy 61 ---ThrsEraIaGlnSerSerGluValleuGlySerGlyLysThrLeuThrIleGlnVal 79
      :::::
Db 324 GTAATATKGACAGACCTGGCCCCCTGACCTGCTCAACGGCTCTTACGTGGTGTCCATGGC 383
Oy 80 LysGluPheGlyAspAlaGlyIleGlyTrpThrCysHisLysGlyGlyLysValLeuSerArg 99
      :::::
Db 384 CTGGAACCTGGCGACAGTGGCTTCACAGCTGCTCTTCACCGTACGACCTCCGACCTGGCC 443
Oy 100 SerLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGlu 119
      :::::
Db 444 CACCAAGATCTCTGCTGATGTC-----GGCTTG----- 470
Oy 120 GlnLysGlnSerLysAsnLysIlePheLeuLysCysGlnAlaLysAsnTyrSerGlyArg 139
      :::::
Db 471 -----CCGCGCGGAGGCTGCTTCTGACCTGGCTCCACACTTACCCCAAGGC 521
Oy 140 PheThrCysTrpTrpLeuThrAlaIleSerThrAspLysPheSerValLysSerSer 159
      :::::
Db 522 TTCTACTGCAAGCTGGCATCTGCCACCCCACTTACAT----- 560
Oy 160 ArgGlyPheSerAspProGlnIleValThrCysGlyAlaValThrLeuSerAlaGlyArg 179
      :::::
Db 561 -----CCCAAC-----ACCTCAATGTACTGCTGCTGATGCTGCCA 599
Oy 180 ValArgValAspAsnArgAspTyrLysLysTyrThrValGlnCysGlnGlnGlySerAla 199
      :::::
Db 600 ATTATGCT-----TGCA-GAAGA----- 619
Oy 200 CysProSerAlaGlnGlnSerLeuProIleGlnValValAspAlaIleHisLysLeu 219
      :::::
Db 620 ---CCAGCGCTCAAGAACCGCTGCCACATTCGTACATGACACCTGTTCCACC--ATC 674
Oy 220 LysTyrGlu-----AsnTyrThrSerSerPhe 228
      :::::
Db 675 AAGTACAAAGCTCTCATAGTGCAGCAATGCCCTGGCCACAAATGCCACACTATCACCC 734
Oy 229 PheIleArg---AspIleIleLysProAspProProThrAsnLeuGlnLeuLysProLeu 247
      :::::
Db 735 TTTGACGAGATTCAACCTTTGTGAAGCTGTATCTCTCCAGAAATGTGTATACCCGGCAGTG 794
Oy 248 ---LysAsnSerArgHisValGluValSerTrpGluTyrProAspThrTrpSerThrPro 266
      :::::
Db 795 CCAGCAACCTCGCGCGCTGGAGGAGTGAGTGAGACCCCTCGACCTGCGCTGAMCCT 854
Oy 267 HisSerTyr 269
      :::::
Db 855 GAGCTCTTTT 863

RESULT 10
LOCUS BG359887
DEFINITION dabb8905.y1 NICHD XGC Emb2 Xenopus laevis cDNA clone IMAGE:4404680
          5' similar to TR:016542 Q16542 INTERLEUKIN-11 RECEPTOR. ; mRNA
          sequence.
ACCESSION BG359887
VERSION BG359887.1 GI:13240578
KEYWORDS EST.
SOURCE Xenopus laevis
          African clawed frog.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoae; Pipidae;
          Xenopodinae; Xenopus.
REFERENCE 1 (bases 1 to 511)
AUTHORS Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D.,
          Martin, J., Wylie, T., Underwood, K., Theisling, B., Bowers, Y., Person
          , B., Gibbons, M., Harvey, N., Riltter, E., Jackson, Y., McCann, R.,
          Waterston, R., and Wilson, R.
          Washu Xenopus EST project, 1999
          Unpublished (1999)
          Other_ESTs: dabb8905.x1
          Contact: Sandy Clifton, Ph.D.
          Washu Xenopus EST project, 1999
          Washington University School of Medicine

```


100

ATCACACATG

QY 316 TyrserserTrpserAspTrpala 324
 Db 397 ATT---GGGACATGGAGTGTGACGAC 420

RESULT 15

AM950312 683 bp mRNA linear EST 01-JUN-2000
 LOCUS EST362382 MAGE resequences, MAGE Homo sapiens cDNA, mRNA sequence.
 DEFINITION AM950312
 ACCESSION AM950312
 VERSION AM950312.1 GI:8139961
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 683)
 Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt,
 I. E., Saeed, A. I., Sharov, V., Lee, N. H., Yeatman, T. J. and
 Quackenbush, J.

TITLE Assessment of gene expression patterns in a model of colon tumor
 metastasis using a 19,200 element cDNA microarray

JOURNAL Unpublished (2000)
 COMMENT Contact: John Quackenbush

The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 3528
 Fax: 301 838 0208

Email: johnq@ligr.org
 Plate: 13

Seq primer: Reverse.

FEATURES
 source Location/Qualifiers
 1..683
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="MAGE resequences, MAGE"
 /note="Vector: pBluescriptSKm"

BASE COUNT 141 a 233 c 190 g 119 t
 ORIGIN

Alignment Scores:

Pred. No.: 0.00031 Length: 683
 Score: 129.50 Matches: 34
 Percent Similarity: 46.22% Conservative: 21
 Best Local Similarity: 28.57% Mismatches: 33
 Query Match: 7.34% Indels: 31
 Ds: 10 Gaps: 6

US-09-917-265-59 (1-329) x AM950312 (1-683)

QY 219 LeuLysTYRGLuAsnTYRTrpSerSerPhePheLeuArgAspIleIleLysProAspPro 238
 Db 22 ATCACCCTTTGACGAGTTTCACG-----ATTGTGAAGCCTGTATCCT 60
 QY 239 ProThrAsnLeuGlnLeuLysProLeu---LysAsnSerArgHisValGluValSerTrp 257
 Db 61 CCAGAAATGTGTGTAAGCCGCGGACAGTCCACCAACCTCGCGGCTGGAGTGTGAGTGG 120
 QY 258 GluTYRProAspThrTrpSerThrProHisSerTYRPheserLeuThrPheCysIleGln 277
 Db 121 CAGACCCCTCGACCTGGCCTGACCTGAGTCT--TTTCCTCTCAAGTTCTTTCTGCC 177
 QY 278 AlaGlnGlyLysAsnAsnArgGluLysLysAspArgLeuCysValAspLys----- 294
 Db 178 TACCGA-----CCCTCATCTCTGGACCACTGGCGACGACAT 210
 QY 295 -----ThrSerAlaLysValValCysHisLysAspAla 305
 Db 211 GTGAGAGTGTCCGAGCGACAGCAGACACATCATCAGATGCCACCGGAAAGAGTAC 270
 QY 306 LysIleArgValGlnAlaIleArgAspArgTYRTrpSerSerSerTrpserAspTrpala 324
 Db 271 ATTATCCAGTGTGAGCGCAAGGACAAATGAGATT--GGGACATGGAGTGTGACGAC 324

Search completed: July 17, 2003, 09:27:13
 Job time : 1567.91 secs

GenCore version 5.1.6
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OM protein - nucleic search, using irame_plus.p2n model

Run on: July 16, 2003, 19:43:49 : Search time 46.3954 Seconds
(without alignments)
2174.711 Million cell updates/sec

Title: US-09-917-265-59
Perfect score: 1764
Sequence: 1 MHPOQLVSWFSVLTLASPL.....QARDRYSSMSDWASVSCS 329

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Xgapop 10.0 , Ygapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Issued-Patents_NA -OPMT=fastlap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS-human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pcr -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCGAPOP=6
-FCGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: Issued-Patents_NA:*
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6: /cgn2_6/prodata/1/ina/pcrus-COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 2 | 1731 | 98.1 | 990 | 4 | US-09-079-984A-11 |
| 3 | 1502.5 | 85.2 | 987 | 4 | US-08-848-760B-24 |
| 4 | 1502.5 | 85.2 | 1623 | 2 | US-08-751-767A-9 |
| 5 | 1502.5 | 85.2 | 1870 | 4 | US-09-310-842-4 |
| 6 | 1502.5 | 85.2 | 2318 | 4 | US-09-851-062-3 |
| 7 | 1502.5 | 85.2 | 6139 | 2 | US-08-751-767A-7 |
| 8 | 1501.5 | 85.1 | 987 | 1 | US-08-186-529-1 |
| 9 | 1501.5 | 85.1 | 987 | 1 | US-08-640-386A-1 |
| 10 | 1501.5 | 85.1 | 1018 | 2 | US-08-184-009-194 |
| 11 | 1501.5 | 85.1 | 1018 | 2 | US-08-458-356-194 |
| 12 | 1501.5 | 85.1 | 1018 | 4 | US-08-460-736-194 |

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|----|--------|------|------|---|-------------------|--------------------|
| 13 | 1501.5 | 85.1 | 1399 | 2 | US-08-751-767A-3 | Sequence 3, Appli |
| 14 | 1501.5 | 85.1 | 2362 | 1 | US-08-265-087-1 | Sequence 1, Appli |
| 15 | 1501.5 | 85.1 | 2362 | 1 | US-08-621-493-1 | Sequence 1, Appli |
| 16 | 1501.5 | 85.1 | 2362 | 2 | US-08-965-688-1 | Sequence 1, Appli |
| 17 | 1501.5 | 85.1 | 2362 | 2 | US-09-260-173-1 | Sequence 1, Appli |
| 18 | 1422.5 | 80.6 | 1560 | 2 | US-08-751-767A-11 | Sequence 11, Appli |
| 19 | 1142.5 | 64.8 | 1095 | 2 | US-08-385-335A-13 | Sequence 13, Appli |
| 20 | 1132.5 | 64.2 | 6295 | 2 | US-08-659-206A-4 | Sequence 4, Appli |
| 21 | 1132.5 | 64.2 | 7287 | 2 | US-08-659-206A-1 | Sequence 1, Appli |
| 22 | 193 | 10.9 | 1074 | 2 | US-08-621-151A-15 | Sequence 15, Appli |
| 23 | 193 | 10.9 | 1404 | 6 | 5171840-8 | Patent No. 5171840 |
| 24 | 193 | 10.9 | 1404 | 6 | 5480796-8 | Patent No. 5480796 |
| 25 | 193 | 10.9 | 1486 | 4 | US-08-795-473B-3 | Sequence 3, Appli |
| 26 | 193 | 10.9 | 1486 | 4 | US-07-439-856-3 | Sequence 3, Appli |
| 27 | 193 | 10.9 | 2061 | 6 | 5171840-1 | Patent No. 5171840 |
| 28 | 193 | 10.9 | 2061 | 6 | 5480796-1 | Patent No. 5480796 |
| 29 | 193 | 10.9 | 3319 | 4 | US-08-795-473B-2 | Sequence 2, Appli |
| 30 | 193 | 10.9 | 3319 | 4 | US-09-439-856-2 | Sequence 2, Appli |
| 31 | 170 | 9.6 | 1591 | 1 | US-07-865-878A-3 | Sequence 3, Appli |
| 32 | 170 | 9.6 | 1591 | 1 | US-07-676-647-1 | Sequence 1, Appli |
| 33 | 170 | 9.6 | 1591 | 1 | US-08-449-329-1 | Sequence 1, Appli |
| 34 | 170 | 9.6 | 1591 | 2 | US-08-448-073-1 | Sequence 1, Appli |
| 35 | 170 | 9.6 | 1591 | 2 | US-08-585-258-1 | Sequence 1, Appli |
| 36 | 170 | 9.6 | 1591 | 2 | US-08-603-010-3 | Sequence 3, Appli |
| 37 | 170 | 9.6 | 1591 | 4 | US-09-211-590-1 | Sequence 1, Appli |
| 38 | 170 | 9.6 | 1591 | 5 | PCT-US91-03896-1 | Sequence 1, Appli |
| 39 | 149.5 | 8.5 | 2456 | 4 | US-09-151-102-1 | Sequence 1, Appli |
| 40 | 149.5 | 8.5 | 2456 | 4 | US-08-929-846-1 | Sequence 1, Appli |
| 41 | 146.5 | 8.3 | 1705 | 4 | US-08-702-665A-2 | Sequence 2, Appli |
| 42 | 146.5 | 8.3 | 1714 | 4 | US-09-151-102-3 | Sequence 3, Appli |
| 43 | 146.5 | 8.3 | 1714 | 4 | US-08-929-846-3 | Sequence 3, Appli |
| 44 | 145 | 8.2 | 1800 | 4 | US-08-702-665A-4 | Sequence 4, Appli |
| 45 | 129 | 7.3 | 1161 | 1 | US-08-383-750-5 | Sequence 5, Appli |

ALIGNMENTS

RESULT 1
US-08-079-984A-11
Sequence 11, Application US/09079984A
Patent No. 6231850
GENERAL INFORMATION:
APPLICANT: Okano, Fumiyoshi, Satoh, Masahiro,
Applicant: Yamada, Katsushige
TITLE OF INVENTION: Canine interleukin 12, a production method thereof, an immune disease treatment method and preventive method using it
TITLE OF INVENTION: method using it
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Miller & Christenbury Intellectual Property
ADDRESS: Department of Schnader, Harrison, Segal and Lewis, LLP
STREET: 1600 Market Street, 39th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079, 984A
FILING DATE: 15-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Austin R. Miller
REGISTRATION NUMBER: 16,602
REFERENCE/DOCKET NUMBER: 1051-98
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-1810
TELEFAX: (215) 568-6946
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:

LENGTH: 990 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 ORIGINAL SOURCE:
 ORGANISM: Canis familiaris
 FEATURE:
 NAME/KEY: Canine IL12
 LOCATION: 1 to 987
 IDENTIFICATION METHOD: Similarity
 US-09-917-984A-11

Alignment Scores:
 Pred. No.: 7,33e-199 Length: 990
 Score: 1764.00 Matches: 329
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 0

US-09-917-265-59 (1-329) x US-09-079-984A-11 (1-990)

QY 1 MethisProglInleuValIleSerTyrPheSerleuValIleuLeuAlaSerProleu 20
 Db 1 ATGCATCCTCAGCAGTTGGTCATCTCTGGTTTCCCTGTTGGCTGGGCTCCCTC 60
 QY 21 MetAlaIleTrrGluLeuGluLysAspValTyrValValGluLeuAspTrrPheSerPro 40
 Db 61 ATGCCAATGCGAAGTGGAGAAAGATGTTATGTGTAGAGTTGGAGCTGGACCCCTGAT 120
 QY 41 AlaProglInleuMetValIleuLeuThrCysHisIsthProglInleuAspAspIleThrTyr 60
 Db 121 GCCCCCGGAGAAATGGTGGTCTCCTACCTGCCATACCCCTGAAGATGACATCCTGG 180
 QY 61 ThrSerAlaInSerSerGluValIleuGlySerGlyThrleuThrIleGlnValLys 80
 Db 181 ACCTCAGCGCAGACAGCTGAAGTCCTAGTTCGTGTAAGCTCGACCATCCAAAGTCAAA 240
 QY 81 GluPheGlyAspAlaGlyInTyrThrCysHisLysGlyGlyLysValLeuSerArgSer 100
 Db 241 GAATTGGAGATCTGGCCAGTATACCTGCCATTAAGAGGAGGCTTTCGAGCCGCTCA 300
 QY 101 LeuLeuLeuIleHisLysLysGluAspGlyIleTrrSerThrAspIleLeuLysGluGln 120
 Db 301 CTCCTGTGATTCACAAAAAGAAAGATGCAATTTGGTCCACTGATATCTTAAAGGAACG 360
 QY 121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
 Db 361 AAAGAAATCCAAAAATTAAGATCTTCTGAATATGAGGCAAGAAATATTCTGGACCTTC 420
 QY 141 ThrCysTrrTrrPheThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArg 160
 Db 421 ACATGCTGTGGTGGTGGCAATCACTACTGATTGAAATTCAGTCTCAAAAGCTGACAA 480
 QY 161 GlyPheSerAspProglInleuValThrCysGlyAlaValThrLeuSerAlaGluArgVal 180
 Db 481 GGCTTCTGACCCCAAGGGGAGACATGTGAGCAGTACACTTTCACACAAGAGGTC 540
 QY 181 ArgValAspAsnArgAspTrrLysLysTyrThrValGluCysGlnGluLysSerAlaCys 200
 Db 541 AGAGTGGACACAGGAGATTATTAAGATACACAGTGAAGTGCAGAGAGGCGAGTCCCTGC 600
 QY 201 ProSerAlaGluGluSerleuProIleGluValValAlaAspAlaIleHisLysLeuLys 220
 Db 601 CCTCTGGCCGAGAGAGCTTACCTCAGAGTCTGGTGGATGCTATTTCACAAGCTCAAG 660
 QY 221 TyrGluAsnTrrTrrSerSerPhePheIleArgAspIleIleLysProAspProProThr 240
 Db 661 TATGAAACTACACAGCAGCTTCTTCATCAGAGCATCATCAAAACCAAGACCCACCCACA 720
 QY 241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrrGluTrrPro 260

Db 721 AACCTGACGCTGAAGCCATTGAAAAATTCGCGCAGCTGGAGGTCACTGGGAATACCC 780
 QY 261 AspThrTrrSerThrProHisSerTyrPheSerleuThrPheCysIleGlnAlaGlnGly 280
 Db 781 GACACCTGGAGACACCCACATTCCTACTTCTCCTGATCTTTGGCATACAGGCCAGGGC 840
 QY 281 LysAsnAsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaValVal 300
 Db 841 AAGAACAAATAGAGAAAAAGAAAGATAGACTCTCGGTGACAAAGACCTCAGCAAGTCTG 900
 QY 301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTrrTrrSerSerTrrP 320
 Db 901 TGGCACAAGGATGCCAAGATCCCGCTGCAAGCCGAGACCGCTACTATAGTTATCCTG 960
 QY 321 SerAspTrrPalAserValSerCysSer 329
 Db 961 AGCGACTGGGCACTCTGTCTCTCAGT 987

RESULT 2
 US-09-079-984A-1
 Sequence 1, Application US/09079984A
 Patent No. 6231850
 GENERAL INFORMATION:
 APPLICANT: Okano, Fumiyoshi, Satoh, Masahiro,
 TITLE OF INVENTION: Canine interleukin 12, a production method
 TITLE OF INVENTION: thereof, an immune disease treatment method and preventive
 NUMBER OF INVENTIONS: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Miller & Christenbury Intellectual Property
 ADDRESS: Department of Schnader, Harrison, Segal and Lewis, LLP
 STREET: 1600 Market Street, 39th Floor
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy Disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Wordperfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/079, 984A
 FILING DATE: 15-MAY-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Austin R. Miller
 REGISTRATION NUMBER: 16,602
 REFERENCE/DOCKET NUMBER: 1051-98
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 563-1810
 TELEFAX: (215) 568-6946
 INFORMATION FOR SEO ID NO.: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 990 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 ORIGINAL SOURCE:
 ORGANISM: Canis familiaris
 FEATURE:
 NAME/KEY: Canine IL12
 LOCATION: 1 to 987
 IDENTIFICATION METHOD: Similarity
 US-09-079-984A-1

Alignment Scores:
 Pred. No.: 5,79e-195 Length: 990
 Score: 1731.00 Matches: 323
 Percent Similarity: 99.69% Conservative: 2
 Best Local Similarity: 99.08% Mismatches: 1
 Query Match: 98.13% Indels: 0

DB: 4 Gaps: 0
US-09-917-265-59 (1-329) x US-09-079-984A-1 (1-990)
QY 4 GlnGlnLeuValIleSerTrpPheSerLeuValLeuLeuAlaSerProLeuMetAlaIle 23
Db 10 CAGCAGTGGTCATCTCTTGCTTTCCCTGCTTTGCTGGCGTCTCCCTCATGSCATA 69
QY 24 TrpGluLeuGluLysAspValTyrValValGluLeuAspTrpHisProAspAlaProGly 43
Db 70 TGGGAACGCGAAGAAAGATGTTATGTTGTAGAGTTGAGCTGCCACCTGATGCCCCGCA 129
QY 44 GluMetValValLeuThrCysHisThrProGluGluAspAlleThrTrpThrSerAla 63
Db 130 GAATGGTGGTCTCCTCACCCTGCCATACCCCTGAAGAAGATGACATCTTGACCTCAGC 189
QY 64 GlnSerSerGluValLeuGlySerCylLysThrLeuThrIleGlnValLysGluPheGly 83
Db 190 CAGACGAGTACGATCTAGCTTCTGTAACACTGCACCATCCAGCTCAAGAAATTTGCA 249
QY 84 AspAlaGlyGlnTyrThrCysHisLysGlyLysValLeuSerArgSerLeuLeu 103
Db 250 GATCGTGGCCAGTATACCTGCCATPAAGGAGGCAAGGTTCTGAGCCGCTCACTGTG 309
QY 104 IleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGluSer 123
Db 310 ATTCACAAAGAAAGATGGAATTTGCTCCACTGATATCTTAAGAAACAGAAAGATCC 369
QY 124 LysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrp 143
Db 370 AAAAATAAATCTTCTGAAATGAGAGCAAGAAATATCTCGACGTTTCACATGCTCG 429
QY 144 TrpLeuAlaIleSerThrAspLeuLysPheSerValLysSerSerArgLysPheSer 163
Db 430 TGGCTGAGCCGATCAGTACTGATTTGAATTCAGTGCACAAAGAGAGAGGCTTCCT 489
QY 164 AspProGlnLysValThrCysGlyAlaValThrLeuSerAlaGluArgValArgValAsp 183
Db 490 GACCCCAAGGGGTGACATGTGAGCAGTGCAGACTTTCAGCAGAGAGGTTGAGAGTGAC 549
QY 184 AsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProSerAla 203
Db 550 AACGAGGATTATAGAGGTACACAGTGCAGTGCAGAGGCGAGTCCCTGCCCTCTGCC 609
QY 204 GluGlnSerLeuProIleGlnValValValAspAlaIleHisLysLeuLysTyrGluAsn 223
Db 610 GAGGAGAGCTTACCATCGAGTGTGGTGGATGCTTATTCACAAAGCTCAAGTATGAAAC 669
QY 224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeuGln 243
Db 670 TACACGACGAGCTTCTTCATCAGAGCATCTCAACAGCAGACCCAGCCACAACCTGCA 729
QY 244 LeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThrTrp 263
Db 730 CTGAGAGCATGGAATAATTCGCGACCTGAGGTCAGCTGGAATATACCCGACACTGG 789
QY 264 SerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 283
Db 790 AGCAGCCCATCTCTCTCTCTCTCTGACATTTTGACATACAGGCCAGGCGAGAGAACAT 849
QY 284 ArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValValCysHisLys 303
Db 850 AGAGAAAGAAAGATAGACTCTGGCTGACAAAGACTAGCCCAAGTGTGCTGCCACAG 909
QY 304 AspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAspTrp 323
Db 910 GATGCCAAGATCCCGCGCAAGCCGAGACCGCTACTACTATGTTATCTCGAGAGCACTGG 969
QY 324 AlaSerValSerCysSer 329
Db 970 GCATCTGTGCCCTGCACT 987
RESULT 3

US-08-848-760B-24
: Sequence 24, Application US/08848760B
: Patent No. 6248721
: GENERAL INFORMATION:
: APPLICANT: Chang, Lung-Ji
: TITLE OF INVENTION: Animal Model For Evaluation Of Vaccines
: NUMBER OF SEQUENCES: 33
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
: STREET: 2421 N.W. 41st Street, Suite A-1
: CITY: Gainesville
: STATE: Florida
: COUNTRY: United States of America
: ZIP: 32606
COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM pc compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/848,760B
: FILING DATE: 25-Jan-2001
: CLASSIFICATION: <unknown>
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: 08/838,702
: FILING DATE: 09-Apr-1997
ATTORNEY/AGENT INFORMATION:
: NAME: PACE, DORAN R.
: REGISTRATION NUMBER: 38,261
: REFERENCE/DOCKET NUMBER: CNG-100C1
TELECOMMUNICATION INFORMATION:
: TELEPHONE: (352) 375-8100
: TELEFAX: (352) 372-5800
: INFORMATION FOR SEQ ID NO: 24:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 987 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: other nucleic acid
: DESCRIPTION: /desc = "DNA"
: SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-08-848-760B-24
Alignment Scores:
Pred. No.: 5,61e-168 Length: 987
Score: 1502.50 Matches: 278
Percent Similarity: 92.02% Conservative: 22
Best Local Similarity: 85.28% Mismatches: 25
Query Match: 85.18% Indels: 1
DB: 4 Gaps: 1
US-09-917-265-59 (1-329) x US-08-848-760B-24 (1-987)
QY 4 GlnGlnLeuValIleSerTrpPheSerLeuValLeuLeuAlaSerProLeuMetAlaIle 23
Db 10 CAGCAGTGGTCATCTCTTGCTTTCCCTGCTTTGCTGGCGTCTCCCTCATGSCATA 69
QY 24 TrpGluLeuGluLysAspValTyrValValGluLeuAspTrpHisProAspAlaProGly 43
Db 70 TGGGAACGCGAAGAAAGATGTTATGTTGTAGAGTTGAGCTGCCACCTGATGCCCCGCA 129
QY 44 GluMetValValLeuThrCysHisThrProGluGluAspAlleThrTrpThrSerAla 63
Db 130 GAATGGTGGTCTCCTCACCCTGCCATACCCCTGAAGAAGATGACATCTTGACCTCAGC 189
QY 64 GlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPheGly 83
Db 190 CAGACGAGTACGATCTAGCTTCTGTAACACTGCACCATCCAGCTCAAGAAATTTGCA 249
QY 84 AspAlaGlyGlnTyrThrCysHisLysGlyLysValLeuSerArgSerLeuLeu 103
Db 250 GATCGTGGCCAGTATACCTGCCATPAAGGAGGCAAGGTTCTGAGCCGCTCACTGTG 309

| | | | |
|---|-----|--|-----|
| Oy | 104 | IIleIsIySylSGlulAspGIyIleTrrPserThraSpIleuLysGIuGlnLysGIuSer | 123 |
| | ... | | |
| Db | 310 | CTTCACAAAGAAAGAAATGGATTTGGTCTCACTGATATTTTAAAGACCAAAAGAACCC | 365 |
| Oy | 124 | LysAsnLysIleIlePheLysCysGIuAlaLysAsnTyrSerGIyArGpHeThrCysTrp | 143 |
| | ... | | |
| Db | 370 | AAAAATAAAGCACTTTCTAAGATGCGGAGCCAAAGAAATTATCTGGACGTTTCACTGCTGG | 429 |
| Oy | 144 | TrpIleuThraIleIleSerThraSpIleuLysPheSerValLysSerSerArgIyPheSer | 163 |
| | ... | | |
| Db | 430 | TGGGTGCGCAATCAAGTACTGATTTGGACATTCAGTCCAAAGCAGAGGCGCTTCT | 489 |
| Oy | 164 | AspProGlnIyAlaThrCysGIuAlaValThrLeuSerAlaGIuArgValArgValAsp | 183 |
| | ... | | |
| Db | 490 | GACCCCAAGGGGTGACGTGGGAGGTGCTACACTCTCGCAGAGAGAGTCAAGGGGAC | 549 |
| Oy | 184 | AsnArgAspTyrIlyLysIlyfThrValGIuLysGIuGIuLysSerAlaCysProSerAla | 203 |
| | ... | | |
| Db | 550 | AACAGAGAGTAT---GAGTACTCAGTGGAGTCCCGAGGAGACAGTCCCTGCCAGCGCT | 606 |
| Oy | 204 | GIuGIuSerLeuProIleGIuValValAlaSpAlaIleHISLysIleLysTyrGIuAsn | 223 |
| | ... | | |
| Db | 607 | GAGGAGAGTGGCCCATTTAGGTGATGTGTGATGCCGTTCACAAAGCTCAAGTATGAAAC | 666 |
| Oy | 224 | TyrThrSerSerPheIleArgAspIleIleLysProAspProPioThraAsnLeuGln | 243 |
| | ... | | |
| Db | 667 | TACACCGCAGCTTCTTCATCAAGGAGCATCATCAACCTGAGCCACCAACCACTTCAG | 726 |
| Oy | 244 | LeuLysProIleuLysAsnSerArgHISValGIuValSerTrpGIuTyrProAspThrTrp | 263 |
| | ... | | |
| Db | 727 | CTGAAGCCATTTAAAGATTTCTGGCGAGGTGGAGTCACTGGGAGTACCTGGACACTGG | 786 |
| Oy | 264 | SerThrProHISerTyrPheSerLeuThrPheCysIleGlnAlaGlnGIyLysAsnAsn | 283 |
| | ... | | |
| Db | 787 | AGTACTCCACATTCCTACTTCTCCCGACATCTCGTTCAAGGTCCAGGCAAGCAAGCAAG | 846 |
| Oy | 284 | ArgGIuLysLysAspArgLeuLysValAspLysThrSerAlaLysValCysHisLys | 303 |
| | ... | | |
| Db | 847 | AGGAAAGAAAGAAATAGAGTCTTCACCGCAAGACCTCAAGCCAGGTATCTGGCCGAAA | 906 |
| Oy | 304 | AspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAspTrp | 323 |
| | ... | | |
| Db | 907 | AATGCCAGCATTTAGCTGGGGGCCGACGAGCGGCTACTTACTCTATCTTGGAGCGAATGC | 966 |
| Oy | 324 | AlaSerValSerCysSer 329 | |
| | ... | | |
| Db | 967 | GCACTCTGCGCCGTCGAGT 984 | |
| RESULT 4 | | | |
| US-08-751-767A-9 | | | |
| Sequence 9, Application US/08751767A | | | |
| Patent No. 5994104 | | | |
| GENERAL INFORMATION: | | | |
| APPLICANT: ANDERSON, ROBERT J. | | | |
| APPLICANT: GRANT, HUGH | | | |
| APPLICANT: MACDONALD, IAN D. | | | |
| TITLE OF INVENTION: INTERLEUKIN-12 FUSION PROTEIN | | | |
| NUMBER OF SEQUENCES: 80 | | | |
| CORRESPONDENCE ADDRESS: | | | |
| ADDRESSEE: NIXON & VANDERHAYE P. C. | | | |
| STREET: 1100 NORTH GLEBE ROAD | | | |
| CITY: ARLINGTON | | | |
| STATE: VA | | | |
| COUNTRY: USA | | | |
| ZIP: 22201 | | | |
| COMPUTER READABLE FORM: | | | |
| MEDIUM TYPE: Floppy disk | | | |
| COMPUTER: IBM PC compatible | | | |
| OPERATING SYSTEM: PC-DOS/MS-DOS | | | |
| SOFTWARE: Patent Release #1.0, Version #1.30 | | | |
| CURRENT APPLICATION DATA: | | | |
| APPLICATION NUMBER: US/08/751,767A | | | |

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? FILING DATE: 08-Nov-1996
? CLASSIFICATION: 536
? ATTORNEY/AGENT INFORMATION:
? NAME: SADOFF, B.J.
? REGISTRATION NUMBER: 36,663
? REFERENCE/DOCKET NUMBER: 117-221
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 7038164091
? TELEFAX: 7038164100
? INFORMATION FOR SRO ID NO: 9:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1623 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..1620
US-08-751-767A-9

Alignment Scores:
Pred. No.: 1 22e-167 length: 1623
Score: 1502.50 Matches: 279
Percent Similarity: 91.49% Conservative: 22
Best Local Similarity: 84.80% Mismatches: 27
Query Match: 85.18% Indels: 1
DB: Gaps: 1

US-09-917-265-59 (1-329) x US-08-751-767A-9 (1-1623)

OY 1 MethisProglIngleuValIleSerTrpPheSerLeuValLleuleuAlaSerProLeu 20
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 ATGGGTCACAGCAGCATTTGCTCATCTTGTGTTTTCCCGATTTTCGGCATCTCCCTC 60

OY 21 MetAlaIleTrpCLeuGlueLuAspaVlTryValValGIuleAsPTPhISProasp 40
    ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 61 GTGGCCATATGGGAAGACTGAAGAAGATTGTTTGTCGTAGAAATTGCATTGTAATCCGAT 120

OY 41 AlaProGLyLueValValLeuThrCysHisIsthPrroglInluAsPaPIleThrTP 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 GCCCTGGAGAAATGGTGGCTCCACCTGTGCACCCTCGAAAGAAAGTAGATCACTCG 180

OY 61 ThrSerAlaGlnSerSergIuValLeuGlySergIylStrPrrleuThrllegInVallys 80
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 ACCGTGGACCAAGCAGCATGAGGCTTGAAGCTTGCAAAACCTGACCATCAAGTCAAAA 240

OY 81 GluPheGIAspaLaGIyIntfYrThrCysHisIstgLyGIyLysValLeuSerArgSer 100
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 GAGTTTGGAGATGCTGCCACATACACCTGTCCAAAGAGGCGAGGTTCTAAGCCATTTC 300

OY 101 LeuLeuLeuIleHisIstgLySGluSpGIyletTrpSerThrAspIleLeuLysGIuIn 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 CTCTCTGCTGCTTCCAAAAAGAAAGATGAAATTGGTCCACTGATATTATTTAAAGACAG 360

OY 121 LysGIUserIstgSmnLysIlePheLeuLysCYsgIuaIalAsanTYrSerGIYArgPhe 140
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 361 AAGAAACCCAAAATTAAGACCTTTCTAAGATCGGAGGCCAAGAAATTATTCGACGTTTC 420

OY 141 ThrCysTrpTrpleuThralIleSerThrAspleuLysPheSerValLysSerSerArg 160
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 421 ACCTGCTGGGCTGCAGCAATCAAGTACTGATTGGACATTCAGTGTCCAAGAACAGACA 480

OY 161 GlyPheSerAsproglInglyValThrCysGIyalaValThrLeuSerAlaGIuArgVal 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 481 GGCTTTCTCACCCCCAAGGGGTGACGTGGAGCTGTCAACCTCTGCAGAGAGATC 540

OY 181 ArgValAspaSnArqSPfYrLysYstrYrThrValGIucYsgInglngJserAlaCys 200
    ||| |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 541 AGAGGGACACACAGAGATAT---GAGTACTAGTGGAGTGTCCAGAGAGACAGTCCCTGC 597

OY 201 ProSerAlaGIuLusLeuProIIegIuValValAspaIalIleHisLysLeuLys 220
    ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

Db 598 CCAGCTCCTGAGAGAGCTTCGCCATTGAGCTCATGTGATGCCGTTGCACAGCTCAAG 657
Qy 221 TycrluasntyrtrhserSerPhePheIleargAspIleIleIysProAsProProthr 240
Db 658 TATGAACACTACACACAGCTTCTTCATCAGGAGCATCATCAACCTGACCCACCCAG 717
Qy 241 AsnleuGlnleuLysProLeuLysAsnSerArgHisValGluValSerTrpGlnTyrPro 260
Db 718 AACCTGCAGTGAAGCATTAAAGATTCTCGCAGGTGAGGTCAGTGGAGTACCT 777
Qy 261 AspThrTrpSerThrProHisSerTyrPheSerLeuthrPheCysIleGlnAlaGlnly 280
Db 778 GACACCTGGAGTACTCCACATTCCTACTCTCCCTGCACATTCTCGTTCAGTCCAGGC 837
Qy 281 LysAsnAsnArgGlnLysLysAspArgLeuCysValAspLysTrpSerAlaLysVal 300
Db 838 AAGAGCAAGAGAGAAAGAAAGATAGAGTCTTCACGGCAAGACCTCAGCCACGGTCATC 897
Qy 301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTrpSerSerTrp 320
Db 898 TGGCCGCAAAATGCGACACATTAGCGTGGGGCCAGCAGCAGCCCTACTATAGCTCATTTGG 957
Qy 321 SerAspTrpAlaSerValSerCysSer 329
Db 958 ACCGAATGGCATCTGTGCCCTGCAGT 984

RESULT 5
US-09-310-842-4
Sequence 4, Application US/09310842A
Patent No. 6451593
GENERAL INFORMATION:
APPLICANT: Wiltig, Prof. Burghardt
APPLICANT: Junghans, Claas
TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene
FILE REFERENCE: XI 597/99
CURRENT APPLICATION NUMBER: US/09/310.842A
CURRENT FILING DATE: 1999-05-12
EARLIER APPLICATION NUMBER: DE 196 48 625.4
EARLIER FILING DATE: 1996-11-13
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 4
LENGTH: 1870
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: gene
LOCATION: (1)..(1870)
OTHER INFORMATION: Interleukin-12 (IL-12, p40-subunit); Oligo DNA Dumbbell
FEATURE:
NAME/KEY: misc_binding
LOCATION: (1)..(2)
OTHER INFORMATION: Intramolecular binding site; the T-nucleotides at position 1 to
OTHER INFORMATION: 2 can be modified with amino or caroxy features
FEATURE:
NAME/KEY: misc_binding
LOCATION: (1869)..(1870)
OTHER INFORMATION: Intramolecular binding site; the T-nucleotides at position 1869
OTHER INFORMATION: to 1870 can be modified with amino or caroxy features
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Strandedness: both: nucleic
OTHER INFORMATION: acid (linear), hypothetical: No. 6451593 anti-sense: No
US-09-310-842-4

Alignment Scores:
Pred. No.: 1,52e-167 Length: 1870
Score: 1502.50 Matches: 278
Percent Similarity: 92.02% Conservative: 22
Best Local Similarity: 85.28% Mismatches: 25
Query Match: 85.18% Indels: 1
DB: 4 Gaps: 1

US-09-917-265-59 (1-329) x US-09-310-842-4 (1-1870)
Qy 4 GlnGlnLeuValIleSerTrpPheSerLeuValIleLeuAlaSerProLeuMetAlaIle 23
Db 642 CAGCGTGGTCACTCTCTGGTTTCCCTGGTTTCTGGCATCTCCCTGGCCATA 701
Qy 24 TrpGlnLeuGlnLysAspValTyrValValGluLeuAspTrpHisProAspAlaProGly 43
Db 702 TGGGACACTGAAGAAAGATCTTATATCTCTAGCAATTGGATTGGTATCCGGATCCCTGGA 761
Qy 44 GluMetValIleLeuThrCysHisThrProGlnGluAspAspIleThrTrpThrSerAla 63
Db 762 GAAATGGTGTCCTCACCCTGTGACACCCCTGAAGAAGATGGATACCTGGACCTTGGAC 821
Qy 64 GlnSerSerGluValLeuGlnLysSerGlnLysThrLeuThrIleGlnValLysGlnPheGly 83
Db 822 CAGACAGTGAAGTCTTGAAGCTGTGGCAAAACCCGTGACCATTCAGTAAAGAGTTTGA 881
Qy 84 AspAlaGlnGlnTyrThrCysHisLysGlnLysValLysSerArgSerLeuLeuLeu 103
Db 882 GATGCTGGCCAGTACACCTGTACAAAGAGCGAGGTTTAAAGCCATTCCCTCTGCTG 941
Qy 104 IleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGlnGlnLysGlnSer 123
Db 942 CTTGCACAAAGAAAGATGGAATTGCTCCACGTATATTAAAGACACAGAAACGCC 1001
Qy 124 LysAsnLysIlePheLeuLysCysGlnAlaLysAsnTyrSerGlyArgPheThrCysTrp 143
Db 1002 AAAAATAAGACCTTCTTAAAGATGCGAGGCCAAGAAATTATCTGACGCTTTCACCTGCGG 1061
Qy 144 TrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerArgGlyPheSer 163
Db 1062 TGGCTGACGACAAATCAGTACTGATTTGACATTTCACTGCTCAAAAGCAGCAGAGGCTTTCT 1121
Qy 164 AspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgValAsp 183
Db 1122 GACCCCAAGGGGTGACGTGGGAGCTCTACACTCTCTGCAGAGACAGTCAAGAGGGGAC 1181
Qy 184 AsnArgAspTyrLysLysTyrThrValGlnLysGlnGlnLysSerAlaCysProSerAla 203
Db 1182 AACAGAGGATAT--GAGTACTCAGTGAAGTCCAGGAGCAGACGTGCTGCCACCTGCT 1238
Qy 204 GluGlnSerLeuProIleGlnValValValAspAlaIleHisLysLeuLysTyrGlnAsn 223
Db 1239 GAGGAGACTTGCCTCATTCAGAGTCACTGATGGATGCCGTTCACAACTCAAGTATATAAAC 1298
Qy 224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeuGln 243
Db 1299 TACACGACGACCTTCTTCATCAGGAGCATTCATCAAACTGACCCACCAACACTTTCGAG 1358
Qy 244 LeuLysProLeuLysAsnSerArgHisValGluValSerTrpGlnTyrTrpAspThrTrp 263
Db 1359 CTGAAGCCATTAAAGAAATTCGCGCAGGTGAGGTCAGCTGGAATACCTGACACCTGG 1418
Qy 264 SerThrProHisSerTyrPheSerLeuthrPheCysIleGlnAlaGlnLysAsn 283
Db 1419 AGTACTGCACATTCCTACTTCTCCCTGCATTCCTGCTTCAGTCCAGGCGCAAGAGCAG 1478
Qy 284 ArgGlnLysLysAspArgLeuCysValAspLysThrSerAlaLysValValCysHisLys 303
Db 1479 AGAGAAAAAGAAAGATAGAGTCTTACCCACCAAGACCTCAGCCAGGTCATCTGCGCGCA 1538
Qy 304 AspAlaLysIleArgValGlnAlaArgAspArgTyrTrpSerSerSerTrpSerAspTrp 323
Db 1539 AATGCCAGCATTTAGCGTGGGCCAGGACCGCTACTATTAATCTATCTTGAAGCAAAATGG 1598
Qy 324 AlaSerValSerCysSer 329
Db 1599 GCATCTGTGCGCTGCAGT 1616
RESULT 6
US-09-851-062-3
Sequence 3, Application US/09851062

```
; Patent No. 6448081
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
; FILE REFERENCE: RTS-0247
; CURRENT APPLICATION NUMBER: US/09/851,062
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 3
; LENGTH: 2318
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (14)...(1000)
US-09-851-062-3

Alignment Scores:
Pred. No.: 2,12e-167 Length: 2318
Score: 1502.50 Matches: 228
Percent Similarity: 92.02% Conservative: 22
Best Local Similarity: 85.28% Mismatches: 25
Query Match: 85.18% Indels: 1
DB: Gaps: 1

US-09-917-265-59 (1-329) x US-09-851-062-3 (1-2318)

QY 4 GlnGlnLeuValIleSerThrPheSerLeuValLeuLeuAlaSerProLeuMetAlaIle 23
DB 23 CAGAGATTGGTCATCTCTGGTTTCCCTGGTTTCCGATCTCCCGCTGGCCATA 82
QY 24 TrpLeuGlnGlnLysAspValTyValValGlnLeuGlnSprHisProAspAlaProGly 43
DB 83 TGGGACTGGAAGAAGATGTTTATGTCGTGAATGGATGGATGTCGATGCCGCTGGA 142
QY 44 GluMetValValLeuThrCysHisThrProGlnGlnAspSerIleThrPheSerAla 63
DB 143 GAAATGCTGTCCCTGACCTGACACCCCTGAGAGAAAGATGATACCTGACCTTGAC 202
QY 64 GluSerSerGluValIleGlnGlnSerGlyLysThrIleGlnValLysGlnPheGly 83
DB 203 CAGAGCTGAGAGGCTTAAAGCTCTGGCAAAACCTGACCATCCAAAGCAAGATTGGA 262
QY 84 AspAlaGlnGlnLysThrCysHisLysGlnGlyLysValLeuSerArgSerLeuLeu 103
DB 263 GATGCTGGCCAGTACCTCTGCAAAAGGAGGAGGTTTAAAGCATTCGCTGCTG 322
QY 104 IleHisLysLysGlnAspGlyIleThrPheSerThrAspIleLeuLysGlnGlnSer 123
DB 323 CTTCACAAAAGAGAAATGGAATTTGCTCAGATATTAAAGCAGCAAGAAACCC 382
QY 124 LysAsnLysIlePheLeuLysCysGlnAlaLysAsnTyrSerGlyArgPheThrCys 143
DB 383 AAAAATRAAGACCTTTCTTAAGATCCGAGGCCAAGAAATTAATTCGAGCTTCACTG 442
QY 144 TrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerArgGlyPheSer 163
DB 443 TGGCTGACGACATCATCTGATGATTGACATTCAGTCAAAAAGCAGCAGAGCTTCT 502
QY 164 AspProGlnGlnValThrCysGlnAlaValThrLeuSerAlaGlnArgValAlaAsp 183
DB 503 GACCCCCAAGGGGTGAGTGGCGAGCTGCTACACTCTGCAAGAGAGACTCAGAGGGGAC 562
QY 184 AsnArgAspTyrLysLysTyrThrValGlnCysGlnGlnGlnSerAlaCysProSerAla 203
DB 563 AACAGAGAGAT---GAGTACTCATGTCAGTCCAGGAGAGACAGTCCCTGCCACTGCT 619
QY 204 GluGlnSerLeuProIleGlnValValAlaAspAlaIleHisLysLeuLysTyrGln 223
DB 620 GAGGAGAGCTTGGCCATGAGGTGATGTCGCTTCAACAGCTCAAGATGATAAAG 679
QY 224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeuGln 243
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DB 680 TACACCACAGCTTCTTATGAGGACATCAAAACCTGACCCACCAACCTTCAG 739
QY 244 LeuLysProLeuLysAsnSerArgHisValGlnValSerTrpGlnTyrProAspThrTrp 263
DB 740 CTGAAGCCATTAAAGAAATTCGCGAGAGTGGAGGCTGAGTCCCTGACACCTGG 799
QY 264 SerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsnAsn 283
DB 800 AGTACTCCACATTCCTACTCTCTCCCTGACATTCCTGAGTCCAGGCGAAGAGCAAG 859
QY 284 ArgGlnLysLysAspArgLeuCysValAspLysThrSerAlaLysValAlaCysHisLys 303
DB 860 AGAGAAAAGAAAGATTAAGTCTTACCCGACAAAGACCTGACGACGTCATCTGCCGCAA 919
QY 304 AspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAspTrp 323
DB 920 AATGCCAGCATTTACCTGCGGCGCCAGGACCGCTACTATAGTCTCATCTTGGACGAAATGG 979
QY 324 AlaSerValSerCysSer 329
DB 980 GCATCTGCTCCCTGCACT 997

RESULT 7
US-08-751-767A-7
; Sequence 7, Application US/08751767A
; Patent No. 5994104
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, ROBERT J.
; APPLICANT: GRANT, HUGH
; APPLICANT: MACDONALD, IAN D.
; TITLE OF INVENTION: INTERLEUKIN-12 FUSION PROTEIN
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHIVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/751,767A
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 117-221
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 7038164091
; TELEFAX: 7038164100
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6139 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3222..4841
; US-08-751-767A-7

Alignment Scores:
Pred. No.: 9.67e-167 Length: 6139
Score: 1502.50 Matches: 279
Percent Similarity: 91.49% Mismatches: 22
Best Local Similarity: 84.80% Gaps: 27
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Query Match: 85.18% Indels: 1
DB: 2 Gaps: 1
US-09-917-265-59 (1-329) x US-08-751-767A-7 (1-6139)

QY 1 MethisProGInGInLeuValIleSerTrpPheSerLeuValIleLeuAlaSerProLeu 20
DB 3222 ATGGGTGACGACGAGTGGTCATCTCTGGTTTCCCGTTTCTTCGCACTCCCTC 3281
QY 21 MetAlaIleTrpGluLeuGluLysAspValTyValValGluLeuAspTrpHisProAsp 40
DB 3282 GTGGCATATCGCAACTCAAGAAAGATCTTATGCTGAGAAATGGATGGATCCGAT 3341
QY 41 AlaProGluGluMetValValLeuThrCysHisTrpProGluGluAspIleThrTrp 60
DB 3342 GCCCTTGAGAAATGGTGGTCTCCACCTGACACCCCTGAAGAAGATGATACCTGG 3401
QY 61 ThrSerAlaGInSerSerGluValLeuGlySerGlyTyThrIleuThrIleGlnValLys 80
DB 3402 ACCTTGGACGACGACGAGTGTCTTACGCTCTGGCAAAACCTGACCATCCAACTCAA 3461
QY 81 GluPheGlyAspAlaGlyGlnTyTrpThrCysHisLysGlyGlyLysValLeuSerArgSer 100
DB 3462 GAGTTTGAGATGCTGGCCAGTACACCTGTCAACAAGGAGGCGAGCTTCAAGCATTCG 3521
QY 101 LeuLeuLeuIleHisLysLysGluAspGlyIleTrpSerTrpAspIleLeuLysGluGln 120
DB 3522 CTCTGCTGCTTCAACAAAGAGAGATGGATTGGTCCACGATATTTTAAAGGACGAG 3581
QY 121 LysGluSerLysAsnLysIlePheLeuLysCysGlnAlaLysAsnTySerGlyArgPhe 140
DB 3582 AAAGAACCCCAAAATAACACTTCTTAGATGCGGCCCAAGAATATTTCGAGAGCTTC 3641
QY 141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArg 160
DB 3642 ACCGTGCTGGTGGTGACGACAAATGACTGATTGACATTGACGTTGCAAAAGCGCAGA 3701
QY 161 GlyPheSerAspProGlnGlyValIleThrCysGlyAlaValIleIleSerAlaGluArgVal 180
DB 3702 GGCCTTCTTGACCCCAAGGGGTGACGTCGGAGCTGCTACACTTCTTCGACAGAGATC 3761
QY 181 ArgValAspAsnArgAspTyTrpLysLysTyTrpValGluCysGlnGluGlySerAlaCys 200
DB 3762 AGACGGCAGACAACAGAGACTAT--GAGTACTCAGTGAGTGCCAGGACGACAGTCCCTGC 3818
QY 201 ProSerAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
DB 3819 CCAGCTGCTGAGGAGACTGCCCATTCAGCTCATGCGATGCCCTTCACCAAGCTCAAG 3878
QY 221 TyrGluAsnTyTrpTrpSerSerPhePheIleArgAspIleIleLysProAspProThr 240
DB 3879 TATTAANAACCTACACGACAGCTTCTTCATFCAGGGACATCATCAACCTGACCCACAG 3938
QY 241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyTrpPro 260
DB 3939 AACTTCGACGTGCAAGCCATTAAACAATTCTGGCAGCGTGGAGCTGAGCTGGAGATCCCT 3998
QY 261 AspThrTrpSerTrpProHisSerTyTrpPheSerLeuThrPheCysIleGlnAlaGlnGly 280
DB 3999 GACACCTGAGACTACTCCACATTTCTACTTCCCTGACATTTCTCGGTCAGGTCCAGCGC 4058
QY 281 LysAsnAsnArgGluLysLysAspArgLeuGlyValAspLysTrpSerAlaLysValAla 300
DB 4059 AAGAGCAAGAGAGAAAGAAAGATAGAGTCTTCACGCGACAGAACCTTCGCCACGGTTCATC 4118
QY 301 CysHisLysAspAlaLysIleArgValGlnAlaIleArgAspArgTyTrpTySerSerSerTrp 320
DB 4119 TGCCGCAAAATATCCACAGATTACCTGGCGGCCGACGAGACCGCTACTATAGCTCATCTTGG 4178
QY 321 SerAspTrpAlaSerValSerCysSer 329
DB 4179 AGCGAATGGGATCTGTCCCTGCAGT 4205

RESULT 8
US-08-186-529-1
Sequence 1, Application US/08186529
Patent No. 5573764
GENERAL INFORMATION:
APPLICANT: Sykes, Megan
APPLICANT: Wolf, Stanley F.
TITLE OF INVENTION: USE OF INTERLEUKIN-12 TO PREVENT
TITLE OF INVENTION: GRAFT-VERSUS-HOST DISEASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Genetics Institute, Inc., Legal Affairs
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/186,529
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, Patricia A.
REGISTRATION NUMBER: 33,194
REFERENCE/DOCKET NUMBER: GI 5225
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-498-8401
TELEFAX: 617-876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 987 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: Lymphoblast
CELL LINE: RPMI 8866
FEATURE:
NAME/KEY: CDS
LOCATION: 1..987
US-08-186-529-1
Alignment Scores:
Pred. No.: 7.37e-168 Length: 987
Score: 1501.50 Matches: 278
Percent Similarity: 92.02% Conservative: 22
Best Local Similarity: 85.28% Mismatches: 25
Query Match: 85.12% Indels: 1
DB: 1 Gaps: 1
US-09-917-265-59 (1-329) x US-08-186-529-1 (1-987)
QY 4 GlnGlnLeuValIleSerTrpPheSerLeuValIleLeuAlaSerProLeuMetAlaIle 23
DB 10 CAGCAGTGGTGCATCTCTGGTTTCCCTGGTTTCTTCGCACTCCCTGCGCATTA 69
QY 24 TrpGluLeuGluLysAspValTyValValGluLeuAspTrpHisProAspAlaProGly 43
DB 70 TGCGAAGTGAAGAAAGATGTTATGCTGAGAAATGGATTCGATCCGATGCCCTGGA 129
QY 44 GluMetValIleLeuThrCysHisTrpProGluGluAspArgIleThrTrpThrSerAla 63
DB 130 GAAATGGTGTCTCCTGACACCCCTGAAGAAGATGGATATCACCCTGAGCTTGAC 189
QY 64 GlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPheGly 83

Db 190 CAGAGCAGTGTGCTTAAAGCTGTGGCAAAACCTGACCATCCAAAGTCTTGA 249
Qy 84 AspaIaGlyGlnTyrThrCysHisLysGlyGlyValLeuSerArgSerLeuLeu 103
Db 250 GATGCTGGCCAGTACCTGTCTCAAAAGAGGAGGTTCTAAAGCCATTGCTCTG 309
Qy 104 THeHisLysLysGluAspGlyLeuTrpSerThrAspIleLeuLysGluGluSer 123
Db 310 CTTCACAAAAGAGAGATGGAATTTGGTCCACATGATTTTAAAGACAGAAAGACC 369
Qy 124 LysAsnLysIlePheLeuLysCysGluAlaLysAsnLysSerGlyArgPheThrCysTrp 143
Db 370 AAAAATTAAGACCTTTCTAAGATGCGAGGCCAAGAAATTAATCTTGACCTTCCCTGG 429
Qy 144 TrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerArgGlyPheSer 163
Db 430 TGGCTGACGACAAATCAGTACGATTTGACATTCAGTGTCAAAAGACAGAGGCTTCT 489
Qy 164 AspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValAsp 183
Db 490 GACCCCAAGGAGGAGTGGAGTGGAGTGTCTGACACTCTGCGAGAGAGTCCAGAGGAG 549
Qy 184 AsnArgAspTyrLysLysTyrThrValGluCysGlnGluLysSerAlaCysProSerAla 203
Db 550 AACAAAGAGATAT--GAGTACTCAGTGGAGTGGAGGAGGAGACAGACTGCTCCAGCTGT 606
Qy 204 GluGluSerLeuProIleGluValValAspAlaIleHisLysLeuLysTyrGluAsn 223
Db 607 GAGGAGAGTGTGCCCATTTGAGAGTATGAGTGTGATGCTGATCCCTTCAAAAGCTCAAGTAA 666
Qy 224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeuGln 243
Db 667 TACACGACGAGCTTCTTCATCAGGAGCATCATCAAACTGACCCCAAGAACTTGCAG 726
Qy 244 LeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThrTrp 263
Db 727 CTGAAGCATTAAGAAATTCCTGGCAGCTGAGGAGTGGAGTGGAGTGGAGTGGAGTGG 786
Qy 264 SerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsnAsn 283
Db 787 AGTACTCCACATTCCTTACTTCTCCCTGACATTCCTGCGCTTCAGTCCAGGCGCAAGACAG 846
Qy 284 ArgGluLysLysAspArgLeuCysValAspLysThrSerAlaValValCysHisLys 303
Db 847 AGAAGAAAAGAAAGATAGAGTCTTCACGACAAAGACCTCAGCCAGGTCATCTGCCGAAA 906
Qy 304 AspaIaLysIleArgValGlnAlaArgAspArgTyrTrpSerSerTrpSerAspTrp 323
Db 907 AATGCCAGCATTAAGCTGTGGGCGCCAGGACCGCTACTATAGCTCATCTTGGAGCGAATGG 966
Qy 324 AlaSerValSerCysSer 329
Db 967 GCATCTGTGGCCTGCACT 984

RESULT 9

US-08-640-386A-1
Sequence 1, Application US/08640386A
Patent No. 5756085
GENERAL INFORMATION:
APPLICANT: Sykes, Megan
APPLICANT: Wolf, Stanley F.
TITLE OF INVENTION: USE OF INTERLEUKIN-12 TO PREVENT
TITLE OF INVENTION: GRAFT-VERSUS-HOST DISEASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc., Legal Affairs
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/640,386A
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: CI 5225A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-498-8224
TELEFAX: 617-876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 987 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: Lymphoblast
CELL LINE: RPMI 8866
FEATURE:
NAME/KEY: CDS
LOCATION: 1..987
US-08-640-386A-1
Alignment Scores:
Pred. No.: 7,37e-168 Length: 987
Score: 1501.50 Matches: 278
Percent Similarity: 92.02% Conservative: 22
Best Local Similarity: 85.28% Mismatches: 25
Query Match: 85.12% Indels: 1
Gaps: 1
US-09-917-265-59 (1-329) x US-08-640-386A-1 (1-987)
Qy 4 GlnGlnLeuValIleSerTrpPheSerLeuValLeuAlaSerProIleuMetAlaIle 23
Db 10 CACAGTGTGTCATCTCTGCTGTTTCCCTGGTTTCTGGACATCTCCCTCGGGCCATA 69
Qy 24 TrpGluLeuLysAspValTyrValValGluLeuAspTrpHisProAspAlaProGly 43
Db 70 TGGGAGCTGAGAAAGATGTTTATGTCGTAAGATTGATTCGATCCGATGCCCTGGA 129
Qy 44 GluMetValValLeuThrCysHisThrProGluGluAspAspIleThrTrpThrSerAla 63
Db 130 GAAATGTTGTTCTCACCCTGTGACACCCCTGAAGAGATGATGATCAGCTGGAGCTGGAC 189
Qy 64 GlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPheGly 83
Db 190 CAGAGCAGTGTGAGCTTAAAGCTGTGGCAAAACCTGACCATCCAAAGATTTGGA 249
Qy 84 AspaIaGlyGlnTyrThrCysHisLysGlyGlyValLeuSerArgSerLeuLeu 103
Db 250 GATGCTGGCCAGTACCTGTCTCAAAAGAGGAGGTTCTAAAGCCATTGCTCTG 309
Qy 104 THeHisLysLysGluAspGlyLeuTrpSerThrAspIleLeuLysGluGluSer 123
Db 310 CTTCACAAAAGAGAGATGGAATTTGGTCCACATGATTTTAAAGACAGAAAGACC 369
Qy 124 LysAsnLysIlePheLeuLysCysGluAlaLysAsnLysSerGlyArgPheThrCysTrp 143
Db 370 AAAAATTAAGACCTTTCTAAGATGCGAGGCCAAGAAATTAATCTTGACCTTCCCTGG 429
Qy 144 TrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerArgGlyPheSer 163
Db 430 TGGCTGACGACAAATCAGTACGATTTGACATTCAGTGTCAAAAGACAGAGGCTTCT 489
Qy 164 AspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValAsp 183

|||||
Db 490 GACCCCAAGGGGTGAGCTGGCGAGCTGCTACACTCTCTGCAGAGAGTACGAGGGGAC 549
Qy 184 AsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProSerAla 203
Db 550 AACAAAGAGATAT--GAGTACTCAGTGGAGTCCAGAGGACGAGTGGCTGGCCAGCTGCT 606
Qy 204 GluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsn 223
Db 607 GAGAGAGTCTGCCCATTTGAGAGTCATGTGGATCCGCTTCAACAAGCTCAAGTATGAAAC 666
Qy 224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProPheThrAsnLeuGln 243
Db 667 TACACGACGAGCTTCTTCATCAGGAGACATCATCAACCTGACCCACCAACAACTGGAG 726
Qy 244 LeuLysProLeuLysAsnSerArgHisValGluValSerTProGluTyrProAspThrTrp 263
Db 727 CTGAAGCCATTAAAGAAATTCCTCGGACGTGAGCTGACCTGGAGTACCCCTGACACCTGG 786
Qy 264 SerThrProHisSerTyrPheSerLeuThrPheCysIleGlnIleGlnGlyLysAsn 283
Db 787 AGTACTCCACATTCCTCTACTCTCTCCCTACATTCCTGCTTCAGTCCAGGCAAGACGAC 846
Qy 284 ArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValValCysHisLys 303
Db 847 AGAAGAAAGAAAGATAGAGCTTCTCAGCAGACGACCTCAGCCAGCTCATCTGCCGCAAA 906
Qy 304 AspAlaLysIleLeuValGlnIleAlaArgAspArgTyrTyrSerSerSerTProSerAspTrp 323
Db 907 AATTCGACGATTAGCCGTGGCGGGCCGAGACCGGCTAATAGCTCATCTTGGAGGCAATCG 966
Qy 324 AlaSerValSerCysSer 329
Db 967 GCATCTGTGGCCCTGCACCT 984

RESULT 10
US-08-184-009-194
: Sequence 194, Application US/08184009
: Patent No. 5833975
: GENERAL INFORMATION:
: APPLICANT: Paoleletti, Enzo
: APPLICANT: Tartaglia, James
: APPLICANT: Cox, William I.
: TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
: NUMBER OF SEQUENCES: 217
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Curtiss, Morris & Safford
: STREET: 530 Fifth Avenue
: CITY: New York
: STATE: NY
: COUNTRY: USA
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/184,009
: FILING DATE: 19-JAN-1994
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Frommer, William S.
: REGISTRATION NUMBER: 25,506
: REFERENCE/DOCKET NUMBER: 454310-2530
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 840-3333
: TELEFAX: (212) 840-0712
: TELEX: 425066CURTMS
: INFORMATION FOR SRO, ID NO: 194:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1018 base pairs
: TYPE: nucleic acid

: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
US-08-184-009-194
Alignment Scores:
Pred. No.: 7.73e-168 Length: 1018
Score: 1501.50 Matches: 278
Percent Similarity: 92.02% Conservative: 22
Best Local Similarity: 85.28% Mismatches: 25
Query Match: 85.12% Indels: 1
Gaps: 1
US-09-917-265-59 (1-329) x US-08-184-009-194 (1-1018)
Qy 4 GlnGlnLeuValIleSerTProPheSerLeuValLeuLeuAlaSerProLeuMetaIle 23
Db 41 CAGCAGTTGGTCATCTCTTGGTTTCCCTGGTTTCTGCGCATCTCCCTGCGGCATA 100
Qy 24 TrpGluLeuGluLysAspValTyrValValGluLeuAspTrpHisProAspAlaProGly 43
Db 101 TGGAGACTGAAGAAAGATGTTATGTGCTAGAAATTTGGATGTGATCCGAGTCCCTGGA 160
Qy 44 GluMetValValLeuThrCysHisThrProGluGluAspIleThrTrpThrSerAla 63
Db 161 GAAATGGTGGTCTCACCCTGTGACACCCCTGAGAAAGATGGTATCACCTGGACCTGGAC 220
Qy 64 GlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPheGly 83
Db 221 CAGAGCAGTGGAGCTTAAAGCTCTGGCAAAACCCCTGACCAATCCAAAGTCAAGTCAAGAGATTGGA 280
Qy 84 AspAlaGlyGlnTyrThrCysHisLysGlyLysValLeuSerArgSerLeuLeuLeu 103
Db 281 GATCTGTGCCAGTACCTGTGTACAAAGAGGCGAGGTTCTTAAGCCATTCCCTCTGCTG 340
Qy 104 IleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGluSer 123
Db 341 CTTCACAAAAGAAAGATGATTTGGTCCACTGATATTATTAAGGACACAGAAAGAACCC 400
Qy 124 LysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrp 143
Db 401 AAAATTAAGACCTTTTAAGATGGAGGCGAGGCAAGAAATTAATTTGGAGCTTACCTGCTGG 460
Qy 144 TrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgIlePheSer 163
Db 461 TGGCTGACGACAAATCAGTACTGATTTTGACATTGAGTGCATAAAGCAGCAGAGGCTTCT 520
Qy 164 AspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgValAsp 183
Db 521 GACCCCAAGGGGTGAGCTGGCGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGAC 580
Qy 184 AsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProSerAla 203
Db 581 AACAAAGAGATAT--GAGTACTCAGTGGAGTCCAGAGGACAGTGGCTGGCCAGCTGCT 637
Qy 204 GluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsn 223
Db 638 GAGAGAGTCTGCCCATTTGAGAGTCATGTGGATCCGCTTCAACAAGCTCAAGTATGAAAC 697
Qy 224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProPheThrAsnLeuGln 243
Db 698 TACACGACGAGCTTCTTCATCAGGAGCATCATCAACCTGACCCACCAAGAACTGGAG 757
Qy 244 LeuLysProLeuLysAsnSerArgHisValGluValSerTProGluTyrProAspThrTrp 263
Db 758 CTGAAGCCATTAAAGAAATTCCTCGGACGTGAGGTCACCTGGAGTACCCGACACCTGG 817
Qy 264 SerThrProHisSerTyrPheSerLeuThrPheCysIleGlnIleGlnGlyLysAsn 283
Db 818 AGTACTCCACATTCCTACTCTCTCCCTGACATTTGCGTTCAGGTCCAGGCAAGACGAC 877
Qy 284 ArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValValCysHisLys 303

DB 878 AGAGAAAGAAAGATAGACTTTCAGCGGACCAAGCCTCAGCCAGCTCATCTGCCGCAAA 937

QY 304 AspalatylsileargvalglnalaargspargtyrtyrserSerSerTrpSerAspTrp 323

DB 998 AATGCCACATTAGCTGCGGGCCAGAGACCGCTACTATGCTCATCTTGAGCGCAATGG 997

QY 324 AlaSerValSerCysSer 329

DB 998 GCATCTGTGCCCTGCAGT 1015

RESULT 11

US-08-458-356-194

Sequence 194, Application US/08458356

Patent No. 5942235

GENERAL INFORMATION:

APPLICANT: Paoletti, Enzo

APPLICANT: Tartaglia, James

APPLICANT: Cox, William I.

TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY

NUMBER OF SEQUENCES: 217

CORRESPONDENCE ADDRESS:

ADDRESSEE: Curtiss, Morris & Safford

STREET: 530 Fifth Avenue

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/458,356

FILING DATE: 02-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/184,009

FILING DATE: 19-JAN-1994

ATTORNEY/AGENT INFORMATION:

NAME: Frommer, William S.

REGISTRATION NUMBER: 25,506

REFERENCE/DOCKET NUMBER: 454310-2530

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 840-3333

TELEFAX: (212) 840-0712

TELEX: 425066CORTMS

INFORMATION FOR SEQ ID NO: 194:

SEQUENCE CHARACTERISTICS:

LENGTH: 1018 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-458-356-194

Alignment Scores:

Pred. No.: 7,73e-168 Length: 1018

Score: 1501.50 Matches: 278

Percent Similarity: 92.02% Conservative: 22

Best Local Similarity: 85.12% Mismatches: 25

Query Match: 85.12% Indels: 1

DB: 2 Gaps: 1

US-09-917-265-59 (1-329) x US-08-458-356-194 (1-1018)

QY 4 GlnGlnLeuValIleSerTrpPheSerLeuValIleLeuAlaSerProLeuMetAlaIle 23

DB 41 CAGCAGTTGGTCATCTCTGTTTCCCTGTTTTCGTCATCTCCCTCGGCCATA 100

QY 24 TrpGlnLeuGlnLysAspValIleValIleGluLeuAspTrpHisProAspAlaProGly 43

DB 101 TGGGAAGTGAAGAAAGATGTTATGTCTGTAATGGATGGTATCCGATCCCGCTGGA 160

QY 44 GlnMetValIleLeuThrCysHisThrProGlnLysAspAlleThrTrpSerAla 63

DB 161 GAAATGGTGGTCTCCACCTGTGACACCCCTGAAGAAAGATGTTACACCTGGACCTTGAC 220

QY 64 GlnSerSerGlnValIleGlnGlySerGlyLysThrLeuThrIleGlnValLysGlnPheGly 83

DB 221 CAGAGCAGTGAAGTCTTAGGCTCTGGCAAAACCTGACCATTCACAGCAAGCAAGAGTTGGA 280

QY 84 AspalaglylnThrCysHisLysGlyLysValLeuSerArgSerLeuLeu 103

DB 281 GATGCTGGCCAGTACACCTGTCAACAAAGAGGAGGAGTTTATAGCCATTGCTCCCTGCTG 340

QY 104 IleHisLysLysGlnLysGlyIleTrpSerThrAspIleLeuLysGlnLysGlnSer 123

DB 341 CTTCACAAAAGAGATGGAATTTGGTCCACGATATTTTAAAGACCAAGAAAGAACCC 400

QY 124 LysAsnLysIlePheLeuLysCysGlnAlaLysAsnTrpSerGlyArgPheThrCysTrp 143

DB 401 AAAAATAGACCTTCTTAAGATCCGAGCCCAAGATTTATTCGTGACCTTTCACCTCTCG 460

QY 144 TrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgLysPheSer 163

DB 461 TGGCTGACGACAATTCAGTACTGATTGACATTCAGTCAAAAGCAGAGAGGCTCTCT 520

QY 164 AspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGlnArgValArgValAsp 183

DB 521 GACCCCAAGGGGTGACGTGGAGGAGCTGCTACACTCTTGCAAGAGAGTCAAGAGGGAC 580

QY 184 AsnArgAspTyrLysLysTyrThrValGlnLysGlnGlnLysSerAlaCysProSerAla 203

DB 581 AACAGAGATAT---CAGTACTCAGTGGAGTGCGAGAGAGACAGAGTGGCCGACAGTCT 637

QY 204 GlnGlnSerLeuProIleGlnValValIleAspAlaIleHisLysLeuLysTyrGlnAsn 223

DB 638 GAGGAGAGTCTGCCATTGAGTCAAGTCAAGTGGATGCGCTTCAACACTCAAGATGAAAAAC 697

QY 224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeuGln 243

DB 698 TACACGACGAGCTTCTTCAATCAGGACATCATCAACCTGACCCCAAGAACTTGCGAG 757

QY 244 LeuLysProLeuLysAsnSerArgHisValGlnValSerTrpGlnLysProAspThrTrp 263

DB 758 CTGAAGCCATTAAAGATCTCTGCGAGGAGGAGTCACTGAGGATACCTCAGCACCTGG 817

QY 264 SerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsnAsn 283

DB 818 AGTACTCCACATTCTCTACTCTCTGACATTTCTCGTTCAGAGTCCAGGCAAGAGCAAG 877

QY 284 ArgGlnLysLysAspArgLeuLysValAspLysTrpSerAlaLysValIleCysHisLys 303

DB 878 AGAGAAAGAAAGATAGAGTCTTTCACGGCAAGACCTCAGCAGCGCTCATCTGCCGCAAA 937

QY 304 AspalatylsileargvalglnalaargspargtyrtyrserSerSerTrpSerAspTrp 323

DB 998 AATGCCACATTAGCTGCGGGCCAGAGACCGCTACTATGCTCATCTTGAGCGCAATGG 997

QY 324 AlaSerValSerCysSer 329

DB 998 GCATCTGTGCCCTGCAGT 1015

RESULT 12

US-08-460-736-194

Sequence 194, Application US/08460736

Patent No. 6265189

GENERAL INFORMATION:

APPLICANT: Paoletti, Enzo

APPLICANT: Tartaglia, James

APPLICANT: Cox, William I.

TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY

NUMBER OF SEQUENCES: 217

CORRESPONDENCE ADDRESS:

ADDRESSEE: Curtiss, Morris & Safford

STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,736
FILING DATE: 02-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/184,009
FILING DATE: 19-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEX: 425066CURTMS
INFORMATION FOR SEQ ID NO: 194:
SEQUENCE CHARACTERISTICS:
LENGTH: 1018 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-460-736-194

Alignment Scores:
Pred. No.: 7.73e-168 Length: 1018
Score: 1501.50 Matches: 278
Percent Similarity: 92.02% Conservative: 22
Best Local Similarity: 85.28% Mismatches: 25
Query Match: 85.12% Indels: 1
DB: Gaps: 1

US-09-917-265-59 (1-329) x US-08-460-736-194 (1-1018)

QY 4 GInGleuValIleSerTPheSerLeuValIleuLeuLaserProleuMetaIalle 23
DB 41 CAGCAGTTGGTCTCTGCTGCTTCCCTGCTTTTCTGGCAGTCCCTCGTGGCCATA 100
QY 24 TTPGluLeuGluLysAspValTyValIValIleuAspTPPhsProAspAlaProGly 43
DB 101 TGGGAGCTGAAGAAATGTTTATGTCGTGAATTCGATTGCGATCCGATGCCCTGGA 160
QY 44 GluMetValIleuThrCysHisThrProGluGluAspIleThrTPthrSerVala 63
DB 161 GAATGTCGTCTCCTCAGCTGACACCCCTGACAGAGATGCTATCAGCTGACCTTGAC 220
QY 64 GlnSerSerGluValIleuGlySerGlyLysThrLeuThrIleGlnValIysGluPheGly 83
DB 221 CAGAGAGTGAAGCTTTAGGCTCTGGCAAAACCTGACCATCAAGCAAGAGTTTGA 280
QY 84 AspAlaGlyGlnTyThrCysHisLysGlyGlyLysValIleuSerArqSerLeuLeu 103
DB 281 GATGCGCCAGTACACCTCTCACAAGAGGCGAGTTTAAAGCCATTCGCTCGCTG 340
QY 104 IleHisLysLysGluAspGlyIleTPPserThrAspIleLeuLysGluGlnLysSer 123
DB 341 CTTCAACAAAAGAGAAATGGAATTCGTCACATATTTTAAAGCAGCAGAAAGAACCC 400
QY 124 LysAsnLysIlePheLeuLysCysGluAlaLysAsnTySerGlyArqPheThrCysTrp 143
DB 401 AAAAATAAGACCTTTCTTAAAGTGGAGGCCAAAGATTAATTCGAGCTTTCACCTG 460
QY 144 TPleuThrAlaIleSerThrAspLeuLysPheSerValIysSerSerArqGlyPheSer 163

DB 461 TGGCTGACGACATCATCTACTGATTTGACATTCAGTGTCAAAGACAGAGGCTCTCT 520
QY 164 AspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArqValArqValAsp 183
DB 521 GACCCCAAGGGGTGAGCTCGGAGCTGCTTACACTCTCTCAGAGAGTACAGGGGAC 580
QY 184 AsnArqAspTyTrpLysTyTrpThrValGluCysGlnGluLysSerAlaCysProSerAla 203
DB 581 AACAGAGATAT--GAGTACTCAGTGGATGCCAGAGACAGATGCTCTCCAGAGCT 637
QY 204 GluLysLeuProIleGluValIValAspAlaIleHisLysLeuLysTyrgLysAsn 223
DB 638 GAGAGAGCTGCGCCATTTGAGGTCATGAGTGGATGCCCTTCACAAGCTCAAGTATGA 697
QY 224 TyTrpThrSerPhePheIleArqAspIleIleLysProAspProPThrAsnLeuGln 243
DB 698 TACACGACGAGCTTCTTCATCAGGACATCATCAAACTGACCCCAAGAACCTTG 757
QY 244 LeuLysProLeuLysAsnSerArqHisValGluValSerTPGluTyTrpProAspTPthr 263
DB 758 CTGAGGCCATTTAAGATTTCTCGGACGAGTGGAGTCACTGGAGTACCTGACACCTG 817
QY 264 SerThrProHisSerTyTrpPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 283
DB 818 AGTACTCAGCATTCCTACTCTCTCCCTGACATTTCTGCTTCAAGTCCAGGCAAGCA 877
QY 284 ArgGluLysLysAspArqLeuCysValAspLysThrSerAlaLysValIValCysHisLys 303
DB 878 AGAGAAAGAAAGACTTAAGTCTTCCACGACAGACCTCACCCAGCATCTGCGGAAA 937
QY 304 AspAlaLysIleArqValIValArqAspArqTyTrpSerSerTPPserAspTrp 323
DB 938 AATGCCAGATTTAGCGGCGGCGGACGAGCGGCTGACTATAGTCACTTGGAGGAAT 997
QY 324 AlaSerValSerCysSer 329
DB 998 GCATCTGTGCGCTGCACT 1015
RESULT 13
US-08-751-767A-3
Sequence 3, Application US/08751767A
Patent No. 5994104
GENERAL INFORMATION:
APPLICANT: ANDERSON, ROBERT J.
APPLICANT: GRANT, HUGH
APPLICANT: MACDONALD, IAN D.
TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,767A
FILING DATE: 08-NOV-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 117-221
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164091
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 3:

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SEQUENCE CHARACTERISTICS:
LENGTH: 1399 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 43..1026
US-08-751-767A-3

Alignment Scores:
Pred. No.: 1,27e-167 Length: 1399
Score: 1501.50 Matches: 278
Percent Similarity: 92.02% Conservative: 22
Best Local Similarity: 85.28% Mismatches: 25
Query Match: 85.12% Indels: 1
DB: Gaps: 1

US-09-917-265-59 (1-329) x US-08-751-767A-3 (1-1399)

QY 4 GlnGlnLeuValIleSerTrpPheSerLeuValLeuValAspProLeuMetAlaIle 23
Db CACAGATGGTCACTCTGCTGTTCCCTGCTTTCGTCATCTCCCTCGGCCATA 111
QY 24 TrpGlnLeuValLysAspValIleValValGlnLeuAspTrpHisProAspAlaProGly 43
Db TGGGAAGTGAAGAAAGTGTATGTCGTAAGATTGATGATGATCGGATGCCCTGCA 171
QY 44 GluMetValValLeuThrCysHisThrProGlnGlnAspAspIleThrTrpHisSerAla 63
Db GAATGGTGTCTCTCACTGACCTGACACCCCGAAGAAAGATGATCATCCTGACCTTGAC 231
QY 64 GlnSerSerGlnValLeuGlySerGlyLysThrLeuThrIleGlnValLysGlnPheGly 83
Db CAGAGAGTAGAGTCTTAGGCTCTGCAAAACCCCTGACCATCCAAAGAGTTTGA 291
QY 84 AspAlaGlyGlnIleThrCysHisLysGlyLysValLeuSerArgSerLeuLeu 103
Db GAGCGTGGCCAGTACACCTCTTCAAAAGAGGAGGATCTTAAGCCATGCTCTGCG 351
QY 104 IleHisLysLysGlnAspGlyIleTrpSerThrAspIleLeuLysGlnGlnLysGlnSer 123
Db CTTCACAAAAGAGAAATGGAATTGTCACATGATATTTAAAGACCAAGAAAGACCC 411
QY 124 LysAsnLysIlePheLeuLysCysGlnAlaLysAsnTrpSerGlyArgPheThrCysTrp 143
Db AAAAATTAAGACCTTTCTTAAGATGCGAGGCCAAAGAAATTAATTCGAGGTTTCACTGCTGG 471
QY 144 TrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPheSer 163
Db TGGCTGACGACATCGTACTGATTTGACATTCACAGTCAAAAGCAGCAGAGGCTCTCT 531
QY 164 AspProGlnGlyValIleThrCysGlyAlaValIleThrLeuSerAlaGlnArgValAsp 183
Db GACCCCAAGGGGTGACGTCGAGAGCTGCTACACTCTCGCAGAGAGTACAGAGGGGAC 591
QY 532 GACCCCAAGGGGTGACGTCGAGAGCTGCTACACTCTCGCAGAGAGTACAGAGGGGAC 591
QY 184 AsnArgAspTrpLysLysThrValGlnCysGlnGlnGlySerAlaCysProSerAla 203
Db AACAAGAGATAT---GAGTACTCATGTCGAGTGCAGAGGACAGTGCCTGCCACTGCT 648
QY 204 GlnGlnSerLeuProIleGlnValValAlaAspAlaIleHisLysLeuLysTrpGlnAsn 223
Db GAGGAGAGTCTCCCATTCAGGTCAATGTCGATGCGCTTCAACACTCAAGATATGAAC 708
QY 224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProTrpThrAsnLeuGln 243
Db TACACACACAGCTTCTTATCATCAGGACATCATCAAAACCTGACCCCAAGAACTTGCAG 768
QY 244 LeuLysProLeuLysAsnSerArgHisValGlnValSerTrpGlnTrpProAspThrTrp 263
Db CTGAAGCCATTAAAGATTTCTGCGAGGTGAGGTCACTGGAGATCCCTGACACCTGCG 828

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QY 264 SerThrProHisSerTrpPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsnAsn 283
Db AGTACTCCACATTTCTTCTTCTCTGACATTTCTGCTCAGGTCCAGGACAGACCAAG 888
QY 284 ArgGlnLysLysAspArgLeuCysValAspLysThrSerAlaLysValValCysHisLys 303
Db AGAGAAAGAAAGATAGAGTCTTCACGACAGACAGACTCAGCCAGGTCTATCTGCCCAAA 948
QY 304 AspAlaLysIleLeuValGlnAlaArgAspArgTrpTrpSerSerSerTrpSerAspTrp 323
Db AATGCCAGCATTAAGCTGCGGCGGACGACCGCTACTATAGCTCATCTTGGAGCGAATGG 1008
QY 324 AlaSerValSerCysSer 329
Db GCATCTGTGCTGCCAGT 1026

RESULT 14
US-08-265-087-1
Sequence 1, Application US/08265087
Patent No. 5571515
GENERAL INFORMATION:
APPLICANT: Scott, Phillip
TITLE OF INVENTION: Compositions and Methods for Use of
TITLE OF INVENTION: IL-12 as an Adjuvant
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Howson and Howson
STREET: Spring House Corporate Center, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/265,087
FILING DATE:
CLASSIFICATION: A24
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/229,282
FILING DATE: 18-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: W5751AUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2362 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 33..1016
US-08-265-087-1

Alignment Scores:
Pred. No.: 2,87e-167 Length: 2362
Score: 1501.50 Matches: 278
Percent Similarity: 92.02% Conservative: 22
Best Local Similarity: 85.28% Mismatches: 25
Query Match: 85.12% Indels: 1
DB: Gaps: 1

US-09-917-265-59 (1-329) x US-08-265-087-1 (1-2362)

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QY      4 GlnGlnLeuValIIEserTrpPheSerLeuValLeuLeuAlaSerProLeuMetaIle 23
Db      42 CAGACGTTGGTCATCTTGTGTTTCCCTGGTTTTCCTGGCATCTCCCTCGTGGCCATA 101
QY      24 TrpGluLeuGluLysAspValTyTrValValGluLeuAspTrpHisProAspAlaProGly 43
Db      102 TGGGAACGAGAAAGATGTTTATCTCTAGCAATTTGATGCTGATCCGATCCCTCGA 161
QY      44 GluMetValValLeuThrCysHisThrProGluGluAspAspIleThrTrpHisSerIa 63
Db      162 GAATGTGTCCTCCTCACCCTGACACCCCTGAAGAGATGTTATCACCCTGGACCTTGGAC 221
QY      64 GluSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPheGly 83
Db      222 CAGAGCAGTGAGGCTTATAGCTCTGGCAAAACCTGACCATCCCAAGTAAAGAGTTTGA 281
QY      84 AspAlaGlyGlnTyTrThrCysHisLysGlyGlyLysValLeuSerArgSerLeuLeu 103
Db      282 GATCTGGCCAGTACACCTCTCACAAAGAGCGACGTTTAAAGCCATTTCCCTCGCTG 341
QY      104 IleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGluSer 123
Db      342 CTTTCACAAAAGAGATGGAATTTGTCCACTGATATTTTAAAGGACCAAGAACACCC 401
QY      124 LysAsnLysIlePheLeuLysCysGlyValAlaLysAsnTyTrSerGlyArgPheThrCysTrp 143
Db      402 AAAAATTAAGACCTTTCTTAAGATGCGAGGCCCAAGAAATATTTCTGGACGTTTACCTCGCTG 461
QY      144 TrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPheSer 163
Db      462 TGCCTGAGCAATACACTACTGATTTGACATTTCAGTGTCAAAAGACAGACAGCGCTCTT 521
QY      164 AspProGlnGlyValIleThrCysGlyAlaValIleThrLeuSerAlaGluArgValArgValAsp 183
Db      522 GACCCCAAGAGGAGTGAGCGGAGCGGAGCTTACACTCTCTGAGAGAGTGAGAGGCGAC 581
QY      184 AsnArgAspTyTrLysLysTyTrThrValGluCysGlnGluGluSerAlaCysProSerAla 203
Db      582 AACAGAGAGTAT--GAGTACTCAGTGGAGTGGCCAGGACGACAGTGCCTGGCCACGCTCT 638
QY      204 GluGluSerLeuProIleGluValValAlaLysAlaIleHisLysLeuLysTyTrGluAsn 223
Db      639 GACGAGAGTCTGCCCATTTGAGGTCATGTGTGATCCGCTTCCACAAAGCTCAAGTATGAAGAAC 698
QY      224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeuGln 243
Db      699 TACACCAAGACGCTTCTTCATCAGGACATTCACAACCTGACCCACCAAGACCAAGACTTGCAG 758
QY      244 LeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyTrProAspThrTrp 263
Db      759 CTGAAGCCATTAAAGATTTCTCGGAGGTGAGGTGACAGTCCAGTACCTGACACACCTCGG 818
QY      264 SerThrProHisSerTyTrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsnAsn 283
Db      819 AGTACTCCACATTCCTCCTCTCCCTGACATTTGCCCTGAGTCCAGGCCAAGACGCAAG 878
QY      284 ArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValValCysHisLys 303
Db      879 AGAGAAAGAAAGATTAAGTCTTACAGACAAAGACCTGAGCCACGTCATCTGCGCGCAA 938
QY      304 AspAlaLysIleArgValGlnAlaArgAspArgTyTrTyTrSerSerSerTrpSerAspTrp 323
Db      939 AATGCCAGCATTTACGCTGCGGCGCCAGACGCGTACATATACCTCATCTTGGAGCGAATGG 998
QY      324 AlaSerValSerCysSer 329
Db      999 GCATCTGTGCCCTGCAGT 1016
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RESULT 15
US-08-621-493-1
; Sequence 1, Application US/08621493
; Patent No. 5723127

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GENERAL INFORMATION:
APPLICANT: Scott, Phillip
APPLICANT: Trinchieri, Giorgio
TITLE OF INVENTION: Compositions and Methods for Use of
TITLE OF INVENTION: IL-12 as an Adjuvant
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Howson and Howson
STREET: Spring House Corporate Center, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,493
FILING DATE: 25-MAR-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/265,087
FILING DATE: 17-JUN-1994
APPLICATION NUMBER: US 08/229,282
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST51AUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2362 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 33..1016
US-08-621-493-1
Alignment Scores:
Pred. No.: 2,87e-167 Length: 2362
Score: 1501.50 Matches: 278
Percent Similarity: 92.02% Conservative: 22
Best Local Similarity: 85.28% Mismatches: 25
Query Match: 85.12% Indels: 1
DB: 1 Gaps: 1
US-09-917-265-59 (1-329) x US-08-621-493-1 (1-2362)
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QY      24 TrpGluLeuGluLysAspValTyTrValValGluLeuAspTrpHisProAspAlaProGly 43
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QY      64 GluSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPheGly 83
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Db      ||||||| 342 CTTCAACAAAAGAGATGAGATTTGGTCCACTGATATTTAAAGAGACAGAAAGAACCC 401
QY      ||||||| 124 LysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrp 143
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QY      ||||||| 224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeuGln 243
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Search completed: July 17, 2003, 09:32:18
Job time : 54.3954 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: July 16, 2003, 19:59:04 : Search time 224.767 Seconds
(without alignments)
3019.692 Million cell updates/sec

Title: US-09-917-265-59

Perfect score: 1764
Sequence: 1 MHPOLVISMSFLVILASPL.....QARDPRYSSMSDMASVSCS 329

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| Ygapop 10.0 | Ygapext 0.5 | | |
| Fgapop 6.0 | Fgapext 7.0 | | |
| Delop 6.0 | Delext 7.0 | | |

Searched: 1439767 seqs, 1031500376 residues

Total number of hits satisfying chosen parameters: 2879534

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : Published.Applications_NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|------------------------------------|
| 1 | 1764 | 100.0 | 987 | 10 | US-09-917-265-58 Sequence 58, Appl |

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|---|----|--------|-------|------|----|-------------------|-------------------|
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| C | 3 | 1764 | 100.0 | 1599 | 10 | US-09-917-265-61 | Sequence 61, Appl |
| C | 4 | 1764 | 100.0 | 1599 | 10 | US-09-917-265-63 | Sequence 63, Appl |
| C | 5 | 1764 | 100.0 | 2267 | 10 | US-09-917-265-107 | Sequence 107, App |
| C | 6 | 1764 | 100.0 | 2267 | 10 | US-09-917-265-109 | Sequence 109, App |
| C | 7 | 1657 | 93.9 | 987 | 10 | US-09-917-265-29 | Sequence 29, Appl |
| C | 8 | 1657 | 93.9 | 987 | 10 | US-09-917-265-31 | Sequence 31, Appl |
| C | 9 | 1653 | 93.7 | 921 | 10 | US-09-917-265-52 | Sequence 52, Appl |
| C | 10 | 1653 | 93.7 | 921 | 10 | US-09-917-265-54 | Sequence 54, Appl |
| C | 11 | 1653 | 93.7 | 985 | 10 | US-09-917-265-55 | Sequence 55, Appl |
| C | 12 | 1653 | 93.7 | 985 | 10 | US-09-917-265-57 | Sequence 57, Appl |
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| C | 15 | 1651 | 93.6 | 2193 | 15 | US-10-079-616-5 | Sequence 5, Appl |
| C | 16 | 1643 | 93.1 | 1599 | 10 | US-09-917-265-38 | Sequence 38, Appl |
| C | 17 | 1643 | 93.1 | 1599 | 10 | US-09-917-265-40 | Sequence 40, Appl |
| C | 18 | 1554 | 88.1 | 921 | 15 | US-10-079-616-6 | Sequence 6, Appl |
| C | 19 | 1554 | 88.1 | 921 | 15 | US-10-079-616-7 | Sequence 7, Appl |
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| C | 21 | 1546 | 87.6 | 921 | 10 | US-09-917-265-28 | Sequence 28, Appl |
| C | 22 | 1546 | 87.6 | 1533 | 10 | US-09-917-265-43 | Sequence 43, Appl |
| C | 23 | 1546 | 87.6 | 1533 | 10 | US-09-917-265-45 | Sequence 45, Appl |
| C | 24 | 1502.5 | 85.2 | 987 | 11 | US-09-826-025-24 | Sequence 24, Appl |
| C | 25 | 1502.5 | 85.2 | 1870 | 15 | US-10-172-399-7 | Sequence 4, Appl |
| C | 26 | 1502.5 | 85.2 | 2318 | 15 | US-10-172-399-7 | Sequence 7, Appl |
| C | 27 | 1502.5 | 85.2 | 8578 | 10 | US-09-828-825-3 | Sequence 1, Appl |
| C | 28 | 1502.5 | 85.2 | 8578 | 10 | US-09-828-825-3 | Sequence 3, Appl |
| C | 29 | 1502.5 | 85.2 | 8608 | 10 | US-09-828-825-7 | Sequence 7, Appl |
| C | 30 | 1502.5 | 85.2 | 8629 | 10 | US-09-828-825-5 | Sequence 5, Appl |
| C | 31 | 1502.5 | 85.2 | 8629 | 10 | US-09-828-825-15 | Sequence 15, Appl |
| C | 32 | 1502.5 | 85.2 | 8638 | 10 | US-09-828-825-9 | Sequence 9, Appl |
| C | 33 | 1502.5 | 85.2 | 8644 | 10 | US-09-828-825-13 | Sequence 13, Appl |
| C | 34 | 1502.5 | 85.2 | 8659 | 10 | US-09-828-825-11 | Sequence 11, Appl |
| C | 35 | 1501.5 | 85.1 | 987 | 11 | US-09-754-014-2 | Sequence 2, Appl |
| C | 36 | 1501.5 | 85.1 | 987 | 11 | US-09-754-014-3 | Sequence 3, Appl |
| C | 37 | 1501.5 | 85.1 | 987 | 11 | US-09-834-014-4 | Sequence 4, Appl |
| C | 38 | 1501.5 | 85.1 | 987 | 11 | US-09-834-014-4 | Sequence 4, Appl |
| C | 39 | 1501.5 | 85.1 | 2362 | 11 | US-09-826-866-2 | Sequence 2, Appl |
| C | 40 | 1141.5 | 64.7 | 1840 | 15 | US-10-172-399-3 | Sequence 3, Appl |
| C | 41 | 193 | 10.9 | 3477 | 11 | US-09-935-868-25 | Sequence 25, Appl |
| C | 42 | 193 | 10.9 | 3477 | 11 | US-10-287-035-25 | Sequence 25, Appl |
| C | 43 | 193 | 10.9 | 3507 | 11 | US-09-935-868-23 | Sequence 23, Appl |
| C | 44 | 193 | 10.9 | 3507 | 15 | US-10-287-035-23 | Sequence 23, Appl |
| C | 45 | 178 | 10.1 | 1363 | 11 | US-09-359-672-6 | Sequence 6, Appl |

ALIGNMENTS

RESULT 1
US-09-917-265-58
Sequence 58, Application US/09917265
Patent No. US20020052030A1
GENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
FILE REFERENCE: IM-5
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 109
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 58
LENGTH: 987
TYPE: DNA
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(987)
OTHER INFORMATION:
US-09-917-265-58

Alignment Scores:
Pred. No.: 1,39e-207 Length: 987
Score: 1764.00 Matches: 329
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-917-265-59 (1-329) x US-09-917-265-58 (1-987)

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Db 61 ATGGCCATATGGAACTGGAGAAAGATGTTATATGTGTAGAGTTGGACTGGCACCCTGAT 120
Oy 41 AlaProGluGluMetValValLeuThrCysHisThrProGluGluAspAspIleThrTrp 60
Db 121 GCCCGCGGAAATGGTGGTCTCCTCCTCCTCCTCCTGAAAGATGACATCCTGG 180
Oy 61 ThrSerAlaGlnSerSerGluValLeuGluSerGlyLysThrLeuThrIleGluValLys 80
Db 181 ACCTCAGCGCAGAGCAGTGAAGTCTCTAGTTCTGTAAACTCTGACCATCCAAAGTCAA 240
Oy 81 GluPheGlyAspAlaGlyLysTrpThrCysHisLysGlyLysValLeuSerArgSer 100
Db 241 GAATTTGGAGATGCTGGCGCAGATACCTGCCATTAAGAGGCAAGTTCTGAGCGGCTCA 300
Oy 101 LeuLeuLeuIleHisLysLysGluAspGlyIleTrpSerTrpAspIleLeuLysGluGln 120
Db 301 CTCCTGTTGATTACAAAAAGAAAGATGAAATTTGGTCTCCTGATATCTTAAGAGAAC 360
Oy 121 LysGlnSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTrpSerGlyArgPhe 140
Db 361 AAAGATATCCAAAATTAAGATCTTCTGTAATGTGAGGCAAGAAATTTCTGGAGGTTTC 420
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Oy 161 GlyPheSerAspProGlnGlyValIleThrCysGlyAlaValIleThrLeuSerAlaGluArgVal 180
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Oy 181 ArgValAspAsnArgAspTrpLysLysTrpThrValGluCysGlnGluIleSerAlaLys 200
Db 541 AGAGTGGCAACAGAGGATTAAGACAGTACAGTGGAGTGTCTCAGAGGAGGAGGCTGCTGC 600
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Db 661 TATGAAAACTACACACGAGCTTCTCTCATCAGAAACATCAACAAACGACCACCCACA 720
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RESULT 2

US-09-917-265-60/c
; Sequence 60, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:

; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 987
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-917-265-60

Alignment Scores:

Pred. No.: 1,39e-207 Length: 987
Score: 1764.00 Matches: 329
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-917-265-59 (1-329) x US-09-917-265-60 (1-987)

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Db 867 GCCCGCGGAAATGGTGGTCTCCTCCTCCTCCTGAAAGATGACATCCTGG 808
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Db 807 ACCTCAGCGCAGACAGTGAAGTCTCTAGTTCTGTAAACTGTGACCATCCAAAGTCAA 748
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QY 321 SerAspTrpAlaSerValSerCysSer 329
Db 27 AGCGACTGGCATCTGTGTATGCAGT 1

RESULT 3

US-09-917-265-61
: Sequence 61, Application US/09917265
: Patent No. US20020052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: APPLICANT: Borouhns, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
: FILE REFERENCE: IM-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: CURRENT FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: PRIOR FILING DATE: 2000-08-04
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 61
: LENGTH: 1599
: TYPE: DNA
: ORGANISM: Canis familiaris
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(1599)
: OTHER INFORMATION:
US-09-917-265-61

Alignment Scores:

Pred. No.: 2,83e-207 Length: 1599
Score: 1764.00 Matches: 329
Percent Similarity: 100.00% Conservatave: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-917-265-59 (1-329) x US-09-917-265-61 (1-1599)

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Db 1 ATGCACCTCAGCAGATGTGTCATCTCCGTGTTTCCCTGTTTCTGTGCGGTCTCCCTC 60
QY 21 MetAlaIleTrpGluLeuGluLysAspValTyTrpValValGIuLeuAspTrpHisProasp 40
Db 61 ATGCCATATGCGAAGTGGAGAAAGATGTTATGTTTGTAGAGTGTGACGTGGACCCGTGAT 120

QY 41 AlaProGluIuMetValIleuThrCysHisIsthrProGluGluAspSIIeThrTrp 60
Db 121 GCGCCCGGAGAAATGTGTGCTCTACCTGCGCTACCTGGAAGAAATGACATGCTTGG 180
QY 61 ThrSerAlaGlnSerSerGluValLeuGlnSerGlyLysTrpLeuThrIIeGlnValIys 80
Db 181 ACCTCAGCGCAGAGAGTGAAGTCTAGTGTCTGTAAACTGTGACCATCCAAAGTCAAA 240
QY 81 GluPheGlyAspAlaGlyGlnTyTrpCysHisLysGlyGlyLysValLeuSerArgSer 100
Db 241 GAATTTGGAGATGCGGCAGTATATCTGCCATAAAGAGCGCAAGGTTCTGAGCCGCTCA 300
QY 101 LeuLeuLeuIIeHisLysLysGluAspGlyIleTrpSerTrpAspIIeLeuIysGluGln 120
Db 301 CTCCTGTGATTACAAAAAAGACATGGAATTTGCTCCTCAGTATATCTTAAAGAGACAG 360
QY 121 LysGluSerLysAsnLysIIePheLeuLysCysGlnAlaLysAsnTyTrpSerGlyArgPhe 140
Db 361 AAGAATCCAAAAATAGATCTTCTGAAATGTGAGCGCAAGAAATATTCTGGAGCTTTC 420
QY 141 ThrCysTrpTrpLeuThrAlaIIeserThrAspLeuLysPheSerValIysSerArg 160
Db 421 ACATGCTGTGCTGACGCGCAATCAGTACTGATTTGAAATTCAAGTCAAAAGTGCAGA 480
QY 161 GlyPheSerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgVal 180
Db 481 GCGTCTCTGACCCCAAGGGGTGACATGTGGAGAGTACACTTTCAGCAGAGAGGCTC 540
QY 181 ArgValaAspAsnArgAspTyTrpLysTyTrpThrValGIuGlyGlnGluIysSerAlaCys 200
Db 541 AGAGTGGACAACAGAGGATTTATAGAAATACACAGTGGAGTGTCCAGAGGCGCGTCTGC 600
QY 201 ProserAlaIgluIuSerLeuProIIeGIuValValAlaSPaIIeHisIysLeuIys 220
Db 601 CCTCTGCCGAGGAGGCTTACCCATTCGAGGTGCGTGAGTCTATTTCACAAAGCTCAAG 660
QY 221 TyrGIuaSnTyTrpSerSerPhePheIIeaRgsAIIeIleYpProAspProThr 240
Db 661 TATGAAAACTACACAGACAGCTTCTTCATCAGACATCATCAAAACCCAGACCCACCA 720
QY 241 AsnLeuGlnLeuIysProLeuIysAsnSerArghIysValGIuValSerTrpSLuTyPro 260
Db 721 AACCTGCAGCTGAACCATTTGAAAAATTCTCGGCACGTGAGAGTCAAGCTGGGAATATACCC 780
QY 261 AspTrpTrpSerTrpProHisSerTrpPheSerLeuThrPheCysIIeGlnAlaInGly 280
Db 781 GACACCTGGAGACCCCATTCCTACTTCTCCCTGCACATTTTGGATACAGGCCCGAGGC 840
QY 281 LysAsnAsnArGluLysLysAspArgLeuCysValaSLyTrpSerAlaIysValaI 300
Db 841 AAGAACAATACAGAAAAAAGATAGACTTCGTGGACAGACCTCAGCCAGAGTCTGTG 900
QY 301 CysHisLysAspAlaLysIIeaRgValGlnAlaArGspArGTrpTrpSerSerTrp 320
Db 901 TGCCACAAGAGATGCCAAGATCCGCTGCAGAGCCGAGACCGCTACTATAGTTCATCTGG 960
QY 321 SerAspTrpAlaSerValSerCysSer 329
Db 961 AGCGACTGGCATCTGTGTATGCAGT 987

RESULT 4

US-09-917-265-63/C
: Sequence 63, Application US/09917265
: Patent No. US20020052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: APPLICANT: Borouhns, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
: FILE REFERENCE: IM-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: CURRENT FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016

```
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-917-265-63

Alignment Scores:
Pred. No.: 2,83e-207      Length: 1599
Score: 1764.00           Matches: 329
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%    Mismatches: 0
Query Match: 100.00%           Indels: 0
DB: 10                      Gaps: 0

US-09-917-265-59 (1-329) x US-09-917-265-63 (1-1599)

QY 1 MethisProgluInleuValIleSerTrpPheSerleuValleuAlaSerProleu 20
D 1599 ATGACCCCTGAGAGTGGTGCATCTCTGTTTCCCTGTTTGGTGGCGTCCCTC 1540
QY 21 MetAlaIleTrpGluLeuGluValAspValTyrValGluLeuAspTrpHisProasp 40
D 1539 ATGGCCATATGGAGACTGGAGAAAGATTTATGTTTATGAGTTGAGCTGGACCTGAT 1480
QY 41 AlaProgluGluMetValIleuThrCysHisThrProgluGluAspAlaIleThrTrp 60
D 1479 GCCCCGGAGAAATGGTGGTCTCCTGACCTGCATACCCCTGAAGAAATGACATCTGG 1420
QY 61 ThSerIaGlnSerSerGluValIleuGlySerGlyThrIleuThrIleGlnVallys 80
D 1419 ACCTCACCGAGAGACAGTGAAGTCTCTAGTTCTGTGTAACCTCGACATCCAAAGTCAA 1360
QY 81 GluPheGlyAspAlaGlyIntYrThrCysHisIlysglyGlyValleuSerArgSer 100
D 1359 GAATTTGGAGTGGTGGCCGATACCTGCTCCATTAAGAGAGCAAGGTTCTGAGCCGCTCA 1300
QY 101 LeuLeuLeuIleHisIlysglyAspGlyIleTrpSerThrAspIleLeuGlyGluGln 120
D 1299 CTCCTGTTGATTCACAAAAGAAAGATGGAATTTGGTCCACTGATCTTAAGAGACAG 1240
QY 121 LysGluSerIlysaNlyIlePheLeuIlycGlyAlaIlysaNlyTrpSerGlyArgPhe 140
D 1239 AAAAATCCCAAAATAAGATCTTCTGAAATGTGAGCAAAAGATTAATTCGACGCTTTC 1180
QY 141 ThrCysTrpIleuThrAlaIleSerThrAspLeuIlyPheSerValIlySerSerArg 160
D 1179 ACATGCTGGTGGCGACGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 1120
QY 161 GlyPheSerAspProGlnGlyValIThrCysGlyAlaValIThrLeuSerAlaGluArgVal 180
D 1119 GGGCTTCTGTACCCCAAGGGGTGACATGTGAGACAGTGCACACTTTCAGCAGAGAGGTC 1060
QY 181 ArgAlaIlysaNlyAspTrpIlyIlyIlyThrValIlycGlyGlnGlyIlySerAlaCys 200
D 1059 AGAGTGGACAAACAGGATTTAAAGATACACAGTGAAGTGTGAGGGGAGGCTGTC 1000
QY 201 ProSerIaGlnGluSerleuProIleGluValAlaValAlaSerAlaIleHisIlyLeuLys 220
D 999 CCGCTGCGCAGAGAGACCTACCATCGAGTCTGTGTGATGCTATTCACAAAGCTCAG 940
QY 221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleIlyProAspProProThr 240
D 939 TATGAAACATAACACAGCAGCTTCTCATCAGACATCATCAAAACAGACCCACCCACA 880
QY 241 AsnLeuGlnleuLysProleuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
D 879 AACCTGAGCTGAAGCCATTGAAAAATTCGCGACCTGAGGCTGACCTGGGATATACCC 820
QY 261 AspThrTrpSerThrProHisSerTyrPheSerleuThrPheCysIleGlnIaGlnGly 280
D 261 AspThrTrpSerThrProHisSerTyrPheSerleuThrPheCysIleGlnIaGlnGly 280
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D 819 GACACCTGGAGACCCCACTTCCTACTCTCCCTGACATTTTCATACAGCCCAAGGC 760
QY 281 LysAsnAsnArgGluIlyIlyAspArgLeuCysValIlyAspIlyThrSerAlaValI 300
D 759 AAGACACATATGAGAAAAGAAAGATAGACTCTGTGGTGGACAAAGCTTCAGCAAGTCTG 700
QY 301 CysHisIlysaNlyIlyIleArgValGlnAlaIlyArgAspArgTyrTrpSerSerTrp 320
D 699 TGGCACAAGGATGCCAAGATCCCGTGCAGAGCCCGAGACCGCTACTATATGTTCTATCTG 640
QY 321 SerAspTrpAlaSerValSerCysSer 329
D 639 AGCGACTGGGCACTGTGTATGACAG 613

RESULT 5
US-09-917-265-107
; Sequence 107, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Borouhgs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917, 265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223, 016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 107
; LENGTH: 2267
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS (154) ..(1140)
; LOCATION: (154) ..(1140)
; OTHER INFORMATION:
US-09-917-265-107

Alignment Scores:
Pred. No.: 4.75e-207      Length: 2267
Score: 1764.00           Matches: 329
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%    Mismatches: 0
Query Match: 100.00%           Indels: 0
DB: 10                      Gaps: 0

US-09-917-265-59 (1-329) x US-09-917-265-107 (1-2267)

QY 1 MethisProgluInleuValIleSerTrpPheSerleuValleuAlaSerProleu 20
D 154 ATGACATCCCTGAGAGTGGTGCATCTCTGTTTCCCTGTTTGGTGGCGTCCCTC 213
QY 21 MetAlaIleTrpGluLeuGluValIlyAspValTyrValIleuLeuAspTrpHisProasp 40
D 214 ATGGCCATATGGAGACTGGAGAAAGATGTTATCTGTAGAGTTGGACAGTGCACCTGAT 273
QY 214 ArgAlaIlysaNlyIlyIlyIlyThrValIlycGlyGlnGlyIlySerAlaCys 200
D 41 AlaProgluGluMetValIleuThrCysHisThrProgluGluAspAlaIleThrTrp 60
D 274 GCCCCGGAGAAATGGTGGTCTCCTGACCTGCATACCCCTGAAGAAATGACATCACTTGG 333
QY 61 ThSerIaGlnSerSerGluValIleuGlySerGlyIlyThrIleuThrIleGlnVallys 80
D 334 ACCTCAGCGCAGAGCAGTGAAGTCTTGTGTAACCTGTGACATCCAAAGTCAA 393
QY 81 GluPheGlyAspAlaGlyIntYrThrCysHisIlysglyGlyValleuSerArgSer 100
D 394 GAATTTGGAGATCTGTGGCCGATTAACCTGCATTAAGAGAGCAAGTTCAGACCCGCTCA 453
QY 101 LeuLeuLeuIleHisIlysglyAspGlyIleTrpSerThrAspIleLeuIlyGluGln 120
D 454 CTCCTGTTGATTCACAAAAGAAAGATGGAATTTGGTTCACATGATATTAAAGAAAGAG 513
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QY 121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
DB 514 AAGAATCCAAAATAAGATCTTCTGAAATGTGAGCAAGAAATTATTCTGGAGCTTTC 573
QY 141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerArg 160
DB 574 ACATCTCTGGTGCCTACCGCAATCAGTACTGATTGAAATTCAGTGTCAAAAAGTAGCAGA 633
QY 161 GlyPheSerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGlnArgVal 180
DB 634 GCGTTCTGTGACCCCAAGGGGTGACATGTGAGAGACATTCCTGACGAGAGGGTTC 693
QY 181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGlySerAlaCys 200
DB 694 AGAGTGCACACAGCAGATTATAGAAAGTACACAGTGGAGTGTGACAGAGGCAAGTCCCTGC 753
QY 201 ProSerAlaGluGluSerLeuProIleGluValValAspAlaIleHisLysLeuLys 220
DB 754 CCTCTGCCGAGAGAACCTTACCCATCGAGCTCGTGGATGCTATTTCACAAAGCTCAAG 813
QY 221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProThr 240
DB 814 TATGAATAACTACACCAGCAGCTTCTTCATCAGACATCATCAACACGACCCACCCACA 873
QY 241 AsnLeuGlnLeuLysProIleLysAsnSerArgHisValGluValSerTyrPoliuTyrPro 260
DB 874 AACCTGACGTGAACCCATGTGAAATAATCTCGGCACTGAGAGTCAAGCTGGGAATACCCC 933
QY 261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGly 280
DB 934 GACACCTGGACACCCCACTTCTTCTCTCCGACATTTTGCATCAGACCCACAGCGC 993
QY 281 LysAsnAsnArgGluLysLysAspArgLeuLysValAspLysThrSerAlaLysValAl 300
DB 994 AAGAACATTAAGAAAGAAAGATAGACTTCTCGTGCAAGACCTCAGCCAGGTCGTG 1053
QY 301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerTrp 320
DB 1054 TGGCAAGAGATGGCAAGATCCGGGTGCAAGCCGAGACCGGTACTATAGTTCAATCCCTGG 1113
QY 321 SerAspTrpAlaSerValSerCysSer 329
DB 1114 AGCGACTGGCATCTGTGCTGCAGT 1140

RESULT 6
US-09-917-265-109/C
: Sequence 109, Application US/09917265
: Patent No. US20020052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: APPLICANT: Borouhous, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
: FILE REFERENCE: IM-5
: CURRENT APPLICATION NUMBER: US/09/917, 265
: PRIOR FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: PRIOR FILING DATE: 2000-08-04
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 109
: LENGTH: 2267
: TYPE: DNA
: ORGANISM: Canis familiaris
US-09-917-265-109

Alignment Scores:
Pred. No.: 4.75e-207 Length: 2267
Score: 1764.00 Matches: 329
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-917-265-59 (1-329) x US-09-917-265-109 (1-2267)
QY 1 MethisProGlnGlnLeuValIleSerTrpPheSerLeuValLeuLeuAlaSerProIleu 20
DB 2114 ATGCATCTCCAGCAGATTGGTATCTCCGTTTTCCCTCGTTTGTGCTGGCGTCCCTC 2055
QY 21 MetAlaIleTyrGluLeuGluLysAspValTyrValValGluLeuAspTrpHisProAsp 40
DB 2054 ATGGCATATATGGAAACTGGACAAAGATTTTATGTGTAGAGTTGGACTGGCACCCTCAT 1995
QY 41 AlaProGlyGluMetValValLeuThrCysHisThrProGluGluAspAspIleThrTrp 60
DB 1994 GCGCCCGGAAGAAATGGTGTCTCTCCTCAGCCCATACCCCTGAAGAAGATGACATCACTGG 1935
QY 61 ThrSerAlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
DB 1934 ACCTCAGCGACAGAGAGTGAAGTCTTACGTTCTGTAAACCTCTCACCATCCAAAGTCAAA 1875
QY 81 GluPheGlyAspAlaGlyGlnTyrThrCysHisLysGlyGlyLysValLeuSerArgSer 100
DB 1874 GAATTTGGAGATCGTCGGCAGATATACCTGCCATTAAGAGGCAAGCTTCGAGCCGCTCA 1815
QY 101 LeuLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGlnGln 120
DB 1814 CTCCGTGTGATTCAACAAAAGAAAGATGAAATTTGGTCCACTGATATCTTAAAGGAACAG 1755
QY 121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
DB 1754 AAGAATCCAAAATAAGATCTTCTGAAATGTGAGGCAAGAAATTATTCTGGAGCTTTC 1695
QY 141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArg 160
DB 1694 ACATCTCTGTGCTGACGCGCATCTGATCTGATTTGAAATTCAGTGTCAAAAAGTAGCAGA 1635
QY 161 GlyPheSerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgVal 180
DB 1634 GCGTTCTGTGACCCCAAGGGGTGACATGTGAGAGAGTGAACCTTTCAGCAGAGAGGGTTC 1575
QY 181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGlySerAlaCys 200
DB 1574 AGAGTGCACACAGGATTTATAGAGTACACAGTGAAGTGTGACAGAGGCAAGTGCCTGC 1515
QY 201 ProSerAlaGluGluSerLeuProIleGluValValAspAlaIleHisLysLeuLys 220
DB 1514 CCTCTGCGAGAGAGGCTTACCCATCGAGGTCGTGGATGCTATTCACAGCTCAAG 1455
QY 221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProThr 240
DB 1454 TATGAATACTACACAGCAGCTTCTTCATCAGACATCATCAAAACGACCCACCCACA 1395
QY 241 AsnLeuGlnLeuLysProIleLysAsnSerArgHisValGluValSerTyrPoliuTyrPro 260
DB 1394 AACCTGACGTGAACCCATTTGAAATAATCTCGGCACTGAGAGTCACTGGGAATACCCC 1335
QY 261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGly 280
DB 1334 GACACCTGGACACCCCACTTCTCTCTCCGATCATTTTGGATTCAGAGCCAGGGC 1275
QY 281 LysAsnAsnArgGluLysLysAspArgLeuLysValAspLysThrSerAlaLysValAl 300
DB 1274 AAGAACAATTAAGAAAGAAAGATAGACTGTGCGGAGCAAGACCTCAGCCCAAGTCTGTG 1215
QY 301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
DB 1214 TGGCAAGAGATGGCAAGATCCGGGTGCAAGCCGAGACCGGTACTATAGTTCAATCCCTGG 1155
QY 321 SerAspTrpAlaSerValSerCysSer 329
DB 1154 AGCGACTGGCATCTGTGCTGCAGT 1128

RESULT 7
US-09-917-265-29
: Sequence 29, Application US/09917265

Patent No. US20020052030A1
 GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT: Borouhgs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265
 PRIOR FILING DATE: 2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 109
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 29
 LENGTH: 987
 TYPE: DNA
 ORGANISM: Felis catus
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(987)
 OTHER INFORMATION:
 US-09-917-265-29

Alignment Scores:
 Pred. No.: 2,18e-194 Length: 987
 Score: 1657.00 Matches: 308
 Percent Similarity: 96.66% Conservative: 10
 Best Local Similarity: 93.62% Mismatches: 11
 Query Match: 93.93% Indels: 0
 Gaps: 0

US-09-917-265-59 (1-329) x US-09-917-265-29 (1-987)

QY 1 MethisProglInleuValIleSerTrpPheSerleuValleuLeuAlaSerProleu 20
 Db 1 ATGCATCCTCAGCAGTTGGTCATCGCTGTTTCCCGTTTGGTGGACCTCCCTC 60
 QY 21 MetAlaIleTrpGluLeuGluValAspValTyrValValGluLeuAspTrpHisProasp 40
 Db 61 ATGGCCATATGGAGACTGGAGAAAACGTTTATGTGTAGAGTTGGAGCTGGACCCCTGAT 120
 QY 41 AlaProGlyGluMetValIleuThrCysHisThrProGluGluAspAspIleThrTrp 60
 Db 121 GCCCCGAGAAATGGTGGTCTCCTGCAATCTCTGTAAGAAATGACATACCTCG 180
 QY 61 ThrSerAlaGlnSerSerGluValleuGlySerGlyLysThrLeuThrIleGlnValLys 80
 Db 181 ACCCTGACGACGACAGTGAAGTCTAGCTGTGTAACCTGACACATCCAAAGTCAAA 240
 QY 81 GluPheGlyAspAlaGlnTrpThrCysHisLysGlyLysValleuSerArgSer 100
 Db 241 GAATTTTCAGATGCTGGCCAGTATACCTGTCAATAAAGAGGCGGTTCTGAGCCATTG 300
 QY 101 LeuLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGln 120
 Db 301 TTCCTCTGATACACAAAAGGAAGATGGAATTTGGTCCACTGATCTTAAGGGAACAG 360
 QY 121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTrpSerGlyArgPhe 140
 Db 361 AAAAATTCAAAATAAGATCTTCTAAATGTGAGCAAAAGAAATTTATTCGAGCGTTTC 420
 QY 141 ThrCysTrpTrpIleuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArg 160
 Db 421 ACCGCTGGTGGGCGGACGATAGTACCGATTGGAATTCACCTGTCACAAAAGCAGAGA 480
 QY 161 GlyPheSerAspProGlnGlyValThrCysGlyValAlaValThrLeuSerAlaGluArgVal 180
 Db 481 GGGCTCCTGACCCCAAGGGGTGACTTGTGGACACGACACTCTGACGAGAGAAGTGC 540
 QY 181 ArgValAspAsnArgAspTrpLysLysLysValIleGluLysGlnGlySerAlaCys 200
 Db 541 AGAGTGGACAACAGGAGATTATTAAGAACTACACAGTGAAGTGCAGAGGCGAGCTGC 600
 QY 201 ProSerIleGluGlnSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220

Db 601 CCGGCTGCCAGAGACCTTACCATTTGAAGTGTGTGGACCTTATTCACAGCTCAAG 660
 QY 221 TyGluAsnTrpThrSerSerPhePheIleArgAspIleIleLysProAspProPhe 240
 Db 661 TACGAACATACACACGACCTTCTTATAGGACATCTCAACACCGACCAACCAAG 720
 QY 241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTrpPro 260
 Db 721 AACCTGCACTGAAGCCATTAAAAATTTCCGCAATCTGGAAGTGAAGTGGAAATACCC 780
 QY 261 AspThrTrpSerThrProHisSerLysTrpPheSerLeuThrPheCysIleGlnAlaGlnGly 280
 Db 781 GACACCTGGAGACCCACATCTCTACTTCTCTTAACATTTGGCGTACAGGTCCAGGGC 840
 QY 281 LysAsnAsnArgGluLysLysAspArgLysCysValAspLysThrSerAlaLysValAla 300
 Db 841 AAGACACACAGACAAAAGAAAGACAGACTCTCCGTGCAAGACCTCAGCAAGGTCTG 960
 QY 301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTrpTrpSerSerSerTrp 320
 Db 901 TGGCACAAGGATGCCAAGATCCGCTGCAAGCCAGACCGCTACTATACCTCATCTG 960
 QY 321 SerAspTrpAlaSerValSerCysSer 329
 Db 961 AGCAACTGGGCAATCCGTCTCTGACAGT 987

RESULT 8
 US-09-917-265-31/c
 Sequence 31. Application US/09917265
 Patent No. US20020052030A1

GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT: Borouhgs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265
 PRIOR FILING DATE: 2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 NUMBER OF SEQ ID NOS: 109
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 31
 LENGTH: 987
 TYPE: DNA
 ORGANISM: Felis catus
 US-09-917-265-31

Alignment Scores:
 Pred. No.: 2,18e-194 Length: 987
 Score: 1657.00 Matches: 308
 Percent Similarity: 96.66% Conservative: 10
 Best Local Similarity: 93.62% Mismatches: 11
 Query Match: 93.93% Indels: 0
 Gaps: 0

US-09-917-265-59 (1-329) x US-09-917-265-31 (1-987)

QY 1 MethisProglInleuValIleSerTrpPheSerleuValleuLeuAlaSerProleu 20
 Db 987 ATGCATCCTCAGCAGTTGGTCATCGCTGTTTCCCGTTTGGTGGACCTCCCTC 928
 QY 21 MetAlaIleTrpGluLeuGluValAspValTyrValValGluLeuAspTrpHisProasp 40
 Db 927 ATGGCCATATGGAGACTGGAGAAAACGTTATGTGTAGAGTTGGAAGTGGACCTGAT 868
 QY 41 AlaProGlyGluMetValIleuThrCysHisThrProGluGluAspAspIleThrTrp 60
 Db 867 GCCCCGAGAAATGGTGGTCTCCTGCAATATCTCGAAGAAATGACATCAGACCTGG 808
 QY 61 ThrSerAlaGlnSerSerGluValleuGlySerGlyLysThrLeuThrIleGlnValLys 80
 Db 807 ACCTTGACCAAGACAGTGAAGTCTTAGCTGTGTAACCTGACACATCCAAAGTCAAA 748

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QY      81  GluPheGlyAspAlaGlyGlnTyrThrCysHisLysGlyGlyLysValLeuSerArgSer 100
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      747  GAATTTGGACATGCTGGCCAGATATACCTGTCATAAGAGGCGAGGCTTCCAGCCATTGG 688

QY      101  LeuLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGln 120
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      687  TTCTCTCTGATACACAAAGAGAGATGCAATTGGTCACATGATATCTTAAGGAGACAG 628

QY      121  LysLysSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      627  AAAAGATTCACAAATAATGATCTTTCTAAATGTAGGCAAGAAATTTCTGGACGTTTC 568

QY      141  ThrCysTrpTrpIleuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArg 160
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      567  ACCGCTGCTGCTGCGACGCGCAATCAGTACCATTTGAATTTCACTGTCAAAAGCAGCCGA 508

QY      161  GlyPheSerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgVal 180
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      507  GCGTCTCTGTACCCCAAGGGGTGACTTGTGACAGCAGCAGCTCTCGAGAGAGGTC 448

QY      181  ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGlnGlySerAlaCys 200
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      447  AGACTGGACACACAGGATTTATAGAGTACACACTGAGTGTCAGAGGGCAGTCCCTGC 388

QY      201  ProSerAlaGluGluSerLeuProIleGluValValAlaAspAlaIleHisLysLeuLys 220
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      387  CCGGCTCCCGAGAGACCTTACCATTGCAAGTCTGCTGCGACGCTATTTCACAGCTCAG 328

QY      221  TyrIleAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProThr 240
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      327  TACGAAAACTACACACACAGCTCTCTCATCAGGAGCATCATCAACCGGACCCACCCAG 268

QY      241  AsnLeuIleLysProLeuLysAsnSerArgHisValGluValSerTrpGlnTyrPro 260
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      267  AACCTGCACACTGAAGCCATTAAAAAATTTCTGGCATGGGAGAGCTGGGAATATCCCT 208

QY      261  AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGly 280
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      207  GACACCTGGAGACACCCACATCTCTACTTCTTCATTGCGCTTACATTGGCGTTACAGTCCAGGCG 148

QY      281  LysAsnAsnArgGlyLysAspArgLeuLysValAspLysThrSerAlaLysValVal 300
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      147  AAGAACACACAGAGGAGAAAGAGACAGACTCTCCCTGACCAAGACCTCAGCCAAAGCTCGTG 88

QY      301  CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTrpSerSerSerTrp 320
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      87  TGCCACACAGATGCCAGATCCGCTGTCAGAGCCGCTACTATAGCTCATCTCTGG 28

QY      321  SerAspTrpAlaSerValSerCysSer 329
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      27  AGCAACTGGGCATCTCGTCTCTGCACT 1

RESULT 9
US-09-917-265-52
: Sequence 52, Application US/09917265
: Patent No. US20020052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: APPLICANT: Borouhns, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
: FILE REFERENCE: IM-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: CURRENT FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: PRIOR FILING DATE: 2000-08-04
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 52
: LENGTH: 921
: TYPE: DNA
: ORGANISM: Canis familiaris
: FEATURE:
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: NAME/KEY: CDS
: LOCATION: (1)..(921)
: OTHER INFORMATION:
US-09-917-265-52

Alignment Scores:
Pred. No.: 6,14e-194 Length: 921
Score: 1653.00 Matches: 307
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 93.71% Indels: 0
DB: 10 Gaps: 0

US-09-917-265-59 (1-329) x US-09-917-265-52 (1-921)

QY      23  IleTrpGluLeuGluLysAspValTyrValValGluLeuAspTrpHisProAspAlaPro 42
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      1  ATATGGGCAACGAGAAAGATGTTATCTTTAGAGTTGGACTGGACCCGATGCCCC 60

QY      43  GlyGluMetValIleuThrCysHisThrProGluGluAspAspIleThrTrpThrSer 62
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      61  GGAGAAATGCTGCTCTCCTGACCTGCCATACCCCTGAGAGATGACATCATTGGACCTCA 120

QY      63  AlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      121  GCGCAGACACTGAAGTCTAGTGTCTGTGTAAACTCGACCATCCAAAGAAATTT 180

QY      83  GlyAspAlaGlyGlnTyrThrCysHisLysGlyLysValLeuSerArgSerLeuLeu 102
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      181  GGAGATGCTGGCCAGTATACCTGCCATMAAGCAGCAAGGTTCTGAGCCGCTCATCTCTG 240

QY      103  LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGlu 122
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      241  TTGATTTCACAAAAAAGAAAGATGAAATTTGGTCCACTGATATCTTAAAGAAACAGAAAGAA 300

QY      123  SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      301  TCCAAAAATAGATCTTCTCTGAATGTGAGCAAAAGAAATTTATCTTGACGTTTCACATGC 360

QY      143  TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 162
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      361  TGGTGGCTGAGGGGAATCAGTACGATTTGAAATTCAGTGCACAAAGTACGAGAGGCTTC 420

QY      163  SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGlnArgValVal 182
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      421  TCTGACCCCGCAAGGGGTGACATGTGAGACACTGACACTTTACGCAAGAGGCTCAGATG 480

QY      183  AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGlnGlySerAlaCysProSer 202
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      481  GACAACAGGATTTATAGAACTACACAGTGAAGTGTGAGAGGACAGTGCCTGCCCTCT 540

QY      203  AlaGluGluSerLeuProIleGluValValAlaLysAlaIleHisLysLeuLysTyrGlu 222
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      541  GCCGAGAGAGCCCTTACCCTAGAGTGTGATGCTATTTCACAACTCAAACTCAATATGAA 600

QY      223  AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeu 242
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      601  AACTACACACAGCAGCTTCTTATCAGAGACTCATCAAAACAGACCCACCCACAACCTG 660

QY      243  GluLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      661  CAGCTGAAGCATTGAAATAATTCGCGACGTGAGAGTCACTGCAATATACCCGACACC 720

QY      263  TrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 282
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      721  TGGAGCACCCCACTTCTCTCTCTGCAATTTTGCATACAGGCCACAGGCAAGAAAC 780

QY      283  AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValValCysHis 302
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      781  AATAGACAAAAGAAAGATAGACTCTGCTGACACAGACTTACGCAAGGTGTGTGTCAC 840

QY      303  LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTrpSerSerSerTrpSerAsp 322
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
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Db 841 AAGATGCCAAGATCCCGCTGCAAGCCGAGACCGCTACTATAGTTCATCTGGAGCGAC 900
Qy 323 TTPalaservAlserCysSer 329
Db 901 TGGCATCTGTGTCTCTGAGT 921
RESULT 10
US-09-917-265-54/c
; Sequence 54, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-917-265-54
Alignment Scores:
Pred. No.: 6,14e-194 Length: 921
Score: 1653.00 Matches: 307
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 93.71% Indels: 0
Gaps: 0
US-09-917-265-59 (1-329) x US-09-917-265-54 (1-921)
Qy 23 ILleTPleuLeuGluysAspValTyrValAluLeuAspTPPhisProAspAlaPro 42
Db 921 ATATGGAGACTGGGAAAGATGTTATGTTGTAGAGTTGGACCTGGACCCGATGCCCCC 862
Qy 43 GlyLumeValValLeuThrCysHisThrProGluGluAspAlaIleThrTriPser 62
Db 861 GGAGAAATGGTGGCTCCACCTGCATACCCCTCAAGAGATGACATCATTGGACCTCA 802
Qy 63 AlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
Db 801 GCCGAGAGCAGTGAAGTCTAGTGTGTTGTTAACTCTGACCATCCAAAGTCAAGAAATTT 742
Qy 83 GlyAspAlaGlyGlnTyrThrCysHisLysGlyLysValLeuSerArgSerLeuLeu 102
Db 741 GGAGATCTGGCCAGTATACCTGCCATTAAGAGGCAAGTTCGAGCCGCTCCTCTG 682
Qy 103 LeuIleHisLysLysGluAspGlyIleTPSerThrAspIleLeuLysGluGlnLysGlu 122
Db 681 TTGATTCACAAAAAGAGATGATTTGGTCCCTATATCTTAAAGAACACAGAAAGAA 622
Qy 123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
Db 621 TCCAAAATAAGATCTTCTGAAATGTGAGCAAAAGAAATTAATCTGACGCTTCACATGC 562
Qy 143 TTPleuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 162
Db 561 TGGGCTGAGCGCAATCAGTACGATTTGAAATTCAGTGCACAAAGATAGCAGAGCTTC 502
Qy 163 SerAspProGlnGlyValThrCysGlyAlaValAlaThrLeuSerAlaGluArgValArgVal 182
Db 501 TCTGACCCCAAGGGGGGACATGTGGACACTGACATCTTCAGCAGAGAGGGGTACAGTGC 442
Qy 183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGlnGlySerAlaCysProSer 202
Db 441 GACAAACAGGATATATAAGATACACAGTGGAGTGTGAGGAGGCAATGCTGCTGCTCT 382

Qy 203 AlaGluLeuSerLeuProIleGluValValAlaAspAlaIleHisLysLysLysTyrGlu 222
Db 381 GCCGAGAGAGCCCTACCCATCGAGCTGTGTGATGCTATTTCACAAAGCTCAAGTATGAA 322
Qy 223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPheAsnLeu 242
Db 321 AACTACACAGCAGCTTCTTCATCAGACATCATCAACCCAGACCCACCAAACTG 262
Qy 243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTPGluTyrProAspThr 262
Db 261 CAGCTGAAGCATTTGAAATAATTCCTGGACAGCTGAGGTGAGTGGAAATACCCGACACC 202
Qy 263 TPserThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 282
Db 201 TGGGACACCCCACTTCTCTCTCCCTGACATTTGCAATAGGCCAGGCCAGCAAGAAC 142
Qy 283 AsnArgGlnLysLysAspArgLeuCysValAspLysThrSerAlaLysValAlaCysHis 302
Db 141 AATGAGAAAAAGAAAGATAGACTCTGCTGGACAGACCTCAGCCAAAGTCTGTGCCAC 82
Qy 303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTPSerAsp 322
Db 81 AAGATGCCAAGATCCGCTGCAAGCCGAGACCGCTACTATATGTTTCATCTGAGCGAC 22
Qy 323 TTPalaservAlserCysSer 329
Db 21 TGGCATCTGTGTCTCTGAGT 1
RESULT 11
US-09-917-265-55
; Sequence 55, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 985
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(984)
; OTHER INFORMATION:
US-09-917-265-55
Alignment Scores:
Pred. No.: 6,78e-194 Length: 985
Score: 1653.00 Matches: 307
Percent Similarity: 96.65% Conservative: 10
Best Local Similarity: 93.60% Mismatches: 11
Query Match: 93.71% Indels: 0
Gaps: 0
US-09-917-265-59 (1-329) x US-09-917-265-55 (1-985)
Qy 1 MethisProGlnGlnLeuValIleSerTPPheSerLeuValLeuLeuAlaSerProLeu 20
Db 1 ATGATCTCTGAGCAGTGTGTCATCGCTGTTTCCCTGTTTGGTGGACCTCCCTC 60
Qy 21 MetAlaIleTPleuLeuGluLysAspValTyrValAluLeuAspTPPhisProAsp 40
Db 61 ATGGCCATATGCGAAGCTGGAAGAAACGTTTATGTTGTAGAGTTGGACTGCACCCCTGAT 120
Qy 41 AlaProGluLumeValValLeuThrCysHisThrProGluGluAspAlaIleThrTriP 60

121 GCGCCCGAGAAATGGTGGTCTCTCACTGCATTAAGAGAGATGACATCACTGG 180

121 TheSerAlaGlnSerSerGluValLeuGlySerGlyThrLeuThrIleGlnVallys 80

181 ACCTGTGACGACAGACATGAGGTCTAGCGCTGGTAAACTGTGACCATCAAGTCAA 240

81 GluPheGlyAspAlaGlyGlnTyrThrCysHisLysGlyGlyValLeuSerArgSer 100

241 GAATTTCAGATGCTGGCCAGCTATACCTGTCATTAAGAGAGCGAGGCTTCGAGCATTCG 300

101 LeuLeuLeuLeuIleHisLysLysGluAspGlyIleLeuPheSerThrAspIleLeuLysGluGln 120

301 TTCTCTCGATACCAAAAAGAGATGGAATTTGGTCCACTGATATCTTAAGGAACAG 360

121 LysGlnSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140

361 AAAAATTCACAAAATTAAGATCTTTCTTAAATGTGAGGCAAAATTAATTCGAGACTTTC 420

141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArg 160

421 ACCTGCTGCTGGCTGACCGCAATCATACCATTTGAAATTCACGTCAAAAGCAGCAGA 480

161 GlyPheSerAspProGlnGlyValThrCysLysAlaValThrLeuSerAlaGluArgVal 180

481 GCGCTCTCTGACCCCAAGGGGTGACTTGTGAGCAGCAGCACTCTCAGCAGAGAAGTTC 540

181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGlnGlnSerAlaCys 200

541 AGAGTGCACAAACAGGATTAATACAGAGTACACAGTGCAGGTTCAGAGAGGCGATGCTGC 600

201 ProSerAlaGluGlnSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220

601 CCGCTGCGCGAGAGACGCTACCCATTCGAATCGTGCGAGCGCTATTCACACACTCAAG 660

221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProThr 240

661 TACCAAAACATACACACACAGCTTCTTCATCAGGACATCATCAAAACCGAGCCACCCAG 720

241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260

721 AACCTGCACACTGAAGCCATTAAAAAATTTCTGGCATGTGGAGAGTACCTGGGAATACCT 780

261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGly 280

781 GACACCTGAGACACCCACATCTCTACTCTCTCTTACATTTGGCGTACAGCTCCAGCGC 840

281 LysAsnAsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValVal 300

841 AAGAACAAACAGAGAAAGAAAGACAGACTCTCCCTGGACAGACCTCAGCCAAAGCTCTG 900

301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320

901 TGCCACAAAGCATGGCAAGATTCGGGTGCACAGCCAGAGACCCCTACTAATAGCTCATCTGG 960

321 SerAspTrpAlaSerValSerCys 328

961 AGCAACATGGGATCCCTCTCTCTGC 984

RESULT 12

US-09-917-265-57/c

Sequence 57, Application US/09917265

Patent No. US20020052030A1

GENERAL INFORMATION:

APPLICANT: Wonderling, Ramani S.

APPLICANT: Boroughs, Karen L.

TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF

FILE REFERENCE: IM-5

CURRENT APPLICATION NUMBER: US/09/917,265

CURRENT FILING DATE: 2001-07-27

PRIOR APPLICATION NUMBER: 60/223,016

PRIOR FILING DATE: 2000-08-04

NUMBER OF SEQ ID NOS: 109

SOFTWARE: patentin version 3.1

| Seq. ID | Length | Score | Percent Similarity | Best Local Similarity | Query Match |
|---|---|---------------|--------------------|-----------------------|-------------|
| SEQ ID NO 57 | 985 | | | | |
| TYPE: DNA | | | | | |
| ORGANISM: <i>Felis catus</i> | | | | | |
| US-09-917-265-57 | | | | | |
| Alignment Scores: | | | | | |
| Pred. No.: | 6,78e-194 | Length: | 985 | | |
| Score: | 1653.00 | Matches: | 307 | | |
| Percent Similarity: | 96.65% | Conservative: | 10 | | |
| Best Local Similarity: | 93.60% | Mismatches: | 11 | | |
| Query Match: | 93.71% | Indels: | 0 | | |
| DB: | 10 | Gaps: | 0 | | |
| US-09-917-265-59 (1-329) x US-09-917-265-57 (1-985) | | | | | |
| QY | 1 MethIaProGInGInleuValIleSerTrpPheSerleuValleuLeuAlaSerProleu | 20 | | | |
| DB | 985 ATGCAATCCACACAGTGGTGCATCGCCGTGTTCCCTGGTTTGGTGGACCTCCCTC | 926 | | | |
| QY | 21 MetaIaIleTregIuIeuGInIuLySaSPVaITyTValValGluIeuAspTrpPHisProAsp | 40 | | | |
| DB | 925 ATGCCCATATGGGAACATGGAGAAAAACGTTTATGTTGTAGAGTTGGACATGCCACCGAT | 866 | | | |
| QY | 41 AlaProGInGInuIeValIleuThrCysHisThrProGInGInuAspAspIleThrTrp | 60 | | | |
| DB | 865 GCCCCCGGAGAAATGGTGGTCCCTCACCTGCATACCTCGAAGAGATGACATCACCTGG | 806 | | | |
| QY | 61 ThrSerAlaGInSerSerGluValleuGlySerGlyIuLyThrIleuThrIleGInValLyS | 80 | | | |
| DB | 805 ACCCTGACCAAGCAGTGAAGTCTGAGCTGTGTAACCTGACCATCCAAATCAGTCAAA | 746 | | | |
| QY | 81 GluPheGlyAspAlaGlyInTrpThrCysHisLySGlyIuLyValLeuSerArgSer | 100 | | | |
| DB | 745 GATTTTGCAGATGCTGGCCAGTATACCTGTCATTAAGAGAGCCAGGTTCTGACCATTCG | 686 | | | |
| QY | 101 LeuLeuLeuIleHisLySLySGInuAspGlyIleTrpSerThrAspIleLeuLySGInGIn | 120 | | | |
| DB | 685 TTCCTCCTGATACACAAAAGAGAGATGGAATTTGGTCCCATGATATCTTAAGGAGACAG | 626 | | | |
| QY | 121 LysGInSerLysAsnLySlePheLeuLySCysGInAlaIuAsnTrpSerGlyArgPhe | 140 | | | |
| DB | 625 AAAGAAATCCAAAATTAAGATCTTTCTTAATAATGAGGCAAAAGAAATTAATTCGACGTTTC | 566 | | | |
| QY | 141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLySlePheSerValLysSerSerArg | 160 | | | |
| DB | 565 ACCTGCTGTGGTGCAGGCAATCACTACCGATTTGAATTCACGTGTCAAAAGACAGCAGA | 506 | | | |
| QY | 161 GlyPheSerAspProGInGInValThrCysGlyAlaValThrLeuSerAlaGluArgVal | 180 | | | |
| DB | 505 GGCTCCTCGACCCCAAGGGGACCTTGTGGAGCAGCAGCACTCTCAGCAGGAAGTGC | 446 | | | |
| QY | 181 ArgValAspAsnArgAspTrpLySLySTyTThrValGluCysGInGlySerAlaCys | 200 | | | |
| DB | 445 AGAGTGAGACAAACAGGATTAATAAGAGTACACAGTGGAGTGCAGGAGGCGCTGC | 386 | | | |
| QY | 201 ProSerAlaGInGInuSerleuProIleGInuValValIuAspAlaIleHisLySleuLyS | 220 | | | |
| DB | 385 CCGGCTGCCGAGAGAGCTTACCATTTGAAGTGTGGTGGACCTATTTCACAAAGCTAAG | 326 | | | |
| QY | 221 TyrGluAsnTyTThrSerSerPhePheIleArgAspIleIleLySProAspProProThr | 240 | | | |
| DB | 325 TACGAAAACTACACCGACGAGCTTCTTCATCAGGACATCATCAACCGGACCCACCGAAG | 266 | | | |
| QY | 241 AsnLeuGInLeuLySProLeuLySAsnSerArgHisValGluValSerTrpGluTyTPro | 260 | | | |
| DB | 265 AACCTGCAACTAAGCCATTAAAAATTCCTCGGCATCTGGAAGTGGAGTGGAAATACCT | 206 | | | |
| QY | 261 AspTrpTrpSerThrProHisSerTyTTrpPheSerleuThrPheCysIleGInAlaGInGly | 280 | | | |
| DB | 205 GACACCTGGAGACCCCATTTCTTACTTCTTAAACATTTGGCGACAGGTCCAGGGC | 146 | | | |
| QY | 281 LysAsnAsnArgGluLySLySAspArgLeuCysValAspTySThrSerAlaLySValVal | 300 | | | |

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|||||
Db 145 AAGAACACAGCAAGAAAGAAAGACAGACTCCCTGGCAGACAGCTAGCCAGCGTGTG 86
Qy 301 CysHisLysAspAlaLysIleArgValGlnAlaIArgAspArgTyrTyrSerSerTirp 320
Db 85 TGCCACAGAGATGCGCAAGATCGCGTGCAGACCGAGACCGCTACTATGCTCATCTGG 26
Qy 321 SerAspTrrPalaservalSerCys 328
Db 25 AGCAACTGGCATCCGTGTCTCTGC 2

RESULT 13
US-09-917-265-66
: Sequence 66, Application US/09917265
: Patent No. US20020052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: APPLICANT: Borouhgs, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
: FILE REFERENCE: IM-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: PRIOR FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 66
: LENGTH: 1533
: TYPE: DNA
: ORGANISM: Canis familiaris
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(1533)
: OTHER INFORMATION:
US-09-917-265-66

Alignment Scores:
Pred. No.: 1,31e-193 Length: 1533
Score: 1653.00 Matches: 307
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 93.71% Indels: 0
Gaps: 0

US-09-917-265-59 (1-329) x US-09-917-265-66 (1-1533)
Qy 23 IleTrrpGluLeuGluLysAspValTyrValGlnLeuAspTrrPhtsProAspAlaPro 42
Db 1 ATATGGGAAGTGGAGAAAGATGTTATGTTGTAGAGTTGGAGTGGACCCCTGATGCCCCC 60
Qy 43 GlyIuMeValValLeuThrCysHisLysThrProGluLysAspAlaLysThrTrrPhtSer 62
Db 61 GGAGAAATGGTGGTCTCAGCTGCCATACCCCTGAGAGAAATGACATTCATTCGACCTCA 120
Qy 63 AlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
Db 121 GCGCAGAGCACTGAGTCTGAGTTCGTGTAACCTGACCATCCAAAGTCAAGAAATTT 180
Qy 83 GlyAspAlaGluGlnTyrThrCysHisLysGlyLysValLeuSerArgSerLeuLeu 102
Db 181 GGAATGCTGGCCAGTATACCTGCCATTAAGAGAGCAAGGTTCTGAGCGCTCATCTCTG 240
Qy 103 LeuIleHisLysLysGluAspGlyIleTrrSerThrAspIleLeuLysGluGlnLysGlu 122
Db 241 TTGATTCCACAAAAGAAAGATGAGATTGGTCCATGATATCTTAAGGAACAGAAAGAA 300
Qy 123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
Db 301 TCCAAAATAGATCTTCTGAAATGTGAGGCAAGAAATATCTGAGACGTTTCACATGC 360
Qy 143 TrrPheLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 162
Db 361 TGGTGGCTGACGGCAATCAGTACTGATTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
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Qy 163 SerAspProGlnGlyValIthrCysGlyAlaValIthrLeuSerAlaGluArgValArgVal 182
Db 421 TCTGATACCCCAAGGCGTACATGTGGAGCAGTGACACTTTCAGAGAGAGGCGCAGAGTG 480
Qy 183 AspAsnArgAspTrrLysLysTyrThrValGluCysGlnGluLysAlaCysProSer 202
Db 481 GACAAACAGGAGATTATTAAGAGTACACAGTGGAGTTCAGAGGCGCATGCTCCCTCT 540
Qy 203 AlaGluGlnSerLeuProIleGlnValValValAspAlaIleHisLysLeuLysTyrGlu 222
Db 541 GCCGAGAGAGACCTACCATTCAGAGCTGTGCTGATCTTTCACAAAGCTCAAGTATGAA 600
Qy 223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPrrrAsnLeu 242
Db 601 AACTACACCAAGCAGACTCTTTCATCAGACATCATCAACCCAGACCCACCAAAACCTG 660
Qy 243 GlnLeuLysProLeuLysAsnSerArgHisValGlnValSerTrrpGluTyrProAspThr 262
Db 661 CAGCTGAAGCCATTGAAAAATTCGCGCAGCTGGAGGTCAGCTGGGAATCCCCGACACC 720
Qy 263 TrrSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 282
Db 721 TGGAGCACCCACATTCCTACTCTCCCTGACATTTTGCAATACAGGCCCGCAGGAGAAC 780
Qy 283 AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValLysHis 302
Db 781 AATGAGAAAAGAAAGATAGACTGTGGTGGACAGACCTCAGCAAGCTCGTGTGCAC 840
Qy 303 LysAspAlaLysIleArgValGlnAlaIArgAspArgTyrTrrSerSerSerTrrPht 322
Db 841 AAGCATGCCAAGATCCCGTGCAGAACCCGAGACCGCTACTATGTTTCATCTCGAGCGAC 900
Qy 323 TrrPalaservalSerCysSer 329
Db 901 TGGCATCTGTGTCATCAGT 921

RESULT 14
US-09-917-265-68/C
: Sequence 68, Application US/09917265
: Patent No. US20020052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: APPLICANT: Borouhgs, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
: FILE REFERENCE: IM-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: PRIOR FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 68
: LENGTH: 1533
: TYPE: DNA
: ORGANISM: Canis familiaris
US-09-917-265-68

Alignment Scores:
Pred. No.: 1,31e-193 Length: 1533
Score: 1653.00 Matches: 307
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 93.71% Indels: 0
Gaps: 0

US-09-917-265-59 (1-329) x US-09-917-265-68 (1-1533)
Qy 23 IleTrrpGluLeuGluLysAspValTyrValGlnLeuAspTrrPhtsProAspAlaPro 42
Db 1533 ATATGGGAAGTGGAGAAAGATGTTATGTTGTAGAGTTGGAGTGGACCCCTGATGCCCCC 1474
Qy 43 GlyIuMeValValLeuThrCysHisLysThrProGluLysAspAlaLysThrTrrPhtSer 62
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Db      1473 GGAGAAATGCTGCTCCTACCTCCATACCCCTGAGAGATGACATCATCTGGACCTCA 1414
Qy      63  AlagInserSerGluValIleuGlySerClyLysThrIleuThrIleGlnValLysGluPhe 82
Db      1413 GCGAGAGCACTGAAGTCTTGAAGTTCTGCTAAACTCTGACCATTCAGTCAAGTCAAGAAATTT 1354
Qy      83  GlyAspAlaGlyGlnTyrThrCysHisLysGlyLysValIleuSerArgSerLeu 102
Db      1353 GGAATGCTGGCCAGTACTACTGCCATTAAGAGCAAGTTCTGAGCCGCTCACTCTG 1294
Qy      103  LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGlnLysGlu 122
Db      1293 TTGATTCACAAAAGAAAGATGAGATTTGGTCCACTGATATCTTAAGACAGAAAGAA 1234
Qy      123  SerLysAsnLysIlePheLeuLysCysGlnAlaLysAsnTyrSerGlyArgPheThrCys 142
Db      1233 TTCAAAATATAGATCTTCTGAAATGTCAGGCAAGAAATVATTCCTGACGTTTCACATGC 1174
Qy      143  TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 162
Db      1173 TGTGGCTGACGCGCATCTAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGCTTC 1114
Qy      163  SerAspProGlnGlyValThrCysGlyAlaValIleuSerAlaGluArgValArgVal 182
Db      1113 TCTGACCCCAAGGCGTGACATGTGACGACGTGACACTTTCAGCAGAGAGGCTCAGAGTG 1054
Qy      183  AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGlySerAlaCysProSer 202
Db      1053 GACACACAGGATTTAAGAAATACACAGTGGAGTGTCAGGAGGCGAGTCCCTGCCCTCT 994
Qy      203  AlaGluGluSerLeuProIleGluValValAlaAspAlaIleHisLysLeuLysTyrGlu 222
Db      993 GCCAGAGAGACCTTACCATCGAGTCTGTGATGATCTATTCCAAAGCTCAAGTATGAA 934
Qy      223  AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPioThrAsnLeu 242
Db      933 AACTACACACGACCTTCTTCATCAGACATCATCAACACAGCCCAACCAACCTG 874
Qy      243  GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
Db      873 CAGTGAAGCATTTGAAAAATTTCTGGCAGCTGAGGTCACCTGGGAATACCCGACACC 814
Qy      263  TrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlyLysAsn 282
Db      813 TGGAGCACCCACACTTCTTCTACTTCTCCCTGACATTTTTCATACAGGCCAGGCAAGAC 754
Qy      283  AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValIleCysHis 302
Db      753 AATGAGAAAAGAAAGATAGACTCTGCTGGACAAGACCTCAGCCAAGCTGCTGGCCAC 694
Qy      303  LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsp 322
Db      693 AAGGATCCCAAGATCCGCTGTCAGAGCCGAGACCGCTAATAGTTCTATCTCTGAGAGCAC 634
Qy      323  TrpAlaSerValSerCysSer 329
Db      633 TGGGCATCTGCTCATGCAGT 613

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STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/079,616
FILING DATE: 22-Feb-2002
CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/011,143
FILING DATE: 04-FEB-1998
APPLICATION NUMBER: PCT/JP97/01824
FILING DATE: 29-MAY-1997
APPLICATION NUMBER: JP 165249/1996
FILING DATE: 04-JUN-1996

ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: IMAMURA-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2193 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-079-616-5

Alignment Scores:
Pred. No.: 3,91e-193 Length: 2193
Score: 1651.00 Matches: 307
Percent Similarity: 96.35% Conservative: 10
Best Local Similarity: 93.31% Mismatches: 12
Query Match: 93.59% Indels: 0
DB: 15 Gaps: 0

US-09-917-265-59 (1-329) x US-10-079-616-5 (1-2193)
Qy      1  MethAspProGlnGlnLeuValIleSerTrpPheSerLeuValIleuLeuAlaSerProLeu 20
Db      64  ATGCATCTCTGACGACAGCTGTCATCGCCCTGTTTAACTGCTGTTTCTGCTGACCTCTCTC 123
Qy      21  MetAlaIleTrpGluLeuGluLysAspValTyrValValGluLeuAspTrpHisProAsp 40
Db      124  ATGGCATATGGAAGAACTGGAGAAACGTTATATGTTAGAGATTGGAGCTGACCTGACCTGAT 183
Qy      41  AlaProGlyGluMetValValLeuThrCysHisThrProGluGluAspIleThrTrp 60
Db      184  GCCCCGGAAGAAATGCTGCTCCTCACCGCAATACTCTCTGAAGAAAGATGACATCACCCTGG 243
Qy      61  ThrSerAlaGlnSerSerGluValIleuGlySerGlyLysThrLeuThrIleGlnValLys 80
Db      244  ACCTCTGACCCAGACAGTGAAGTCTTAGGCTCTGTGTAACCTTGACCATTCAAAGTCAAA 303
Qy      81  GluPheGlyAspAlaGlyGlnTyrThrCysHisLysGlyLysValIleuSerArgSer 100
Db      304  GAATTTGAGATGCTGGCCAGTATACCTGATCAAGAGGCGAGGTTCTGAGCCATTCG 363
Qy      101  LeuLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGln 120
Db      364  TTCTCTGATACCAAAAAGAAAGATGGAATTTTGGTCCACTGATATCTTAAGGGAACAG 423
Qy      121  LysGluSerLysAsnLysIlePheLeuLysCysGlnAlaLysAsnTyrSerGlyArgPhe 140

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QY 141 ThrcYstrPTpleuThrAlaIleSerThrAspleuLysPheSerValLysSerArg 160
Db 484 ACCTGCTGGTGGCTGACGGCAATCAGTACCATTTGAATTCAGTCTCAAAAGCAGCAGA 543
QY 161 GlyPheSerAspProGlnGlyValThrCysGlyValAlaValThrLeuSerAlaGluArgVal 180
Db 544 GGCTCTCTGTGACCCCAAGGGGTGACTGTGTGACAGGACACTCTCAGCAGAGAGGTC 603
QY 181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
Db 604 AGACTGGACACACAGGAGATTATTAAGAGTACACAGTGGAGTGTCTCAGAGGGCAGTCCCTGC 663
QY 201 ProSerAlaGlnGluSerLeuProIleGluValAlaValAspAlaIleHisLysLeuLys 220
Db 664 CCGGCTCGCCGAGGAGAGCTTACCATTTGAAGTCTGCTGGAGGCTATTTCACAGCTCAAG 723
QY 221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProThr 240
Db 724 TACGAAACTACACACAGAGCTTCTTCATCAGGACATCATCAAAACCGAGCCACCCAG 783
QY 241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTTPGluTyrPro 260
Db 784 AACCTGCACTGAAGCCATTAAAAATTCGCGCATGTGGAAGTGGAGCTGGGAATTACCT 843
QY 261 AspThrTTPSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGly 280
Db 844 GACACCTGGAGACACCCACATTCCTACTTCTCCTTAACATTGGCGTACAGCTCCAGGGC 903
QY 281 LysAsnAsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysVal 300
Db 904 AAGAACACACAGAGAAAAAGACAGACTCTCCGTGGACAAAGACCTCAGCCAAAGTGTG 963
QY 301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTyr 320
Db 964 TGGCACAAGGATGCCAAGATCCGGGTGCAAGCCAGAGACCGCTACTATAGCTCATCTCTGG 1023
QY 321 SerAspTTPAlaSerValSerCysSer 329
Db 1024 AGCAACTGGGATCCGTCTCTGCAGT 1050
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Search completed: July 17, 2003, 09:56:19
Job time : 229.767 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 13:16:38 ; Search time 84.9175 Seconds
(without alignments)
5774.736 Million cell updates/sec

Title: US-09-917-265-61

Sequence: 1 atgacaccctcagcagttgtg.....tgctcacttgaaactcttc 1599

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 15338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 802724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Issued_Patents_NA:*
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6: /cgn2_6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|-------------------|-------------------|
| 1 | 974 | 60.9 | 990 | 4 | US-09-079-984A-11 | Sequence 11, Appl |
| 2 | 798 | 49.9 | 990 | 4 | US-09-079-984A-1 | Sequence 1, Appl |
| 3 | 494 | 30.9 | 669 | 4 | US-09-079-984A-12 | Sequence 12, Appl |
| 4 | 443 | 27.7 | 669 | 4 | US-09-079-984A-2 | Sequence 2, Appl |
| 5 | 59 | 3.7 | 660 | 1 | US-08-186-529-3 | Sequence 3, Appl |
| 6 | 59 | 3.7 | 660 | 1 | US-08-640-386A-3 | Sequence 3, Appl |
| 7 | 59 | 3.7 | 721 | 2 | US-08-184-009-199 | Sequence 199, App |
| 8 | 59 | 3.7 | 721 | 2 | US-08-458-356-199 | Sequence 199, App |
| 9 | 59 | 3.7 | 721 | 4 | US-08-460-736-199 | Sequence 199, App |
| 10 | 59 | 3.7 | 762 | 4 | US-08-848-760B-21 | Sequence 21, Appl |
| 11 | 59 | 3.7 | 1026 | 2 | US-08-751-767A-1 | Sequence 1, Appl |
| 12 | 59 | 3.7 | 1316 | 2 | US-08-684-687-3 | Sequence 3, Appl |
| 13 | 59 | 3.7 | 1316 | 4 | US-09-851-520-3 | Sequence 3, Appl |
| 14 | 59 | 3.7 | 1364 | 1 | US-08-265-087-3 | Sequence 3, Appl |
| 15 | 59 | 3.7 | 1364 | 1 | US-08-621-493-3 | Sequence 3, Appl |
| 16 | 59 | 3.7 | 1364 | 4 | US-08-965-688-3 | Sequence 3, Appl |
| 17 | 59 | 3.7 | 1364 | 4 | US-09-260-173-3 | Sequence 3, Appl |
| 18 | 59 | 3.7 | 1560 | 2 | US-08-751-767A-11 | Sequence 11, Appl |
| 19 | 59 | 3.7 | 1623 | 2 | US-08-751-767A-9 | Sequence 9, Appl |
| 20 | 59 | 3.7 | 1645 | 4 | US-09-310-842-2 | Sequence 2, Appl |
| 21 | 59 | 3.7 | 6139 | 1 | US-08-751-767A-7 | Sequence 7, Appl |
| 22 | 46 | 2.9 | 987 | 1 | US-08-186-529-1 | Sequence 1, Appl |
| 23 | 46 | 2.9 | 987 | 4 | US-08-640-386A-1 | Sequence 1, Appl |
| 24 | 46 | 2.9 | 987 | 4 | US-08-848-760B-24 | Sequence 24, Appl |
| 25 | 46 | 2.9 | 1018 | 2 | US-08-184-009-194 | Sequence 194, App |
| 26 | 46 | 2.9 | 1018 | 2 | US-08-458-356-194 | Sequence 194, App |
| 27 | 46 | 2.9 | 1018 | 4 | US-08-460-736-194 | Sequence 194, App |

| | | | | | | |
|----|----|-----|------|---|-------------------|-------------------|
| 28 | 46 | 2.9 | 1399 | 2 | US-08-751-767A-3 | Sequence 3, Appl |
| 29 | 46 | 2.9 | 1870 | 4 | US-09-310-842-4 | Sequence 4, Appl |
| 30 | 46 | 2.9 | 2318 | 4 | US-09-851-062-3 | Sequence 3, Appl |
| 31 | 46 | 2.9 | 2362 | 1 | US-08-265-087-1 | Sequence 1, Appl |
| 32 | 46 | 2.9 | 2362 | 1 | US-08-621-493-1 | Sequence 1, Appl |
| 33 | 46 | 2.9 | 2362 | 2 | US-08-965-688-1 | Sequence 1, Appl |
| 34 | 46 | 2.9 | 2362 | 4 | US-09-260-173-1 | Sequence 1, Appl |
| 35 | 31 | 1.9 | 713 | 2 | US-08-385-335A-10 | Sequence 10, Appl |
| 36 | 31 | 1.9 | 6295 | 2 | US-08-659-206A-4 | Sequence 4, Appl |
| 37 | 31 | 1.9 | 7287 | 2 | US-08-659-206A-1 | Sequence 1, Appl |
| 38 | 24 | 1.5 | 39 | 4 | US-09-079-984A-13 | Sequence 13, Appl |
| 39 | 20 | 1.3 | 20 | 3 | US-08-621-841-52 | Sequence 52, Appl |
| 40 | 20 | 1.3 | 20 | 4 | US-09-851-520-28 | Sequence 28, Appl |
| 41 | 20 | 1.3 | 20 | 4 | US-09-851-520-31 | Sequence 31, Appl |
| 42 | 20 | 1.3 | 20 | 4 | US-09-851-520-58 | Sequence 58, Appl |
| 43 | 20 | 1.3 | 20 | 4 | US-09-851-062-17 | Sequence 17, Appl |
| 44 | 20 | 1.3 | 20 | 4 | US-09-851-062-23 | Sequence 23, Appl |
| 45 | 20 | 1.3 | 20 | 4 | US-09-851-062-33 | Sequence 33, Appl |

ALIGNMENTS

RESULT 1
US-09-079-984A-11
Sequence 11, Application US/09079984A
Patent No. 6231850
GENERAL INFORMATION:
APPLICANT: Okano, Fumiyoshi, Satoh, Masahiro,
APPLICANT: Yamada, Katsushige
TITLE OF INVENTION: Canine interleukin 12, a production method
thereof, an immune disease treatment method and preventive
TITLE OF INVENTION: thereof, an immune disease treatment method and preventive
TITLE OF INVENTION: method using it
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Miller & Christenbury Intellectual Property
ADDRESS: Department of Schnader, Harrison, Segal and Lewis, LLP
STREET: 1600 Market Street, 39th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079, 984A
FILING DATE: 15-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Austin R. Miller
REGISTRATION NUMBER: 16,602
REFERENCE/DOCKET NUMBER: 1051-98
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-1810
TELEFAX: (215) 568-6946
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 990 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: Canine IL12
LOCATION: 1 to 987
IDENTIFICATION METHOD: Similarity
US-09-079-984A-11
Query Match 60.9% ; Score 974 ; DB 4 ; Length 990 ;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 974; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 7 CCTCAGAGATTGTCATCTCTGTTTCCCTTTTGGTGGCGTCCCTCATGGCC 66
OY 67 ATATGGAACTGGAGAAAGATGTTATGTTAGAGTTGGACCTGATGCCCC 126
Db 67 ATATGGAACTGGAGAAAGATGTTATGTTAGAGTTGGACCTGATGCCCC 126
OY 127 GGAGAAATGGTGGTCCCTGACCTGCAATCCCTGAAGAATGACATCTTGACCTCA 186
Db 127 GGAGAAATGGTGGTCCCTGACCTGCAATCCCTGAAGAATGACATCTTGACCTCA 186
OY 187 GCGCAGACAGTGAAGTCTAGTTCTGTAAATCTGACCAATCCAAAGTCAATTT 246
Db 187 GCGCAGACAGTGAAGTCTAGTTCTGTAAATCTGACCAATCCAAAGTCAATTT 246
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OY 307 TTGATTCACAAAAAAGATGGAATTTGGTCCCTGATATCTTAAAGAGCAAGAA 366
Db 307 TTGATTCACAAAAAAGATGGAATTTGGTCCCTGATATCTTAAAGAGCAAGAA 366
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OY 607 GCGGAGAGAGCTTACCATCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 666
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OY 667 AACTACACAGGACCTTCTCATCAGACATCATCAACCAAGCCCAACCAAGCTG 726
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OY 727 CAGCTGAAGCATTTGAAATTTCTGCGACGTGAGGTGAGTGTGAGTGTGAGTGTGAG 786
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OY 787 TGGAGCAGCCCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 846
Db 787 TGGAGCAGCCCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 846
OY 847 AATGAGCAAAAGAAAGATAGACTGTGCTGAGCAAGCAAGCAAGCAAGCAAGCAAG 906
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OY 907 AAGGATGCCAAGATCCCGTGCAGAGCCGAGACGCTACTATAGTTCATCTGAGAGC 966
Db 907 AAGGATGCCAAGATCCCGTGCAGAGCCGAGACGCTACTATAGTTCATCTGAGAGC 966
OY 967 TGGGCACTCTGTGC 980
Db 967 TGGGCACTCTGTGC 980

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RESULT 2

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US-09-079-984A-1
: Sequence 1, Application US/09079984A
: Patent No. 6231850
: GENERAL INFORMATION:
: APPLICANT: Okano, Fumiyoshi, Satoh, Masahiro,
: APPLICANT: Yamada, Katsushige
: TITLE OF INVENTION: Canine Interleukin 12, a production method
: TITLE OF INVENTION: thereof, an immune disease treatment method and preventive
: NUMBER OF SEQUENCES: 16
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Miller & Christenbury Intellectual Property
: ADDRESSEE: Department of Schneider, Harrison, Segal and Lewis, LLP
: STREET: 1600 Market Street, 39th Floor
: CITY: Philadelphia
: STATE: PA
: COUNTRY: USA
: ZIP: 19103
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy Disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Wordperfect 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/079,984A
: FILING DATE: 15-MAY-1998
: ATTORNEY/AGENT INFORMATION:
: NAME: Austin R. Miller
: REGISTRATION NUMBER: 16,602
: REFERENCE/DOCKET NUMBER: 1051-98
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215) 563-1810
: TELEFAX: (215) 568-6946
: INFORMATION FOR SEO ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 990 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: ORIGINAL SOURCE:
: ORGANISM: Canis familiaris
: FEATURE:
: NAME/KEY: Canine IL12
: LOCATION: 1 to 987
: IDENTIFICATION METHOD: Similarity
US-09-079-984A-1
Query Match 49.9%; Score 798; DB 4; Length 990;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 948; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 28 TGGTTTCCCTGTTTGGTGGCGTCCCTCATGATGGCAATGAGAAAGAT 87
Db 28 TGGTTTCCCTGTTTGGTGGCGTCCCTCATGATGGCAATGAGAAAGAT 87
OY 88 GTTTATGTTAGAGTTGAGCTGCAACCTGATGCCCGGAGAAATGTGTCTCAAC 147
Db 88 GTTTATGTTAGAGTTGAGCTGCAACCTGATGCCCGGAGAAATGTGTCTCAAC 147
OY 148 TGGCATACCCCTTAAGAAAGTGAATGATCTGAGCTCAGCGAGAGAGTGAAGTCTTA 207
Db 148 TGGCATACCCCTTAAGAAAGTGAATGATCTGAGCTCAGCGAGAGAGTGAAGTCTTA 207
OY 208 GTTTCTGTTAAACTGTGACATCCAAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 267
Db 208 GTTTCTGTTAAACTGTGACATCCAAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 267
OY 268 TGGCATAAAGAGAGAGGTTCTGAGCCGCTCACTCTGTTGATTCACAAAAAAGAAAT 327
Db 268 TGGCATAAAGAGAGAGGTTCTGAGCCGCTCACTCTGTTGATTCACAAAAAAGAAAT 327
OY 328 GGAATTTGCTCAGTATCTTAAAGAGAGAGAAAGATCCAAAAATGAATCTTCTG 387

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|||||
Db 328 GGAATTGGTCCACTGATATCTTAAAGCAGAGAAAGATCCAAAATTAAGATCTTTCTG 387
Qy 388 AAATGTAGCGCAAGAATTAATTCGACGCTTTCACATGCTGCTGGCTGACGGCATACT 447
Db 388 AAATGTAGCGCAAGAATTAATTCGACGCTTTCACATGCTGCTGGCTGACGGCATACT 447
Qy 448 ACTGATTTGAAATTCACGTGCAAAAGTAGCAGAGGCTTCTGTGACCCCAAGGGGTACA 507
Db 448 ACTGATTTGAAATTCACGTGCAAAAGTAGCAGAGGCTTCTGTGACCCCAAGGGGTACA 507
Qy 508 TGTGAGCAGTGCACATTTTCAGCAGAGAGGTCAGAGTGCACAACAGGATTTATAGAG 567
Db 508 TGTGAGCAGTGCACATTTTCAGCAGAGAGGTCAGAGTGCACAACAGGATTTATAGAG 567
Qy 568 TACACAGTGAAGTGTAGAGAGGCGAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTG 627
Db 568 TACACAGTGAAGTGTAGAGAGGCGAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTG 627
Qy 628 GAGTGTGTGTGATGCTATTTCAACAGCTCAAGTATGAAATGACACAGAGCTTCTG 687
Db 628 GAGTGTGTGTGATGCTATTTCAACAGCTCAAGTATGAAATGACACAGAGCTTCTG 687
Qy 688 ATCAGAGACATCATCAAAACAGAGCCACCCCAAAACCTGACGCTGAAGCCTTGAATAAT 747
Db 688 ATCAGAGACATCATCAAAACAGAGCCACCCCAAAACCTGACGCTGAAGCCTTGAATAAT 747
Qy 748 TCTCGGACAGTGCAGAGTGTGGAAATACCCGACACCTGAGAGACCCCATCTGTAC 807
Db 748 TCTCGGACAGTGCAGAGTGTGGAAATACCCGACACCTGAGAGACCCCATCTGTAC 807
Qy 808 TTTCTCCCTGACATTTTGCATACAGGCGCAGGCAAGACATAGAGAAAAAGATAGA 867
Db 808 TTTCTCCCTGACATTTTGCATACAGGCGCAGGCAAGACATAGAGAAAAAGATAGA 867
Qy 868 CTCTGCGTGACAAAGACCTCAGCCCAAGGTGTGCCCAAGATGCCAATCCGGCTG 927
Db 868 CTCTGCGTGACAAAGACCTCAGCCCAAGGTGTGCCCAAGATGCCAATCCGGCTG 927
Qy 928 CAAGCCCGAGACGCTACTACTTCTCTGAGAGCGCAGCTGCGATCTGTG 978
Db 928 CAAGCCCGAGACGCTACTACTTCTCTGAGAGCGCAGCTGCGATCTGTG 978

RESULT 3
US-09-079-984A-12
Sequence 12, Application US/09079984A
Patent No. 6231850
GENERAL INFORMATION:
APPLICANT: Okano, Fumiyoshi, Satoh, Masahiro,
APPLICANT: Yamada, Katsushige
TITLE OF INVENTION: Canine interleukin 12, a production method
TITLE OF INVENTION: thereof, an immune disease treatment method and preventive
TITLE OF INVENTION: method using it
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Miller & Christenbury Intellectual Property
ADDRESSEE: Department of Schnader, Harrison, Segal and Lewis, LLP
STREET: 1600 Market Street, 39th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,984A
FILING DATE: 15-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Austin R. Miller

REGISTRATION NUMBER: 16,602
REFERENCE/DOCKET NUMBER: 1051-98
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-1810
TELEFAX: (215) 568-6946
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 669 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: Canine IL12
LOCATION: 1 to 666
IDENTIFICATION METHOD: Similarity
US-09-079-984A-12

Query Match 30.9% Score 494 DB 4: Length 669;
Best Local Similarity 100.0%; Pred. No. 2,9e-235;
Matches 494; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1076 TGAGAGCGCTCAGCAGACCGCTTCAGAGGCGCAGACAACTCTGAATTTATATCTGCA 1135
Db 143 TGAGAGCGCTCAGCAGACCGCTTCAGAGGCGCAGACAACTCTGAATTTATATCTGCA 202
Qy 1136 CTTCGGAAGAGATTGATCATGATATATACAAAGATATAAACAGCAGACAGTGGAGCCT 1195
Db 203 CTTCGGAAGAGATTGATCATGATATATACAAAGATATAAACAGCAGACAGTGGAGCCT 262
Qy 1196 GCTTACACAGTGAATTAACATGATGATGAGAGTGTGCTGCTGCTGCTGCTGCTGCTG 1255
Db 263 GCTTACACAGTGAATTAACATGATGATGAGAGTGTGCTGCTGCTGCTGCTGCTGCTG 322
Qy 1256 TAACTAACGGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1315
Db 323 TAACTAACGGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 382
Qy 1316 GCACCATCTATGAGAGCTTGAGATGTACAGATGGAATTCAGAGCCATGAGCCAAAGC 1375
Db 383 GCACCATCTATGAGAGCTTGAGATGTACAGATGGAATTCAGAGCCATGAGCCAAAGC 442
Qy 1376 TTTTAATGATCCCAAGAGGAGATCTTCTGATGCTCAAAACATGCTGACGCTATGATG 1435
Db 443 TTTTAATGATCCCAAGAGGAGATCTTCTGATGCTCAAAACATGCTGACGCTATGATG 502
Qy 1436 AGCTGTTACAGGCGCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCCTTGAAG 1495
Db 503 AGCTGTTACAGGCGCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCCTTGAAG 562
Qy 1496 AGCCGATTTTATAAACTAAATCAAGCTGTGACATCTTCTGATGCTTTCAGAAATTC 1555
Db 563 AGCCGATTTTATAAACTAAATCAAGCTGTGACATCTTCTGATGCTTTCAGAAATTC 622
Qy 1556 GTGCGGTGACCATC 1569
Db 623 GTGCGGTGACCATC 636

RESULT 4
US-09-079-984A-2
Sequence 2, Application US/09079984A
Patent No. 6231850
GENERAL INFORMATION:
APPLICANT: Okano, Fumiyoshi, Satoh, Masahiro,
APPLICANT: Yamada, Katsushige
TITLE OF INVENTION: Canine interleukin 12, a production method
TITLE OF INVENTION: thereof, an immune disease treatment method and preventive
TITLE OF INVENTION: method using it
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:

ADDRESSEE: Miller & Christendbury Intellectual Property
ADDRESSEE: Department of Schnader, Harrison, Segal and Lewis, LLP
STREET: 1600 Market Street, 39th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/079,984A

FILING DATE: 15-MAY-1998

ATTORNEY/AGENT INFORMATION:

NAME: Austin R. Miller

REGISTRATION NUMBER: 16,602

REFERENCE/DOCKET NUMBER: 1051-98

TELEPHONE: (215) 563-1810

TELEFAX: (215) 568-6946

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 669 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

ORIGINAL SOURCE:

ORGANISM: Canis familiaris

FEATURE:

NAME/KEY: Canine IL12

LOCATION: 1 to 666

IDENTIFICATION METHOD: Similarity

US-09-079-984A-2

Query Match 27.7%; Score 443; DB 4; Length 669;
Best Local Similarity 99.8%; Pred. No. 5.5e-210;
Matches 493; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1076 TGAAGCGCTGACAGACGCTTCAGAAAGCCAGACAACTAGATATATATCTCGCA 1135
143 TGAGAGCGCTGACAGACGCTTCAGAAAGCCAGACAACTAGATATATATCTCGCA 202
1136 CTTCGAGAGATTGATGATGAAGATATCAAAAGATATAAACCAGACAGTGGAGCCT 1195
203 CTTCGAGAGATTGATGATGAAGATATCAAAAGATATAAACCAGACAGTGGAGCCT 262
1196 GCTTACCACTGGATTAACCATGAATGAGAGTTGCTGCTCCAGAGAGATCTTTGA 1255
263 GCTTACCACTGGATTAACCATGAATGAGAGTTGCTGCTCCAGAGAGATCTTTGA 322
1256 TAACTAAGGAGATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1315
323 TAACTAAGGAGATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 382
1316 GCAGCATCTATGAGGACTTGAAGATGTACAGATGGAATTAAGGCCATGAAGCAAGC 1375
383 GCAGCATCTATGAGGACTTGAAGATGTACAGATGGAATTAAGGCCATGAAGCAAGC 442
1376 TTTTATGATCCCAAGAGGAGATCTTTCTGATCAAAACATGCTGACAGCTATCGATG 1435
443 TTTTATGATCCCAAGAGGAGATCTTTCTGATCAAAACATGCTGACAGCTATCGATG 502
1436 ACCTGTTACAGGCGCTGATTTCAACAGTGTGTCGACAGAAATCCCTCTTGAAG 1495
503 ACCTGTTACAGGCGCTGATTTCAACAGTGTGTCGACAGAAATCCCTCTTGAAG 562
1496 ACCCGATTTTATATAAATCAAGCTCTGATATCTTCTCATGCTTCAAGATTC 1555
563 ACCCGATTTTATATAAATCAAGCTCTGATATCTTCTCATGCTTCAAGATTC 622

QY 1556 GTGCGTGATCATT 1569
Db 623 GTGCGTGATCATT 636

RESULT 5

US-08-186-529-3
Sequence 3, Application US/08186529

Patent No. 5573764

GENERAL INFORMATION:

APPLICANT: Sykes, Megan

TITLE OF INVENTION: USE OF INTERLEUKIN-12 TO PREVENT

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESS: Genetics Institute, Inc., Legal Affairs

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: MA

COUNTRY: USA

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/186,529

FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: McDaniel, Patricia A.

REGISTRATION NUMBER: 33,194

REFERENCE/DOCKET NUMBER: GI 5225

TELEPHONE: 617-498-8401

TELEFAX: 617-876-5851

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 660 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

CELL TYPE: Lymphoblast

CELL LINE: RPMI 8866

FEATURE:

NAME/KEY: CDS

LOCATION: 1..660

US-08-186-529-3

Query Match 3.7%; Score 59; DB 1; Length 660;
Best Local Similarity 100.0%; Pred. No. 1.2e-19;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1498 CCGGATTTTATAAATAAATCAAGCTCTGATATCTTCTCATGCTTCAAGATTC 1556
Db 556 CCGGATTTTATAAATAAATCAAGCTCTGATATCTTCTCATGCTTCAAGATTC 614

RESULT 6

US-08-640-386A-3
Sequence 3, Application US/08640386A

Patent No. 5756085

GENERAL INFORMATION:

APPLICANT: Sykes, Megan

TITLE OF INVENTION: USE OF INTERLEUKIN-12 TO PREVENT

NUMBER OF SEQUENCES: 4

```

CORRESPONDENCE ADDRESS:
ADDRESS: Genetics Institute, Inc., Legal Affairs
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/640,386A
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: GI 5225A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-498-8224
TELEFAX: 617-876-5851
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 660 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORGANISM: Homo sapiens
CELL TYPE: Lymphoblast
CELL LINE: RPMI 8866
FEATURE:
NAME/KEY: CDS
LOCATION: 1..660
US-08-640-386A-3

Query Match          3.7%; Score 59; DB 1; Length 660;
Best Local Similarity 100.0%; Pred. No. 1.2e-19;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1498 CCGGATTTTATAAACTAAATCAAGCTCTGCATCTTTCATGCTTTCAGATTGC 1556
DB 556 CCGGATTTTATAAACTAAATCAAGCTCTGCATCTTTCATGCTTTCAGATTGC 614

RESULT 7
US-08-184-009-199
Sequence 199, Application US/08184009
Patent No. 5833975
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: Tartaglia, James
APPLICANT: Cox, William I.
TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
NUMBER OF SEQUENCES: 217
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtlis, Morris & Safford
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/184,009
FILING DATE: 19-JAN-1994
```

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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEX: 425066CURTMS
INFORMATION FOR SEQ ID NO: 199:
SEQUENCE CHARACTERISTICS:
LENGTH: 721 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-184-009-199

Query Match          3.7%; Score 59; DB 2; Length 721;
Best Local Similarity 100.0%; Pred. No. 1.2e-19;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1498 CCGGATTTTATAAACTAAATCAAGCTCTGCATCTTTCATGCTTTCAGATTGC 1556
DB 617 CCGGATTTTATAAACTAAATCAAGCTCTGCATCTTTCATGCTTTCAGATTGC 675

RESULT 8
US-08-458-356-199
Sequence 199, Application US/08458356
Patent No. 5942235
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: Tartaglia, James
APPLICANT: Cox, William I.
TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
NUMBER OF SEQUENCES: 217
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtlis, Morris & Safford
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,356
FILING DATE: 02-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/184,009
FILING DATE: 19-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEX: 425066CURTMS
INFORMATION FOR SEQ ID NO: 199:
SEQUENCE CHARACTERISTICS:
LENGTH: 721 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-458-356-199
```



```

:
:   REGISTRATION NUMBER: 36,663
:   REFERENCE/DOCKET NUMBER: 117-221
:   TELECOMMUNICATION INFORMATION:
:   TELEPHONE: 7038164091
:   TELEFAX: 7038164100
:   INFORMATION FOR SEQ ID NO: 1:
:   SEQUENCE CHARACTERISTICS:
:   LENGTH: 1026 base pairs
:   TYPE: nucleic acid
:   STRANDEDNESS: double
:   TOPOLOGY: linear
:   MOLECULE TYPE: cDNA
:   FEATURE:
:   NAME/KEY: CDS
:   LOCATION: 170..826
:   US-08-751-767A-1

Query Match          3.7%; Score 59; DB 2; Length 1026;
Best Local Similarity 100.0%; Pred. No. 1.2e-19;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1498 CCGGATTTTATAAACAATAATCAAGCTGCGATCTTCTTCATGCTTTGAGAATTGC 1556
Db      725 CCGGATTTTATAAACAATAATCAAGCTGCGATCTTCTTCATGCTTTGAGAATTGC 783

RESULT 12
US-08-684-687-3
: Sequence 3, Application US/08684687
: Patent No. 5830451
: GENERAL INFORMATION:
: APPLICANT: KIEFF, ELLIOTT D.
: APPLICANT: DEVERGNE, ODLIE.
: TITLE OF INVENTION: A NOVEL HAEMATOPHOETIC CYTOKINE AND USES
: TITLE OF INVENTION: THEREFOR
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
: STREET: 600 ATLANTIC AVENUE
: CITY: BOSTON
: STATE: MA
: COUNTRY: USA
: ZIP: 02210
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/684.687
: FILING DATE:
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/005,092
: FILING DATE: 11-OCT-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: GATES, EDWARD R.
: REGISTRATION NUMBER: 31,616
: REFERENCE/DOCKET NUMBER: B0801/7051
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-720-3500
: TELEFAX: 617-720-2441
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1316 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: HOMO SAPIENS
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:   FEATURE:
:   NAME/KEY: CDS
:   LOCATION: 102..863
:   US-08-684-687-3

Query Match          3.7%; Score 59; DB 2; Length 1316;
Best Local Similarity 100.0%; Pred. No. 1.2e-19;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1498 CCGGATTTTATAAACAATAATCAAGCTGCGATCTTCTTCATGCTTTGAGAATTGC 1556
Db      759 CCGGATTTTATAAACAATAATCAAGCTGCGATCTTCTTCATGCTTTGAGAATTGC 817

RESULT 13
US-09-851-520-3
: Sequence 3, Application US/09851520
: Patent No. 6399379
: GENERAL INFORMATION:
: APPLICANT: Brenda F. Baker
: APPLICANT: Susan M. Freier
: TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
: FILE REFERENCE: RTS-0241
: CURRENT APPLICATION NUMBER: US/09/851,520
: CURRENT FILING DATE: 2001-05-07
: NUMBER OF SEQ ID NOS: 88
: SEQ ID NO 3
: LENGTH: 1316
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (102)...(863)
: US-09-851-520-3

Query Match          3.7%; Score 59; DB 4; Length 1316;
Best Local Similarity 100.0%; Pred. No. 1.2e-19;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1498 CCGGATTTTATAAACAATAATCAAGCTGCGATCTTCTTCATGCTTTGAGAATTGC 1556
Db      759 CCGGATTTTATAAACAATAATCAAGCTGCGATCTTCTTCATGCTTTGAGAATTGC 817

RESULT 14
US-08-265-087-3
: Sequence 3, Application US/08265087
: Patent No. 5571515
: GENERAL INFORMATION:
: APPLICANT: Scott, Phillip
: APPLICANT: Trincheri, Giorgio
: TITLE OF INVENTION: Compositions and Methods for Use of
: TITLE OF INVENTION: IL-12 as an Adjuvant
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Howson and Howson
: STREET: Spring House Corporate Center, PO Box 457
: CITY: Spring House
: STATE: Pennsylvania
: COUNTRY: USA
: ZIP: 19477
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/265,087
: FILING DATE:
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/229,282
: FILING DATE: 18-APR-1994
```

ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: MST51AUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1364 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 101..859
US-08-265-087-3

Query Match 3.7%; Score 59; DB 1; Length 1364;
Best Local Similarity 100.0%; Pred. No. 1.2e-19;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1498 CCGGATTTTATATAAATAAATCAAGCTCTGCACTTCTTCATGCTTTCAGAAATTCG 1556
|||||
DB 758 CCGGATTTTATATAAATAAATCAAGCTCTGCACTTCTTCATGCTTTCAGAAATTCG 816

RESULT 15
US-08-621-493-3
Sequence 3, Application US/08621493
Patent No. 5723127
GENERAL INFORMATION:
APPLICANT: Scott, Phillip
TITLE OF INVENTION: Compositions and Methods for Use of
TITLE OF INVENTION: IL-12 as an Adjuvant
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Center, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,493
FILING DATE: 25-MAR-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/265,087
FILING DATE: 17-JUN-1994
APPLICATION NUMBER: US 08/229,282
FILING DATE: 18-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: MST51AUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1364 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA

FEATURE:
NAME/KEY: CDS
LOCATION: 101..859
US-08-621-493-3

Query Match 3.7%; Score 59; DB 1; Length 1364;
Best Local Similarity 100.0%; Pred. No. 1.2e-19;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1498 CCGGATTTTATATAAATAAATCAAGCTCTGCACTTCTTCATGCTTTCAGAAATTCG 1556
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DB 758 CCGGATTTTATATAAATAAATCAAGCTCTGCACTTCTTCATGCTTTCAGAAATTCG 816

Search completed: July 16, 2003, 19:43:44
Job time : 85.9175 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 13:21:13 : Search time 302.749 Seconds
(without alignments)
8432.179 Million cell updates/sec

Title: US-09-917-265-61

Perfect score: 1599
Sequence: 1 atgcacccctcagcagtttgt.....tgccctactgaactcttc 1599

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1114047 seqs, 798260406 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2228094

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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13: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Query Length | DB ID | Description |
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| 1 | 1599 | 100.0 | 1599 | 10 | US-09-917-265-61 Sequence 61, Appl |
| 2 | 1599 | 100.0 | 1599 | 10 | US-09-917-265-63 Sequence 63, Appl |
| 3 | 1533 | 95.9 | 1533 | 10 | US-09-917-265-66 Sequence 66, Appl |
| 4 | 1533 | 95.9 | 1533 | 10 | US-09-917-265-68 Sequence 68, Appl |
| 5 | 987 | 61.7 | 987 | 10 | US-09-917-265-58 Sequence 58, Appl |
| 6 | 987 | 61.7 | 987 | 10 | US-09-917-265-60 Sequence 60, Appl |
| 7 | 974 | 60.9 | 2267 | 10 | US-09-917-265-107 Sequence 107, App |
| 8 | 974 | 60.9 | 2267 | 10 | US-09-917-265-109 Sequence 109, App |
| 9 | 914 | 57.2 | 921 | 10 | US-09-917-265-52 Sequence 52, Appl |
| 10 | 914 | 57.2 | 921 | 10 | US-09-917-265-54 Sequence 54, Appl |
| 11 | 494 | 30.9 | 591 | 10 | US-09-917-265-49 Sequence 49, Appl |
| 12 | 494 | 30.9 | 591 | 10 | US-09-917-265-51 Sequence 51, Appl |
| 13 | 494 | 30.9 | 666 | 10 | US-09-917-265-46 Sequence 46, Appl |
| 14 | 494 | 30.9 | 666 | 10 | US-09-917-265-48 Sequence 48, Appl |
| 15 | 494 | 30.9 | 1455 | 10 | US-09-917-265-104 Sequence 104, App |
| 16 | 494 | 30.9 | 1455 | 10 | US-09-917-265-106 Sequence 106, App |
| 17 | 81 | 5.1 | 561 | 10 | US-09-917-265-101 Sequence 101, App |
| 18 | 81 | 5.1 | 561 | 10 | US-09-917-265-103 Sequence 103, App |
| 19 | 81 | 5.1 | 591 | 10 | US-09-917-265-35 Sequence 35, Appl |

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| C | 20 | 81 | 5.1 | 591 | 10 | US-09-917-265-37 | Sequence 37, Appl |
| | 21 | 81 | 5.1 | 591 | 12 | US-10-079-616-9 | Sequence 9, Appl |
| | 22 | 81 | 5.1 | 666 | 10 | US-09-917-265-32 | Sequence 32, Appl |
| C | 23 | 81 | 5.1 | 666 | 10 | US-09-917-265-34 | Sequence 34, Appl |
| | 24 | 81 | 5.1 | 1441 | 12 | US-10-079-616-8 | Sequence 8, Appl |
| | 25 | 81 | 5.1 | 1533 | 10 | US-09-917-265-43 | Sequence 43, Appl |
| C | 26 | 81 | 5.1 | 1533 | 10 | US-09-917-265-45 | Sequence 45, Appl |
| | 27 | 81 | 5.1 | 1599 | 10 | US-09-917-265-38 | Sequence 38, Appl |
| C | 28 | 81 | 5.1 | 1599 | 10 | US-09-917-265-40 | Sequence 40, Appl |
| | 29 | 66 | 4.1 | 921 | 10 | US-09-917-265-26 | Sequence 26, Appl |
| C | 30 | 66 | 4.1 | 921 | 10 | US-09-917-265-28 | Sequence 28, Appl |
| | 31 | 66 | 4.1 | 921 | 12 | US-10-079-616-6 | Sequence 6, Appl |
| C | 32 | 66 | 4.1 | 985 | 10 | US-09-917-265-55 | Sequence 55, Appl |
| | 33 | 66 | 4.1 | 985 | 10 | US-09-917-265-57 | Sequence 57, Appl |
| C | 34 | 66 | 4.1 | 987 | 10 | US-09-917-265-29 | Sequence 29, Appl |
| | 35 | 66 | 4.1 | 987 | 10 | US-09-917-265-31 | Sequence 31, Appl |
| C | 36 | 66 | 4.1 | 2193 | 12 | US-10-079-616-5 | Sequence 5, Appl |
| | 37 | 63 | 3.9 | 921 | 12 | US-10-079-616-7 | Sequence 7, Appl |
| C | 38 | 59 | 3.7 | 60 | 10 | US-09-917-265-83 | Sequence 83, Appl |
| | 39 | 59 | 3.7 | 60 | 10 | US-09-917-265-84 | Sequence 84, Appl |
| C | 40 | 59 | 3.7 | 660 | 10 | US-09-754-014-6 | Sequence 6, Appl |
| | 41 | 59 | 3.7 | 660 | 10 | US-09-836-866-4 | Sequence 4, Appl |
| | 42 | 59 | 3.7 | 689 | 12 | US-10-079-616-26 | Sequence 26, Appl |
| | 43 | 59 | 3.7 | 762 | 9 | US-09-826-025-21 | Sequence 21, Appl |
| | 44 | 59 | 3.7 | 1026 | 9 | US-10-172-399-5 | Sequence 5, Appl |
| | 45 | 59 | 3.7 | 1395 | 10 | US-09-924-703-5 | Sequence 5, Appl |

ALIGNMENTS

RESULT 1
US-09-917-265-61
Sequence 61, Application US/09917265
Patent No. US20020052030A1

GENERAL INFORMATION:

APPLICANT: Wonderling, Ramani S.

TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH

FILE REFERENCE: IM-5

CURRENT FILING DATE: 2001-07-27

PRIOR APPLICATION NUMBER: 60/223,016

PRIOR FILING DATE: 2000-08-04

NUMBER OF SEQ ID NOS: 109

SOFTWARE: PatentIn version 3.1

SEQ ID NO 61

LENGTH: 1599

TYPE: DNA

ORGANISM: Canis familiaris

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(1599)

OTHER INFORMATION:

US-09-917-265-61

Query Match Best local Similarity 100.0%; Score 1599; DB 10; Length 1599;

Matches 1599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| Oy | 1 | ATGACCCCTCAGCAGTTCATCTCCGTTTCCCTGTTTTCCTGCGTTCGCGTCCCTC | 60 |
| | | | |
| Db | 1 | ATGACCCCTCAGCAGTTCATCTCCGTTTCCCTGTTTTCCTGCGTTCGCGTCCCTC | 60 |
| Oy | 61 | ATGGCCATATGGAAGTGGAGAAAGATTTATGTTAGATTGAGCTGCACCTGAT | 120 |
| | | | |
| Db | 61 | ATGGCCATATGGAAGTGGAGAAAGATTTATGTTAGATTGAGCTGCACCTGAT | 120 |
| Oy | 121 | GGCCCCGGAAGAAATGCTGCTCCTCACCCTGCATACCCCTGAAGAAGATGACATCTGG | 180 |
| | | | |
| Db | 121 | GGCCCCGGAAGAAATGCTGCTCCTCACCCTGCATACCCCTGAAGAAGATGACATCTGG | 180 |
| Oy | 181 | ACCTCAGCGCAGAGCAGTGAAGTCTAGTTCTGTGTAAGTCTGACCATCAAGTCAA | 240 |

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Db      181 ACCACGCGAGACAGTGAAGTCTGAGTTCTGTTAAACCTGCACCATCCAGTCAAA 240
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Db      241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATTAAGGAGCAAGTTCTGAGCCGCTCA 300
QY      301 CTCCTGTTGATTACCAAAAAAGAGATGAAATTTGGTCGACGTATATCTTAAAGAACAG 360
Db      301 CTCCTGTTGATTACCAAAAAAGAGATGAAATTTGGTCGACGTATATCTTAAAGAACAG 360
QY      361 AAAGAAATCCAAAAATAGATCTTCTGAATGTGAGGCAAAAGATTTATCTGACGTTTC 420
Db      361 AAAGAAATCCAAAAATAGATCTTCTGAATGTGAGGCAAAAGATTTATCTGACGTTTC 420
QY      421 ACATGCTGTGGCTGACGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGACA 480
Db      421 ACATGCTGTGGCTGACGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGACA 480
QY      481 GGGCTTCTTGACCCCAAGGGGTGACATGTGAGACAGTGAACACTTTCAGACAGAGGCTC 540
Db      481 GGGCTTCTTGACCCCAAGGGGTGACATGTGAGACAGTGAACACTTTCAGACAGAGGCTC 540
QY      541 AGAGTGGACACAGGGGATTATAGAGTACACAGTGGAGTGTGAGAGGCGACATGCCCTGC 600
Db      541 AGAGTGGACACAGGGGATTATAGAGTACACAGTGGAGTGTGAGAGGCGACATGCCCTGC 600
QY      601 CCCTGTGCGAGAGAGAGCCCTACCCATCGAGGTCTGTGTGATCTATTCACAAGTCAAG 660
Db      601 CCCTGTGCGAGAGAGAGCCCTACCCATCGAGGTCTGTGTGATCTATTCACAAGTCAAG 660
QY      661 TATGAAACTATACCCGACAGCTTCTTCATCAGAGACATATCAACCCAGACCCACACA 720
Db      661 TATGAAACTATACCCGACAGCTTCTTCATCAGAGACATATCAACCCAGACCCACACA 720
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QY      781 GACACTGGAACACCCCATTCCTTACTTCTCCCTGACATTTTGTGATACAGGCCAGGGC 840
Db      781 GACACTGGAACACCCCATTCCTTACTTCTCCCTGACATTTTGTGATACAGGCCAGGGC 840
QY      841 AAGAACATAGAGAAAAAGAAAGATGACTCTGCTGAGCAAAACCTCAGCCAAAGTCTG 900
Db      841 AAGAACATAGAGAAAAAGAAAGATGACTCTGCTGAGCAAAACCTCAGCCAAAGTCTG 900
QY      901 TGCCACAAAGATGCCAAGATCCGCTGCAAGCCCGAGACCCGCTACTATAGTTCATCTGG 960
Db      901 TGCCACAAAGATGCCAAGATCCGCTGCAAGCCCGAGACCCGCTACTATAGTTCATCTGG 960
QY      961 AAGGACTGGGATCTGTGTCATGCAAGTGTGCGGTGGCGGAGATCTAGAAACTTGCCA 1020
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Db      1021 ACCCTTACCTCATCCCGGGGTATGTTCCAAATGTTTGAACCACTCCCAAACTTGTGAGA 1080
QY      1081 GCGCTGACGACACGCTTCAGAAAGCCAGACAAACTCTAGAAATTAATTTCTGCACTTCC 1140
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QY      1141 GAAGGATGATGATGAGATATTCACAAAGGATAAACACGACAGCTGAGAGCCGCTGTA 1200
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QY      1261 AAGGGAATGCTGCGCTCTGGAAGGCTCTTTATGAGGTCCTTGCTTACGACG 1320
Db      1261 AAGGGAATGCTGCGCTCTGGAAGGCTCTTTATGAGGTCCTTGCTTACGACG 1320

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Db      1261 AAGGGAATGCTGCGCTCTGGAAGGCTCTTTATGAGGTCCTTGCTTACGACG 1320
QY      1321 ATCTATGAGACTTGAAGATGTACAGATGGAATTAAGGCCCTYGAACCAAGCTTTTA 1380
Db      1321 ATCTATGAGACTTGAAGATGTACAGATGGAATTAAGGCCCTYGAACCAAGCTTTTA 1380
QY      1381 ATGATCCCAAGAGCAGATCTTCTGATCAAAACATGCTGCACACTATCATGATGAGCTG 1440
Db      1381 ATGATCCCAAGAGCAGATCTTCTGATCAAAACATGCTGCACACTATCATGATGAGCTG 1440
QY      1441 TTACAGCCCTGAATTTCAACAGTGTGACTGTGCGCACAGAAATCTCTCTTGAAGAGCG 1500
Db      1441 TTACAGCCCTGAATTTCAACAGTGTGACTGTGCGCACAGAAATCTCTCTTGAAGAGCG 1500
QY      1501 GATTTTATTAATAAATAAATAAAGCTCTGATATCTTCTCATGCTTTCAGAAATGCTGCG 1560
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Db      1561 GTGACCATCAATGAAATGATGTCTTACTTGAACCTTTC 1599

RESULT 2
US-09-917-265-63/c
; Sequence 63, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-917-265-63

Query Match      100.0%; Score 1599; DB 10; Length 1599;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1119 GGCCTCTCTGACCCCAAGGGGTGACATGTGAGCAGTGTGACACTTTCAGCAGAGAGGGTTC 1060
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Db 1059 AGAGTGGACAACAGGATTTATAGAAGTACACAGTGTGAGAGTGTGAGAGGGCAGTGCCTGC 1000
QY 601 CCCCTGCGCGAGAGAGCCTACCCATGAGAGTGTGTGGTGTGATTCATTCACAGTCAAG 660
Db 999 CCCCTGCGCGAGAGAGCCTACCCATGAGAGTGTGTGGTGTGATTCATTCACAGTCAAG 940
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QY 781 GACACCTGGAGCACCCCAATCTTCTACTCTCTCCCTGACATTTTGGATACAGCCCAAGGC 840
Db 819 GACACCTGGAGCACCCCAATCTTCTACTCTCTCCCTGACATTTTGGATACAGCCCAAGGC 860
QY 841 AAGACACATAGAGAAAAAGAAAGATAGACTGTGCGTGCAGACAGCTCGAGCCAGGTCGTG 900
Db 759 AAGACACATAGAGAAAAAGAAAGATAGACTGTGCGTGCAGACAGCTCGAGCCAGGTCGTG 700
QY 901 TGCCACAAGGATGCCAAGATCCGCTGCAAGCCCGAGACCGCTACTATAGTTTCATCTGG 960
Db 699 TGCCACAAGGATGCCAAGATCCGCTGCAAGCCCGAGACCGCTACTATAGTTTCATCTGG 640
QY 961 AGGCACGTGGCATCTGTGTCTCATGTGAGTGTGGCGGTGGCGGGGATCTAGAAACTGTGCA 1020
Db 639 AGGCACGTGGCATCTGTGTCTCATGTGAGTGTGGCGGTGGCGGGGATCTAGAAACTGTGCA 580
QY 1021 ACCCTACTGCACTCCCGGGATGTCCAAATGTTTGAACCACTCCCAAAACCTTTGTGAGA 1080
Db 579 ACCCTACTGCACTCCCGGGATGTCCAAATGTTTGAACCACTCCCAAAACCTTTGTGAGA 520
QY 1081 GCGCTGAGCAACAGCTTTCAGAAAGCCAGACAAACTAGAAATTAATTCCTGCACTTCC 1140
Db 519 GCGCTGAGCAACAGCTTTCAGAAAGCCAGACAAACTAGAAATTAATTCCTGCACTTCC 460
QY 1141 GAACAGATGATFCTGMAAGATATCACAAGAGATAAAACACACAGTGTGAGCGCTGCTTA 1200
Db 459 GAACAGATGATFCTGMAAGATATCACAAGAGATAAAACACACAGTGTGAGCGCTGCTTA 400
QY 1201 CCATGTGAATTAACCATGAATGAGAGTTCCTGCTTCACAGAGATTCCTTTGTAATCT 1260
Db 399 CCATGTGAATTAACCATGAATGAGAGTTCCTGCTTCACAGAGATTCCTTTGTAATCT 340
QY 1261 AACGGAGTTCCTGCGCTCTGAAAGGCCCTTTTATGACGGTCTGTCGCTTAAGCAGC 1320
Db 339 AACGGAGTTCCTGCGCTCTGAAAGGCCCTTTTATGACGGTCTGTCGCTTAAGCAGC 280
QY 1321 ATCTATAGAGACTTGAAGATGTACACAGATGAATTCAAAGGCCATGAAGCAAGCTTTTA 1380
Db 279 ATCTATAGAGACTTGAAGATGTACACAGATGAATTCAAAGGCCATGAAGCAAGCTTTTA 220
QY 1381 ATGAGATCCCAAGAGCGAGATCTTCTGTGATCAAAAACATGCTGACAGCATATGATGAGTG 1440
Db 219 ATGAGATCCCAAGAGCGAGATCTTCTGTGATCAAAAACATGCTGACAGCATATGATGAGTG 160
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QY 1501 GATTTTATAAACTAAATCAAGTGTGCATCTTCTTCATGCTTTGAGATTTGCTGCG 1560
Db 99 GATTTTATAAACTAAATCAAGTGTGCATCTTCTTCATGCTTTGAGATTTGCTGCG 40
QY 1561 GTGACCATCAATAGAAATGATGCTCTACTCTTGAACCTTTCG 1599
Db 39 GTGACCATCAATAGAAATGATGCTCTACTTGAACCTTTCG 1

RESULT 3
US-09-917-265-66
: Sequence 66, Application US/09917265
: Patent No. US20020052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: APPLICANT: Boroughs, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
: FILE REFERENCE: IM-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: PRIOR FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: PRIOR FILING DATE: 2000-08-04
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 66
: LENGTH: 1533
: TYPE: DNA
: ORGANISM: Canis familiaris
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(1533)
: OTHER INFORMATION:
US-09-917-265-66

Query Match          95.9%; Score 1533; DB 10; Length 1533;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATATGGAACTGAGAGAAAGATGTTATGTTGTAGAGTTGAGCTGCGACCCCTGATGCCCC 60
QY 127 GGAAGAAATGTTGTCCTCACTGCCATACCCCTGAAAGAAAGATACATCACTTGGACCTCA 186
Db 61 GGAGAAATGTTGTCCTCACTGCCATACCCCTGAAAGAAAGATACATCACTTGGACCTCA 120
QY 187 GCGCAGACAGTGAAGTCTAGTGTCTGTAATACTGTGACCATCAAGTCAAAAGATTT 246
Db 121 GCGCAGACAGTGAAGTCTAGTGTCTGTAATACTGTGACCATCAAGTCAAAAGATTT 180
QY 247 GGAGATGCTGGCCATATACCTGCGATAAAGGAGCGAGTTCTGAGCGGCTCACTCTCG 306
Db 181 GGAGATGCTGGCCATATACCTGCGATAAAGGAGCGAGTTCTGAGCGGCTCACTCTCG 240
QY 307 TTGATTTCAAAAAAAGAGATGGAATTTTGTGTCATGATATCTTAAAGCAAGAAAGAA 366
Db 241 TTGATTTCAAAAAAAGAGATGGAATTTTGTGTCATGATATCTTAAAGCAAGAAAGAA 300
QY 367 TCACAAAATAAGATCTTCTGAAATGTGAGCGCAAGAAATTTATCTGAGCGTTTCACATGC 426
Db 301 TCACAAAATAAGATCTTCTGAAATGTGAGCGCAAGAAATTTATCTGAGCGTTTCACATGC 360
QY 427 TGTGGCTGACGGCAATCAGTACTGATTTTGAATTTCACTGTGCAAAAGTAGCAGAGCTTC 486
Db 361 TGTGGCTGACGGCAATCAGTACTGATTTTGAATTTCACTGTGCAAAAGTAGCAGAGCTTC 420
QY 487 TCTGACCCCAAGGGGTACATGTGTGAGACAGTGCACCTTTTACGAGAGAGGCTCAGAGTG 546
Db 421 TCTGACCCCAAGGGGTACATGTGTGAGACAGTGCACCTTTTACGAGAGAGGCTCAGAGTG 480
QY 547 GACAAGACGAGATTTAAGAAAGTACACAGTGTGAGTGTGAGAGGCGAGTGCCTGCCCTCT 606
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Db      481 GACAAAGGATTTAAGATACACAGTGGAGTGTGAGAGGAGAGTGGCTTCT 540
Oy      607 GCGGAGAGGAGCTACCATGAGAGTCTGGTGGATGCTATTTCACAGCTCAAGTATGAA 666
Db      541 GCGGAGAGGAGCTACCATGAGAGTGTGGTGGATGCTATTTCACAGCTCAAGTATGAA 600
Oy      667 AACTACACAGAGCTTCTCATGAGACATCATCAACAGAGCCGACCAACAACTG 726
Db      601 AACTACACAGAGCTTCTCATGAGACATCATCAACAGAGCCGACCAACAACTG 660
Oy      727 CAGCTGAAGCATTGAAAAATTCTCGGACGTGAGAGTCACTGGGAATTACCCGACAC 786
Db      661 CAGCTGAAGCATTGAAAAATTCTCGGACGTGAGAGTCACTGGGAATTACCCGACAC 720
Oy      787 TGGAGCACCCACATTCCTACTCTCCCTGACATTTTTCATACAGGCCGACGAGAAAC 846
Db      721 TGGAGCACCCACATTCCTACTCTCCCTGACATTTTTCATACAGGCCGACGAGAAAC 780
Oy      847 AATAGAGAAAAAAGATAGACTCTGCTGGACAAAGCCTGACCAAGTCTGTGGCAC 906
Db      781 AATAGAGAAAAAAGATAGACTCTGCTGGACAAAGCCTGACCAAGTCTGTGGCAC 840
Oy      907 AAGATGCAAGATCCGGTGCAGCCGAGACCCGCTACTATATAGTTATCTGTGAGCGAC 966
Db      841 AAGATGCAAGATCCGGTGCAGCCGAGACCCGCTACTATATAGTTATCTGTGAGCGAC 900
Oy      967 TGGGCACTCTGTGATCAGTGTGTGGGCTGGGCGGAGTCTGAAACTTGGCAACCCCT 1026
Db      901 TGGGCACTCTGTGATCAGTGTGTGGGCTGGGCGGAGTCTGAAACTTGGCAACCCCT 960
Oy      1027 ACTGCATCCCGGGTATGTTCCATATGTTTGAACCATCTCCCAACCTTGTGAGAGCCGTC 1086
Db      961 ACTGCATCCCGGGTATGTTCCATATGTTTGAACCATCTCCCAACCTTGTGAGAGCCGTC 1020
Oy      1087 AGCAACAGCTTGAAGAGCCAGCAAACTCTAGAAATATATTCCTGCACTTCCGAGAG 1146
Db      1021 AGCAACAGCTTGAAGAGCCAGCAAACTCTAGAAATATATTCCTGCACTTCCGAGAG 1080
Oy      1147 ATTGATCATGAATATACAAAGAGATAAACAGCAGCAGCAGTGGAGGCTGCTTACCACTG 1206
Db      1081 ATTGATCATGAATATACAAAGAGATAAACAGCAGCAGCAGTGGAGGCTGCTTACCACTG 1140
Oy      1207 GAATTAACCATGATGAGAGTGTGCTGGCTTCCAGAGAGATCTTTGATTAATACAGGG 1266
Db      1141 GAATTAACCATGATGAGAGTGTGCTGGCTTCCAGAGAGATCTTTGATTAATACAGGG 1200
Oy      1267 AGTTGGCTGGCTCTGGAAGAGCTCTTTTATGAGGCTCTGTGCTTACAGCATCTAT 1326
Db      1201 AGTTGGCTGGCTCTGGAAGAGCTCTTTTATGAGGCTCTGTGCTTACAGCATCTAT 1260
Oy      1327 GAGGACTTGAAGATGACAGATGGAATTCAGAGGCCATGAAGGCAAGCTTTTATAGAT 1386
Db      1261 GAGGACTTGAAGATGACAGATGGAATTCAGAGGCCATGAAGGCAAGCTTTTATAGAT 1320
Oy      1387 CCCAAGAGCAGATCTTTCTGATCAAAACATGCTGACAGCTATGAGTGTATACAG 1446
Db      1321 CCCAAGAGCAGATCTTTCTGATCAAAACATGCTGACAGCTATGAGTGTATACAG 1380
Oy      1447 GCGCTAATTTCAACGCTGACTGTGCGACAGAAATCTCCCTTGAAGAGCCGATTTT 1506
Db      1381 GCGCTAATTTCAACGCTGACTGTGCGACAGAAATCTCCCTTGAAGAGCCGATTTT 1440
Oy      1507 TATAAAACTAAATCAAGCTGTGATCTTCTTCAATGCTTTCAGAAATTCGCGGTGAC 1566
Db      1441 TATAAAACTAAATCAAGCTGTGATCTTCTTCAATGCTTTCAGAAATTCGCGGTGAC 1500
Oy      1567 ATCAATAGATATGCTCTACTTGAACCTTCC 1599
Db      1501 ATCAATAGATATGCTCTACTTGAACCTTCC 1533

```

RESULT 4

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US-09-917-265-68/c
; Sequence 68, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Borroughs, Karen L.
; TITLE OR INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
; FILE REFERENCE: 1M-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: Patent version 3.1
; SEQ ID NO 68
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-917-265-68

```

Query Match 95.9%; Score 1533; DB 10; Length 1533;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy      67 ATATGGGAACGTGAGAAAGATGTTATGTTGTAAGACTGCGACCCCTGATGCCCC 126
Db      1533 ATATGGGAACGTGAGAAAGATGTTATGTTGTAAGACTGCGACCCCTGATGCCCC 1474
Oy      127 GGAGAAATGTTGTGCTCCACCTGCCATACCCCTGAAAGAGATGACATCTTGGACCTCA 186
Db      1473 GGAGAAATGTTGTGCTCCACCTGCCATACCCCTGAAAGAGATGACATCTTGGACCTCA 1414
Oy      187 GCGCAGAGCAGTGAAGTCTCTAGTCTCTGTTAACTCTGACATCCAAAGTAAATTT 246
Db      1413 GCGCAGAGCAGTGAAGTCTCTAGTCTCTGTTAACTCTGACATCCAAAGTAAATTT 1354
Oy      247 GGAGATGCTGGCCAGTATACCTGCCATTAAGAGGCAAGGTTCTGAGCGCTCACTCTG 306
Db      1353 GGAGATGCTGGCCAGTATACCTGCCATTAAGAGGCAAGGTTCTGAGCGCTCACTCTG 1294
Oy      307 TTGATTCACAAAAAAGAGATGGAAATTTGCTCAGTATCTTAAAGAAACAGAAAGAA 366
Db      1293 TTGATTCACAAAAAAGAGATGGAAATTTGCTCAGTATCTTAAAGAAACAGAAAGAA 1234
Oy      367 TCACAAAATTAAGATCTTTCTGAAATGTGAGCAAAAGATTTATTCGAGCTTTCACATGC 426
Db      1233 TCACAAAATTAAGATCTTTCTGAAATGTGAGCAAAAGATTTATTCGAGCTTTCACATGC 1174
Oy      427 TGGTGGCTGAGGCGCATATGATGATTTGAAATTCAGTGTGCAAAAGTAGCAGAGCTTC 486
Db      1173 TGGTGGCTGAGGCGCATATGATGATTTGAAATTCAGTGTGCAAAAGTAGCAGAGCTTC 1114
Oy      487 TCTGACCCCAAGAGGAGTACATGTGAGACAGTGCACACTTATGAGAGAGGAGTCAAGTG 546
Db      1113 TCTGACCCCAAGAGGAGTACATGTGAGACAGTGCACACTTATGAGAGAGGAGTCAAGTG 1054
Oy      547 GACAACAGGATTTATAGAGTATACACAGTGTGAGAGGAGGAGTGCCTGCCCTCT 606
Db      1053 GACAACAGGATTTATAGAGTATACACAGTGTGAGAGGAGGAGTGCCTGCCCTCT 994
Oy      607 GCGGAGAGAGCCTTAACCATGAGAGTGTGAGTGTGATCTATTCACAAGCTCAAGTATGAA 666
Db      993 GCGGAGAGAGCCTTAACCATGAGAGTGTGAGTGTGATCTATTCACAAGCTCAAGTATGAA 934
Oy      667 AACTACACAGCAGCTTCTTCATCAGAGACATCATCAACAGAGCCGACCAACAACTG 726
Db      933 AACTACACAGCAGCTTCTTCATCAGAGACATCATCAACAGAGCCGACCAACAACTG 874
Oy      727 CAGCTGAAGCATTGAAAAATTCTCGGACGTGTGAGGTCAGCTGGGAATACCCGACAC 786
Db      873 CAGCTGAAGCATTGAAAAATTCTCGGACGTGTGAGGTCAGCTGGGAATACCCGACAC 814
Oy      787 TGGAGCACCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCGACGAGCAAGAAC 846

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Db      813  TGGAGCACCACCATCTCTACTTCTCCCTGACATTTTGATACAGGCCAGGCAAGAAC 754
Oy      847  AATAGAGAAAGAAAGATAGACTCTGCGTGGACAGAGCTCAGCCAAAGTGTGTGCCAC 906
Db      753  AATAGAGAAAGAAAGATAGACTCTGCGTGGACAGAGCTCAGCCAAAGTGTGTGCCAC 694
Oy      907  AAGGATGCCAAGATCCCGGTGCACAGCCGAGACCCCTACTATAGTTTCATCTCGAGCGAC 966
Db      693  AAGGATGCCAAGATCCCGGTGCACAGCCGAGACCCCTACTATAGTTTCATCTCGAGCGAC 634
Oy      967  TGGGCATCTGTGTATGAGTGTGTGGCGGTGGCGGAGTCTAGAACTTGGCAACCCCT 1026
Db      633  TGGGCATCTGTGTATGAGTGTGTGGCGGTGGCGGAGTCTAGAACTTGGCAACCCCT 574
Oy      1027  ACTGCATCCCGGGGTATGTTCCCATGTTTGAACCACTCCCAACCTTTGTGAGACCGTC 1086
Db      573  ACTGCATCCCGGGGTATGTTCCCATGTTTGAACCACTCCCAACCTTTGTGAGACCGTC 514
Oy      1087  AGCAACACGCTTCAGAGCGCAGACAACTAGATATATCTTCCGACCTTCCGAGAG 1146
Db      513  AGCAACACGCTTCAGAGCGCAGACAACTAGATATATCTTCCGACCTTCCGAGAG 454
Oy      1147  ATTGATCATGAGATATACAAAAGGATAAAACACAGAGTGGAGGCGCTTGAACACGTG 1206
Db      453  ATTGATCATGAGATATACAAAAGGATAAAACACAGAGTGGAGGCGCTTGAACACGTG 394
Oy      1207  GAATTAACCATGATGAGAGTGGCTGGCTTCAGAGAGATCTCTTTGATACTAACGGG 1266
Db      393  GAATTAACCATGATGAGAGTGGCTGGCTTCAGAGAGATCTCTTTGATACTAACGGG 334
Oy      1267  AGTTGCGTGGCGCTGGAAGAGCGCTTTTATGAGGTCGCTGGCTTACGACGATCTAT 1326
Db      333  AGTTGCGTGGCGCTGGAAGAGCGCTTTTATGAGGTCGCTGGCTTACGACGATCTAT 274
Oy      1327  GAGGACTTGAAGATGTACCAAGATGGAATTCAGAGGCAATGAAGCAAGCTTTTAATGAT 1386
Db      273  GAGGACTTGAAGATGTACCAAGATGGAATTCAGAGGCAATGAAGCAAGCTTTTAATGAT 214
Oy      1387  CCCAAGAGGCAATCTTTCTGATGATAAAACATGCTGACAGATGATGAGTGTACAG 1446
Db      213  CCCAAGAGGCAATCTTTCTGATGATAAAACATGCTGACAGATGATGAGTGTACAG 154
Oy      1447  GCCCTGAATTCACAGTGTGACTGTGCACAGAAATCCTCCCTTGAAGAGCGGATTTT 1506
Db      153  GCCCTGAATTCACAGTGTGACTGTGCACAGAAATCCTCCCTTGAAGAGCGGATTTT 94
Oy      1507  TATAAACCTAAATCAAGCTCTGCATACTTCTTCATCTTCAGAAATTCGTGCGGTGAC 1566
Db      93  TATAAACCTAAATCAAGCTCTGCATACTTCTTCATCTTCAGAAATTCGTGCGGTGAC 34
Oy      1567  ATCAATAGATGATGTCTCTACTTGACACTTCC 1599
Db      33  ATCAATAGATGATGTCTCTACTTGACACTTCC 1
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RESULT 5

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US-09-917-265-58
; Sequence 58, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Karen L.
; APPLICANT: Borroughs, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917_265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 987
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; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(987)
; OTHER INFORMATION:
US-09-917-265-58
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Query Match 61.7%; Score 987; DB 10; Length 987;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 987; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy      1  ATGACACCCACAGATGGTGCATCTTCCTGTTTCCCTGCTTTCCTGCGCTCCCTC 60
Db      1  ATGACACCCACAGATGGTGCATCTTCCTGTTTCCCTGCTTTCCTGCGCTCCCTC 60
Oy      61  ATGGCCATATGSGAACTGAGAAAGATGTTATGTTGATGAGTTGAGTGCACCCCTGAT 120
Db      61  ATGGCCATATGSGAACTGAGAAAGATGTTATGTTGATGAGTTGAGTGCACCCCTGAT 120
Oy      121  GCGCCCGGAGAAATGTTGTTCTCTCACTCCCTACCTCCCTACCTCCCTGAGAGATGACATCACTTGG 180
Db      121  GCGCCCGGAGAAATGTTGTTCTCTCACTCCCTACCTCCCTACCTCCCTGAGAGATGACATCACTTGG 180
Oy      181  ACCTCAGCCGACAGCAGTGAAGTCTAGTTCGTGTAACCTGACCATCCAGTCAAA 240
Db      181  ACCTCAGCCGACAGCAGTGAAGTCTAGTTCGTGTAACCTGACCATCCAGTCAAA 240
Oy      241  GAATTTGGAGATGCTGGCCAGTATACCTGCAATAAAGAGGCAAGGTTCTGAGCCGCTCA 300
Db      241  GAATTTGGAGATGCTGGCCAGTATACCTGCAATAAAGAGGCAAGGTTCTGAGCCGCTCA 300
Oy      301  CTCCTGTTGATTCACAAAAAAGAGATGGAATTTTGGTCCACGATATCTTTAAAGAACAG 360
Db      301  CTCCTGTTGATTCACAAAAAAGAGATGGAATTTTGGTCCACGATATCTTTAAAGAACAG 360
Oy      361  AAAGATCCAAAAATTAAGATCTTTCTGAAATGTGAGGCAAGAAATATCTGACGCTTTC 420
Db      361  AAAGATCCAAAAATTAAGATCTTTCTGAAATGTGAGGCAAGAAATATCTGACGCTTTC 420
Oy      421  ACATGCTGCTGCTGACGGCAATCACTGATGTTTGAATTCAGTGTCAAAAGTACAGA 480
Db      421  ACATGCTGCTGCTGACGGCAATCACTGATGTTTGAATTCAGTGTCAAAAGTACAGA 480
Oy      481  GCGTTCTGACACCCCAAGGGGTGACATGTGAGCAGTACACTTTTCACAGAGAGGTC 540
Db      481  GCGTTCTGACACCCCAAGGGGTGACATGTGAGCAGTACACTTTTCACAGAGAGGTC 540
Oy      541  AGAGTGCACACAGGATATTAAGAAGTACACAGTGAAGTGCAGAGAGGCGAGTGCCTGC 600
Db      541  AGAGTGCACACAGGATATTAAGAAGTACACAGTGAAGTGCAGAGAGGCGAGTGCCTGC 600
Oy      601  CCCTTGCCGAGAGAGCCCTACCCATCGAGGTGCTGGTGATGCTATTTCACAAGCTCAAG 660
Db      601  CCCTTGCCGAGAGAGCCCTACCCATCGAGGTGCTGGTGATGCTATTTCACAAGCTCAAG 660
Oy      661  TATGAAACCTACACAGCAGCTTCTTCATCAAGACATCATCAAAACCAACCCACCACCA 720
Db      661  TATGAAACCTACACAGCAGCTTCTTCATCAAGACATCATCAAAACCAACCCACCACCA 720
Oy      721  AACCTGACAGCTGAACCATTTGAATAATCTCGGACGTGAGAGTCAAGTGGGAATACCC 780
Db      721  AACCTGACAGCTGAACCATTTGAATAATCTCGGACGTGAGAGTCAAGTGGGAATACCC 780
Oy      781  GACACCTGAGACACCCACATTCCTTCTCCCTGACATTTTGCATACAGGCCAGGCG 840
Db      781  GACACCTGAGACACCCACATTCCTTCTCCCTGACATTTTGCATACAGGCCAGGCG 840
Oy      841  AAGAACATATAGGAAAGAAAGATAGACTCTGCTGGACAAAGCCTGACCAAGGTCGG 900
Db      841  AAGAACATATAGGAAAGAAAGATAGACTCTGCTGGACAAAGCCTGACCAAGGTCGG 900
Oy      901  TGCCACAAGGATGCCAAGATCCGCTGCAAGCCGAGACCGCTACTATATGTCATCTGG 960
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Db 901 TGGCACAAGATGCGCAAGATCCGCTCAAGCCCGAGACCCCTACTATAGTTCAATCCTGG 960
 QY 961 AGGACTGGGCGATCTGTCTATGAGT 987
 Db 961 AGGACTGGGCGATCTGTCTATGAGT 987

RESULT 6

US-09-917-265-60/c
 ; Sequence 60, Application US/09917265
 ; Patent No. US20020052030A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wonderling, Ramani S.
 ; APPLICANT: Boroughs, Karen L.
 ; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
 ; FILE REFERENCE: IM-5
 ; CURRENT APPLICATION NUMBER: US/09/917,265
 ; PRIOR APPLICATION NUMBER: 2001-07-27
 ; PRIOR FILING DATE: 2000-08-04
 ; NUMBER OF SEQ ID NOS: 109
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 60
 ; LENGTH: 987
 ; TYPE: DNA
 ; ORGANISM: Canis familiaris
 US-09-917-265-60

Query Match 61.7%; Score 987; DB 10; Length 987;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 987; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCCACCTCTAGCAGTGTGTCATCTCTGTTTCCCTGTTTGGTGGCTCTCCCTC 60
 Db 987 ATCCACCTCTAGCAGTGTGTCATCTCTGTTTCCCTGTTTGGTGGCTCTCCCTC 928
 QY 61 ATGGCCATATGGGAAGTGGGAAAGATGTTTATGTTGTAGAGTTGGACCTGGAT 120
 Db 927 ATGGCCATATGGGAAGTGGGAAAGATGTTTATGTTGTAGAGTTGGACCTGGAT 868
 QY 121 GCCCGCGAAGATGTTGTCCTCACCCTGCATACCCCTGAAGAAGATGATCATCTGG 180
 Db 867 GCCCGCGAAGATGTTGTCCTCACCCTGCATACCCCTGAAGAAGATGATCATCTGG 808
 QY 181 ACCTCAGCGCAGCAGTGAAGTCTAGTCTGTGTAAGTCTGACCATCCAAAGTCAA 240
 Db 807 ACCTCAGCGCAGCAGTGAAGTCTAGTCTGTGTAAGTCTGACCATCCAAAGTCAA 748
 QY 241 GAATTGGAGATCTGCGCAGTATACCTGCCATAAAGGAGGCAAGTCTTGAGCCCTCA 300
 Db 747 GAATTGGAGATCTGCGCAGTATACCTGCCATAAAGGAGGCAAGTCTTGAGCCCTCA 688
 QY 301 CTCCTGTTGATTCACAAAAAGATGGAATTTGTCACATGATCTTAAAGAAACAG 360
 Db 687 CTCCTGTTGATTCACAAAAAGATGGAATTTGTCACATGATCTTAAAGAAACAG 628
 QY 361 AAAGATTCAAAAATTAAGATCTTTTGAATGTGAGGCAAGAAATTAATTTGAGCTTTC 420
 Db 627 AAAGATTCAAAAATTAAGATCTTTTGAATGTGAGGCAAGAAATTAATTTGAGCTTTC 568
 QY 421 ACATGCTGTGCTGCGCAGTATGATCTGTTGAATTCAGTGTCAAAAGTACAGCA 480
 Db 567 ACATGCTGTGCTGCGCAGTATGATCTGTTGAATTCAGTGTCAAAAGTACAGCA 508
 QY 481 GGCCTTCTGACCCCAAGGGGTGACATGTGAGCAGTACACTTTCACAGAGAGGGTC 540
 Db 507 GGCCTTCTGACCCCAAGGGGTGACATGTGAGCAGTACACTTTCACAGAGAGGGTC 448
 QY 541 AGAGTGGACACAGGAGATTATTAAGATACACAGTGAAGTGTACAGAGGCGAGTCCCTGC 600
 Db 447 AGAGTGGACACAGGAGATTATTAAGATACACAGTGAAGTGTACAGAGGCGAGTCCCTGC 388

QY 601 CCTCTGCGAGGAGAGACCTTACCATGAGCTGTGTGATGTCTATTCACAAAGTCAAG 660
 Db 387 CCTCTGCGAGGAGAGACCTTACCATGAGCTGTGTGATGTCTATTCACAAAGTCAAG 328
 QY 661 TATGAANAATACACACAGCAGCTTCTTCATAGAGACATCAATCAACACAGCCACCCACA 720
 Db 327 TATGAANAATACACACAGCAGCTTCTTCATAGAGACATCAATCAACACAGCCACCCACA 268
 QY 721 AACCTGACGTGAAGCCATTGAAATAATCTCGCAGCTGAGAGTCACTGGGAATACCC 780
 Db 267 AACCTGACGTGAAGCCATTGAAATAATCTCGCAGCTGAGAGTCACTGGGAATACCC 208
 QY 781 GACACCTGGAGCAGCCCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
 Db 207 GACACCTGGAGCAGCCCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 148
 QY 841 AAGAACATAGAAAAAAGATAGACTCTGCTGAGCAAGACCTCAGCCAAAGTCTGTG 900
 Db 147 AAGAACATAGAAAAAAGATAGACTCTGCTGAGCAAGACCTCAGCCAAAGTCTGTG 88
 QY 901 TGGCACAAGATGCGCAAGATCCGCGTGAAGCCCGAGACCCGCTACTATAGTTCCTGG 960
 Db 87 TGGCACAAGATGCGCAAGATCCGCGTGAAGCCCGAGACCCGCTACTATAGTTCCTGG 28
 QY 961 AGGACTGGGCGATCTGTCTATGAGT 987
 Db 27 AGGACTGGGCGATCTGTCTATGAGT 1

RESULT 7

US-09-917-265-107
 ; Sequence 107, Application US/09917265
 ; Patent No. US20020052030A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wonderling, Ramani S.
 ; APPLICANT: Boroughs, Karen L.
 ; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
 ; FILE REFERENCE: IM-5
 ; CURRENT APPLICATION NUMBER: US/09/917,265
 ; PRIOR FILING DATE: 2001-07-27
 ; PRIOR APPLICATION NUMBER: 2000-08-04
 ; NUMBER OF SEQ ID NOS: 109
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 107
 ; LENGTH: 2267
 ; TYPE: DNA
 ; ORGANISM: Canis familiaris
 ; NAME/KEY: CDS
 ; LOCATION: (154)..(1140)
 ; OTHER INFORMATION:
 US-09-917-265-107

Query Match 60.9%; Score 974; DB 10; Length 2267;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 974; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCTCAGCAGTGGTATCTCTGTTTCCCTGTTTGGTGGCTCTCCCTCATAGCC 66
 Db 160 CCTCAGCAGTGGTATCTCTGTTTCCCTGTTTGGTGGCTCTCCCTCATAGCC 219
 QY 67 ATATGGAACTGAGAAAGATGTTTATGTTGTAGAGTGTGAGCTGACACCTGATAGCC 126
 Db 220 ATATGGAACTGAGAAAGATGTTTATGTTGTAGAGTGTGAGCTGACACCTGATAGCC 279
 QY 127 GGAGAAATGTTGTTCTTACCTGCCATACCCCTGAAGAAAGATGACATCACTTGGACCTCA 186
 Db 280 GGAGAAATGTTGTTCTTACCTGCCATACCCCTGAAGAAAGATGACATCACTTGGACCTCA 339
 QY 187 GCGCAGACGACGAAAGTCTAGGTTCTGTGTAAGTCTGACCATTCGAAGTCAAAAGATT 246
 Db 340 GCGCAGACGACGAAAGTCTAGGTTCTGTGTAAGTCTGACCATTCGAAGTCAAAAGATT 399

QY 247 GGAGATGCTGGCCAGTATACCTGCCATAAAGAGGCAAGGTTCTGAGCCGCTACTCTG 306
|||||
Db 400 GGAATCTCTGCCGCTTACCTGCCATTAAGAGGCAAGGTTCTGAGCCGCTACTCTG 459
QY 307 TTGATTCACAAAAAAGAAGATGGAATTTGCTCCACTGATATCTTAAAGAAACAGAAAGAA 366
|||||
Db 460 TTGATTCACAAAAAAGAAGATGGAATTTGCTCCACTGATATCTTAAAGAAACAGAAAGAA 519
QY 367 TCCAAAAATAAATCTTCTGAAATGTGAGGCAAAAGATTTCTTGCACGTTTCACATGC 426
|||||
Db 520 TCCAAAAATAAATCTTCTGAAATGTGAGGCAAAAGATTTCTTGCACGTTTCACATGC 579
QY 427 TGGTGGCTGACGGCAATCAGTACTGATTTTGAATTTGATGCAAAAGAGCAGAGGGCTC 486
|||||
Db 580 TGGTGGCTGACGGCAATCAGTACTGATTTTGAATTTGATGCAAAAGAGCAGAGGGCTC 639
QY 487 TCTGACCCCAAGGGGTGAGATGTGAGCACTGACACTTTTCAGCAGAGAGGGTCAAGTG 546
|||||
Db 640 TCTGACCCCAAGGGGTGAGATGTGAGCACTGACACTTTTCAGCAGAGAGGGTCAAGTG 599
QY 547 GACACACGGGATTTAAAGAGTACACAGTGTGAGTCAAGAGGGGAGTGCCTGCTCT 606
|||||
Db 700 GACACACGGGATTTAAAGAGTACACAGTGTGAGTCAAGAGGGGAGTGCCTGCTCT 759
QY 607 GCCGAGAGAGCCTACCCATCGAGTGTGATGCTATTCACAAAGCTCAAGTATGAA 666
|||||
Db 760 GCCGAGAGAGCCTACCCATCGAGTGTGATGCTATTCACAAAGCTCAAGTATGAA 819
QY 667 AACTACACAGACGCTTCTTCATCAGACATCATCAACAGCAGACCCACCAACCTG 726
|||||
Db 820 AACTACACAGACGCTTCTTCATCAGACATCATCAACAGCAGACCCACCAACCTG 879
QY 727 CAGCTGAAGCATTGAAAAATTTCTGCGACCTGAGAGTCACTGGGAATACCCGACACC 786
|||||
Db 880 CAGCTGAAGCATTGAAAAATTTCTGCGACCTGAGAGTCACTGGGAATACCCGACACC 939
QY 787 TGGAGCACCCAGCATCT 846
|||||
Db 940 TGGAGCACCCAGCATCT 999
QY 847 AATAGAGAAAAAAGATAGACTGTGCTGAGACAAAGCTCAACCAAGTCTGTGCTCAC 906
|||||
Db 1000 AATAGAGAAAAAAGATAGACTGTGCTGAGACAAAGCTCAACCAAGTCTGTGCTCAC 1059
QY 907 AAGGATGCCAAGATCCCGGTCGAAGCCCGAGACCGCTACTATAGTTATCTTGAAGCGAC 966
|||||
Db 1060 AAGGATGCCAAGATCCCGGTCGAAGCCCGAGACCGCTACTATAGTTATCTTGAAGCGAC 1119
QY 967 TGGGCATCTGTCT 980
|||||
Db 1120 TGGGCATCTGTCT 1133

RESULT 8
US-09-917-265-109/c

: Sequence 109, Application us/09917265
: Patent No. US20020052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: APPLICANT: Borouhgs, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
: FILE REFERENCE: IM-5
: CURRENT APPLICATION NUMBER: US/09/917, 265
: PRIOR APPLICATION NUMBER: 2001-07-27
: PRIOR FILING DATE: 2000-08-04
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 109
: LENGTH: 2267
: TYPE: DNA
: ORGANISM: Canis familiaris

US-09-917-265-109

Query Match 60.9%; Score 974; DB 10; Length 2267;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 974; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCTGACGAGTTGGTCATCTCTGTTTCCCTGTTTGGTGGGTCCTCCCTCATGCGC 66
|||||
Db 2108 CCTGACGAGTTGGTCATCTCTGTTTCCCTGTTTGGTGGGTCCTCCCTCATGCGC 2049
QY 67 ATATGGCAACTGGAAAAAGATGTTTANGTTTGAAGTTGAGCTGGACCCCTGATGCCCC 126
|||||
Db 2048 ATATGGCAACTGGAAAAAGATGTTTANGTTTGAAGTTGAGCTGGACCCCTGATGCCCC 1989
QY 127 GGAGAAATGGTGGTCTCCTCCTGCTATACCCCTGAAGAAGTACATCTTGGACCTCA 186
|||||
Db 1988 GGAGAAATGGTGGTCTCCTCCTGCTATACCCCTGAAGAAGTACATCTTGGACCTCA 1929
QY 187 GCCGAGAGCAGTGAAGTCTAGTGTGCTGCTAAACCTGACCATCCCAAGAAATTT 246
|||||
Db 1928 GCCGAGAGCAGTGAAGTCTAGTGTGCTGCTAAACCTGACCATCCCAAGAAATTT 1869
QY 247 GGAGATGCTGGCCAGTATACCTGCCATTAAGAGGCAAGGTTCTGAGCCGCTCACTCCTG 306
|||||
Db 1868 GGAGATGCTGGCCAGTATACCTGCCATTAAGAGGCAAGGTTCTGAGCCGCTCACTCCTG 1809
QY 307 TTGATTCACAAAAAAGAAGATGGAATTTGCTCCACTGATATCTTAAAGAAACAGAAAGAA 366
|||||
Db 1808 TTGATTCACAAAAAAGAAGATGGAATTTGCTCCACTGATATCTTAAAGAAACAGAAAGAA 1749
QY 367 TCCAAAAATAAATCTTCTGAAATGTGAGGCAAAAGATTTCTTGCAGCTTTCACATGC 426
|||||
Db 1748 TCCAAAAATAAATCTTCTGAAATGTGAGGCAAAAGATTTCTTGCAGCTTTCACATGC 1689
QY 427 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTTCACTGTCAAAAGTAGAGAGGCTTC 486
|||||
Db 1688 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTTCACTGTCAAAAGTAGAGAGGCTTC 1529
QY 487 TCTGACCCCAAGGGGTGACATGTGAGCACTGTACCTTTACAGAGAGAGGTCAGAGTG 546
|||||
Db 1528 TCTGACCCCAAGGGGTGACATGTGAGCACTGTACCTTTACAGAGAGAGGTCAGAGTG 1569
QY 547 GACAAACAGGATTTAAGAAATGACACAGTGAAGTGTGAGAGGCGAGTGCCTGCTCT 606
|||||
Db 1568 GACAAACAGGATTTAAGAAATGACACAGTGAAGTGTGAGAGGCGAGTGCCTGCTCT 1509
QY 607 GCCGAGAGAGCCTACCCATCGAGTGTGCTGATGCTATTCACAAAGCTCAAGTATGAA 666
|||||
Db 1508 GCCGAGAGAGCCTACCCATCGAGTGTGCTGATGCTATTCACAAAGCTCAAGTATGAA 1449
QY 667 AACTACACAGCAGCTTCTTCATGAGACATCATCAACAGCAGACCCACCAACCTG 726
|||||
Db 1448 AACTACACAGCAGCTTCTTCATGAGACATCATCAACAGCAGACCCACCAACCTG 1389
QY 727 CAGCTGAAGCATTGAAAAATTTCTGCGACCTGAGAGGTCAGCTGGGAATACCCGACACC 786
|||||
Db 1388 CAGCTGAAGCATTGAAAAATTTCTGCGACCTGAGAGGTCAGCTGGGAATACCCGACACC 1329
QY 787 TGGAGCACCCAGCATCT 846
|||||
Db 1328 TGGAGCACCCAGCATCT 1269
QY 847 AATAGAGAAAAAAGATAGACTGTGCTGAGACAAAGCTTACGCAAGGTCGTGCTCAC 906
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Db 1268 AATAGAGAAAAAAGATAGACTGTGCTGAGACAAAGCTTACGCAAGGTCGTGCTCAC 1209
QY 907 AAGGATGCCAAGATCCCGGTCGAAGCCCGAGACCGCTACTATAGTTATCTTGAAGCGAC 966
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Db 1208 AAGGATGCCAAGATCCCGGTCGAAGCCCGAGACCGCTACTATAGTTATCTTGAAGCGAC 1149
QY 967 TGGGCATCTGTCT 980
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Db 1148 TGGGCATCTGTCT 1135

RESULT 9
US-09-917-265-52
; Sequence 52, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917, 265
; CURRENT FILING DATE: 2001-07-27
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(921)
; OTHER INFORMATION:
US-09-917-265-52

Query Match 57.2%; Score 914; DB 10; Length 921;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 914; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATATGGAACTGGAGAAAGATGTTATGTTAGAGTTGAGTCGACCGCTGATGCCCC 126
DB 1 ATATGGAACTGGAGAAAGATGTTATGTTAGAGTTGAGTCGACCGCTGATGCCCC 60
QY 127 GGAGAAATGGTGTCTCTCACTCCATACCCCTGAGAGAGATACATCACTTGACCTCA 186
DB 61 GGAGAAATGGTGTCTCTCACTCCATACCCCTGAGAGAGATACATCACTTGACCTCA 120
QY 187 GCGCAGAGCAGTGAAGTCTCTAGAGTTCTGTAAGTCTGACATCCAGTCAAGAAATT 246
DB 121 GCGCAGAGCAGTGAAGTCTCTAGAGTTCTGTAAGTCTGACATCCAGTCAAGAAATT 180
QY 247 GGAGATCTGCGCCAGTATACCTGCTCCATTAAGAGGAGAGGTTCTGAGCCGCTACTCTG 306
DB 181 GGAGATCTGCGCCAGTATACCTGCTCCATTAAGAGGAGAGGTTCTGAGCCGCTACTCTG 240
QY 307 TTGATTCACAAAAAAGAGATGGAATTTGGTCCACTGATATCTTAAGAGAGAGAA 366
DB 241 TTGATTCACAAAAAAGAGATGGAATTTGGTCCACTGATATCTTAAGAGAGAGAA 300
QY 367 TCCAAAAATAGATCTTTCTGAAATGTGAGGCAAGAAATTAATCTGGAGCTTACATGC 426
DB 301 TCCAAAAATAGATCTTTCTGAAATGTGAGGCAAGAAATTAATCTGGAGCTTACATGC 360
QY 427 TGGTGGCTACGGCAGTACGTAAGTCTGAAATTAAGTCTGAAATTAAGTCTGAAATTAAG 486
DB 361 TGGTGGCTACGGCAGTACGTAAGTCTGAAATTAAGTCTGAAATTAAGTCTGAAATTAAG 420
QY 487 TCTGACCCCAAGGGGTGACATGTGAGAGAGTGAACCTTCAGCAGAGAGGGGTCAAGTG 546
DB 421 TCTGACCCCAAGGGGTGACATGTGAGAGAGTGAACCTTCAGCAGAGAGGGGTCAAGTG 480
QY 547 GACAACAGGATTAATAGAAATGACACAGTGGATGTCAGAGAGGAGTCTGCTGCCCTT 606
DB 481 GACAACAGGATTAATAGAAATGACACAGTGGATGTCAGAGAGGAGTCTGCTGCCCTT 540
QY 607 GCGGAGAGAGAGCTTACCTGAGAGTCTGCTGGATGCTATTCACAGCTCAAGTATGAA 666
DB 541 GCGGAGAGAGAGCTTACCTGAGAGTCTGCTGGATGCTATTCACAGCTCAAGTATGAA 600
QY 667 AACTACACGAGAGCTTCTTCATCAGAGATCATCAAAAGCAGACCCCAAGAACCTG 726
DB 600 AACTACACGAGAGCTTCTTCATCAGAGATCATCAAAAGCAGACCCCAAGAACCTG 726

DB 601 AACTACACGAGAGCTTCTTCATCAGAGATCATCAAAAGCAGACCCCAAGAACCTG 660
QY 727 CAGCTGAAGCCATTGAAAAATTTCTCGGACAGTGGAGTCAAGTGGGAATACCCCGACAC 786
DB 661 CAGCTGAAGCCATTGAAAAATTTCTCGGACAGTGGAGTCAAGTGGGAATACCCCGACAC 720
QY 787 TGGAGCACCACCATTCCTACTTCTCCGACATTTTGGATACAGCCCGACAGGAGAAC 846
DB 721 TGGAGCACCACCATTCCTACTTCTCCGACATTTTGGATACAGCCCGACAGGAGAAC 780
QY 847 AATAGAAAAAAGATAGACTCTGCTGGACAGACCTCAGCAGAGTCTGTGCCAC 906
DB 781 AATAGAAAAAAGATAGACTCTGCTGGACAGACCTCAGCAGAGTCTGTGCCAC 840
QY 907 AAGATGCCAAGATCCGCGTCAAGGCCGAGACCGCTACTATATGTCATCTGGAGCAGAC 966
DB 841 AAGATGCCAAGATCCGCGTCAAGGCCGAGACCGCTACTATATGTCATCTGGAGCAGAC 900
QY 967 TGGGCACTGTGTCTC 980
DB 901 TGGGCACTGTGTCTC 914

RESULT 10
US-09-917-265-54/C
; Sequence 54, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917, 265
; CURRENT FILING DATE: 2001-07-27
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-917-265-54

Query Match 57.2%; Score 914; DB 10; Length 921;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 914; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATATGGAACTGGAGAAAGATGTTATGTTAGAGTTGAGTCGACCGCTGATGCCCC 126
DB 921 ATATGGAACTGGAGAAAGATGTTATGTTAGAGTTGAGTCGACCGCTGATGCCCC 862
QY 127 GGAGAAATGGTGTCTCTCACTCCATACCCCTGAGAGAGATACATCACTTGAGCTCA 186
DB 861 GGAGAAATGGTGTCTCTCACTCCATACCCCTGAGAGAGATACATCACTTGAGCTCA 802
QY 187 GCGCAGAGCAGTGAAGTCTCTAGAGTTCTGTAAGTCTGACCATCCAAAGAAATT 246
DB 801 GCGCAGAGCAGTGAAGTCTCTAGAGTTCTGTAAGTCTGACCATCCAAAGAAATT 742
QY 247 GGAGATCTGCGCCAGTATACCTGCTCAATAAGAGGCAAGGTTCTGAGCCGCTACTCTG 306
DB 741 GGAGATCTGCGCCAGTATACCTGCTCAATAAGAGGCAAGGTTCTGAGCCGCTACTCTG 682
QY 307 TTGATTCACAAAAAAGAGATGGAATTTGGTCCACTGATATCTTAAGAGAGAGAA 622
DB 681 TTGATTCACAAAAAAGAGATGGAATTTGGTCCACTGATATCTTAAGAGAGAGAA 622
QY 621 TCCAAAAATAGATCTTTCTGAAATGTGAGGCAAGAAATTAATCTGGAGCTTACATGC 426
DB 621 TCCAAAAATAGATCTTTCTGAAATGTGAGGCAAGAAATTAATCTGGAGCTTACATGC 562
QY 427 TGGTGGCTGAGGCAATCAGTATGTAATTTGAAATTCAGTGTCAAAAGTAGAGAGGCTTC 486

|||||
Db 561 TGTGGCTAGCGGCATCAGTACTGATTTGAATTCAGTGTCAAAAGTAGCAGAGGCTTC 502
Qy 487 TCTGACCCCAAGGGGTACATGTGAGCAGTACACACTTTTCAGCAGAGAGGTGAGAGT 546
Db 501 TCTGACCCCAAGGGGTACATGTGAGCAGTACACACTTTTCAGCAGAGAGGTGAGAGT 442
Qy 547 GACAACAGGATTTAAGAGTACACAGTGGAGTGCAGAGAGGAGTGGCTGGCCCTCT 606
Db 441 GACAACAGGATTTAAGAGTACACAGTGGAGTGCAGAGAGGAGTGGCTGGCCCTCT 382
Qy 607 GCCGAGAGAGCCTTACCCATCGAGGTCGTGTGATGCTATTACAGCTCAAGTATGAA 656
Db 381 GCCGAGAGAGCCTTACCCATCGAGGTCGTGTGATGCTATTACAGCTCAAGTATGAA 322
Qy 667 AACTACACAGCAGCTTCTTATCAGAGACATCATCAAAACGAGCCCAACCAACTG 726
Db 321 AACTACACAGCAGCTTCTTATCAGAGACATCATCAAAACGAGCCCAACCAACTG 262
Qy 727 CAGCTGAGCATTGAAAAATTTCTGGCAGCGTGGAGTGCAGCTGGGAATACCCCGAC 786
Db 261 CAGCTGAGCATTGAAAAATTTCTGGCAGCGTGGAGTGCAGCTGGGAATACCCCGAC 202
Qy 787 TGCAGCACCCACATCTCTACTTCTCCCTGACATTTTGCATACAGGCCGAGCAAGAC 846
Db 201 TGCAGCACCCACATCTCTACTTCTCCCTGACATTTTGCATACAGGCCGAGCAAGAC 142
Qy 847 AATACGAAAAAAGATAGACTCTGCGTGCAGCAAGACTTACGCCAAGTGTGCGCAC 906
Db 141 AATACGAAAAAAGATAGACTCTGCGTGCAGCAAGACTTACGCCAAGTGTGCGCAC 82
Qy 907 AAGATGCCAAGATCCGCTGCAAGCCGAGACCGCTACTACTTACTTCTGAGAGCAG 966
Db 81 AAGATGCCAAGATCCGCGGTGCAAGCCGAGACCGCTACTACTTACTTCTGAGAGCAG 22
Qy 967 TGGCATCTGTGTC 980
Db 21 TGGCATCTGTGTC 8

RESULT 11

US-09-917-265-49
: Sequence 49, Application US/09917265
: Patent No. US20020052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: APPLICANT: Boroughs, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
: FILE REFERENCE: IM-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: PRIOR FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 49
: LENGTH: 591
: TYPE: DNA
: ORGANISM: Canis familiaris
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(591)
: OTHER INFORMATION:
US-09-917-265-49

Query Match

Best Local Similarity 30.9%; Score 494; DB 10; Length 591;
Pred. No. 5.8e-251;
Matches 494; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1076 TGAGAGCCGTGACGACACGCTTCGAGAGCCAGCAACACTTAAATTATATTCCTGCA 1135
Db 68 TGAGAGCCGTGACGACACGCTTCGAGAGCCAGCAACACTTAAATTATATTCCTGCA 127

Qy 1136 CTTCCGAAGAGATGATCATGAGATATTCACAAAGATAAACAGCACAGTGGAGCCT 1195
Db 128 CTTCCGAAGAGATGATCATGAGATATTCACAAAGATAAACAGCACAGTGGAGCCT 187
Qy 1196 GCTTACACAGTGAATTAACCATGAGATGAGAGTTGCTG6CTTCAGAGAGATCTTTGA 1255
Db 188 GCTTACACAGTGAATTAACCATGAGATGAGAGTTGCTG6CTTCAGAGAGATCTTTGA 247
Qy 1256 TAACTAACGGGAGTTGCCCTGCGCTCTGGAAAGGCTCTTTTATGACGCTCTGCTTTA 1315
Db 248 TAACTAACGGGAGTTGCCCTGCGCTCTGGAAAGGCTCTTTTATGACGCTCTGCTTTA 307
Qy 1316 GCAGCATCTATGAGACCTTGAAGATGTCACAGATGGAATTAAGGCCATGGAAGCAAGC 1375
Db 308 GCAGCATCTATGAGACCTTGAAGATGTCACAGATGGAATTAAGGCCATGGAAGCAAGC 367
Qy 1376 TTTTATGATGCCCAAGAGGAGATCTTTCTGGATCAAAACATGCTGACAGTATGATG 1435
Db 368 TTTTATGATGCCCAAGAGGAGATCTTTCTGGATCAAAACATGCTGACAGTATGATG 427
Qy 1436 AGCTGTACAGGCCCTGTAATTTCAACAGTGTACTGTGCGCACAGAAATCTCCCTGAA 1495
Db 428 AGCTGTACAGGCCCTGTAATTTCAACAGTGTACTGTGCGCACAGAAATCTCCCTGAA 487
Qy 1496 AGCCGATTTTATATAACTAAATCAAGCTGTGATCTTCTTATGCTTTCAGAAATTC 1555
Db 488 AGCCGATTTTATATAACTAAATCAAGCTGTGATCTTCTTATGCTTTCAGAAATTC 547
Qy 1556 GTGCGGTGACCATC 1569
Db 548 GTGCGGTGACCATC 561

RESULT 12

US-09-917-265-51/c
: Sequence 51, Application US/09917265
: Patent No. US20020052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: APPLICANT: Boroughs, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
: FILE REFERENCE: IM-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: PRIOR FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 51
: LENGTH: 591
: TYPE: DNA
: ORGANISM: Canis familiaris
US-09-917-265-51

Query Match

Best Local Similarity 30.9%; Score 494; DB 10; Length 591;
Pred. No. 5.8e-251;
Matches 494; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1076 TGAGAGCCGTGACGACACGCTTCGAGAGCCAGCAACACTTAAATTATATTCCTGCA 1135
Db 524 TGAGAGCCGTGACGACACGCTTCGAGAGCCAGCAACACTTAAATTATATTCCTGCA 465
Qy 1136 CTTCCGAAGAGATGATCATGAGATATTCACAAAGATAAACAGCACAGTGGAGCCT 1195
Db 464 CTTCCGAAGAGATGATCATGAGATATTCACAAAGATAAACAGCACAGTGGAGCCT 405
Qy 1196 GCTTACACAGTGAATTAACCATGAGATGAGAGTTGCTG6CTTCAGAGAGATCTTTGA 1255
Db 404 GCTTACACAGTGAATTAACCATGAGATGAGAGTTGCTG6CTTCAGAGAGATCTTTGA 345
Qy 1256 TAACTAACGGGAGTTGCCCTGCGCTCTGGAAAGGCTCTTTTATGACGCTCTGCTTTA 1315
Db 344 TAACTAACGGGAGTTGCCCTGCGCTCTGGAAAGGCTCTTTTATGACGCTCTGCTTTA 285

| Query Match | 30.9% | Score 494 | DB 10 | Length 666 |
|-----------------------|----------------|---|----------|------------|
| Best Local Similarity | 100.0% | Pred. No. 5_9e-251 | | |
| Matches 499 | Conservative 0 | Mismatches 0 | Indels 0 | Gaps 0 |
| QY | 1076 | TGAGAGCCGTGACGACACGCGCTTGAGAGGCCAGACAACTGTAGAATTTATTTCTGCA | 1135 | |
| Db | 524 | TGAGAGCCGTGACGACACACGCGCTTGAGAGGCCAGACAACTGTAGAATTTATTTCTGCA | 465 | |
| QY | 1136 | CTTCCGAGAGGATTTGATCATGAGATATTCACAAAGGATAAACCCAGACAGTGGAGCGCT | 1195 | |
| Db | 464 | CTTCCGAGAGGATTTGATCATGAGATATTCACAAAGGATAAACCCAGACAGTGGAGCGCT | 405 | |
| QY | 1196 | GCTTACCACCTGGAATTTACCATGTAATGAGAGTTGCTGCTGCCTCCACAGAGATCTCTTTGA | 1255 | |
| Db | 404 | GCTTACCACCTGGAATTTACCATGTAATGAGAGTTGCTGCTGCCTCCACAGAGATCTCTTTGA | 345 | |
| QY | 1256 | TAACTAAAGGAGATTTGCGTGGCCTCTGGAAAGGCGCTTTTATGACGGTCCGCGCTTA | 1315 | |
| Db | 344 | TAACTAAAGGAGATTTGCGTGGCCTCTGGAAAGGCGCTTTTATGACGGTCCGCGCTTA | 285 | |
| QY | 1316 | GCAGCATCTATGAGGACTTGAGAGTGTACCAGATGGAATTTCAAGGCCATGAAAGCAAAGC | 1375 | |
| Db | 284 | GCAGCATCTATGAGGACTTGAGAGTGTACCAGATGGAATTTCAAGGCCATGAAAGCAAAGC | 225 | |
| QY | 1376 | TTTTATATGATGCCAGAGGCGAGATCTTCTGGATGCAAAAACATGCTGACAGCTATGATG | 1435 | |
| Db | 224 | TTTTATATGATGCCAGAGGCGAGATCTTCTGGATGCAAAAACATGCTGACAGCTATGATG | 165 | |
| QY | 1436 | AGCTGTTACAGGCCCTGGAATTTTCACAGTGTGACTGTGCACAGAAATCCTCCCTTGAAG | 1495 | |
| Db | 164 | AGCTGTTACAGGCCCTGGAATTTTCACAGTGTGACTGTGCACAGAAATCCTCCCTTGAAG | 105 | |
| QY | 1496 | AGCGGATTTTATATAAACTAAATTAAGCTCTGCACTACTTCTCATGCTTTAGAAATTC | 1555 | |
| Db | 104 | AGCGGATTTTATATAAACTAAATTAAGCTCTGCACTACTTCTCATGCTTTTAGAAATTC | 45 | |
| QY | 1556 | GTGCGGTGACCAATC | 1569 | |

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 10:34:53 ; Search time 2747.57 Seconds
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Title: US-09-917-265-61

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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 809774376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST: *
1: em_estbda:*
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12: gb_estl3:*
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26: em_gss_pro:*
27: em_gss_rnd:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 40 | 2.5 | 1099 | 13 | B1523344 | B1523344 603175938 |
| 3 | 31 | 1.9 | 589 | 9 | A1050362 | A1050362 ub30807.r |
| 4 | 30 | 1.9 | 373 | 12 | BF552757 | BF552757 UT-R-C0-1 |
| 5 | 29 | 1.8 | 832 | 13 | B1523569 | B1523569 603175938 |
| 6 | 26 | 1.6 | 342 | 13 | BM257856 | BM257856 521721 MA |

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| 7 | 26 | 1.6 | 812 | 12 | BG702253 | BG702253 602683459 | |
| C | 9 | 22 | 1.4 | 529 | 13 | B1725614 | B1725614 1031079H1 |
| 8 | 22 | 1.4 | 642 | 13 | BM600965 | BM600965 170006870 | |
| 10 | 22 | 1.4 | 662 | 17 | AG049786 | AG049786 Pan troy1 | |
| 11 | 21 | 1.3 | 369 | 17 | A2884788 | A2884788 RPI1-23-1 | |
| C | 12 | 21 | 1.3 | 489 | 17 | A0393691 | A0393691 CITR1-E1- |
| 13 | 21 | 1.3 | 552 | 13 | BM085578 | BM085578 sa126g11- | |
| C | 14 | 21 | 1.3 | 564 | 13 | BJ030774 | BJ030774 BJO30774 |
| 15 | 21 | 1.3 | 571 | 13 | B1032049 | B1032049 BJO32049 | |
| C | 16 | 21 | 1.3 | 638 | 13 | B1099266 | B1099266 TPI-40-G0 |
| 17 | 21 | 1.3 | 646 | 10 | BB038225 | BB038225 BB038225 | |
| 18 | 21 | 1.3 | 667 | 13 | BJ042592 | BJ042592 BJ042592 | |
| 19 | 21 | 1.3 | 679 | 14 | BU002107 | BU002107 OCG30D21- | |
| C | 20 | 21 | 1.3 | 733 | 17 | AO631366 | AO631366 RPI1-11-4 |
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| C | 22 | 21 | 1.3 | 975 | 17 | CNS04W1 | AL310995 Tetradon |
| 23 | 20 | 1.3 | 136 | 13 | BM140498 | BM140498 WHE0484_a | |
| C | 24 | 20 | 1.3 | 167 | 10 | AW472465 | AW472465 s125102.Y |
| 25 | 20 | 1.3 | 173 | 13 | BJ006287 | BJ006287 BJ006287 | |
| C | 26 | 20 | 1.3 | 239 | 17 | BH870361 | BH870361 hm61b07.b |
| C | 27 | 20 | 1.3 | 241 | 17 | AZ891891 | AZ891891 RPI1-24-2 |
| 28 | 20 | 1.3 | 266 | 10 | AW101097 | AW101097 sd74a01.Y | |
| 29 | 20 | 1.3 | 296 | 13 | BI498525 | BI498525 sa115c08. | |
| C | 30 | 20 | 1.3 | 305 | 9 | A1441440 | A1441440 sa59h11.Y |
| 31 | 20 | 1.3 | 316 | 13 | BM522480 | BM522480 sam93e09. | |
| 32 | 20 | 1.3 | 333 | 10 | AW311474 | AW311474 sg40b04.Y | |
| 33 | 20 | 1.3 | 338 | 14 | BQ770669 | BQ770669 UT-M-F10- | |
| 34 | 20 | 1.3 | 340 | 17 | A0373901 | A0373901 RPI11-14 | |
| 35 | 20 | 1.3 | 341 | 13 | BI973274 | BI973274 sa186c03. | |
| 36 | 20 | 1.3 | 346 | 10 | AW164696 | AW164696 se76d07.Y | |
| 37 | 20 | 1.3 | 352 | 10 | BE610397 | BE610397 sa55b10.Y | |
| 38 | 20 | 1.3 | 366 | 13 | BI424493 | BI424493 sa55b10.Y | |
| C | 39 | 20 | 1.3 | 374 | 14 | T99581 | T99581 ye6508.r1 |
| C | 40 | 20 | 1.3 | 385 | 12 | BE703854 | BE703854 MR2-NM111 |
| 41 | 20 | 1.3 | 421 | 17 | A0673149 | A0673149 HS_5496_A | |
| 42 | 20 | 1.3 | 433 | 14 | BQ610072 | BQ610072 sap36e02. | |
| C | 43 | 20 | 1.3 | 436 | 10 | AV792889 | AV792889 AV792889 |
| 44 | 20 | 1.3 | 439 | 9 | A1442207 | A1442207 sa49b01.Y | |
| 45 | 20 | 1.3 | 475 | 12 | BF704417 | BF704417 MI-P-E6-a | |

ALIGNMENTS

RESULT 1
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LOCUS 603033580F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5175018 5',
DEFINITION B1824638
ACCESSION B1824638
VERSION B1824638.1 GI:15936188
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 447)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LHAM1435 row: O column: 19
High quality sequence start: 3
High quality sequence stop: 445.
Location/Qualifiers

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source
1. .447
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/db_xref="taxon:9606"
/clone="IMAGE:5175018"
/clone_1id="NIH_MGC_115"
/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector:
pcmv-SpOrf6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

BASE COUNT      149 a      63 c      87 g      148 t
ORIGIN

Query Match      2.6%; Score 41; DB 13; Length 447;
Best Local Similarity 100.0%; Pred. No. 8.0e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1516  AAATCAGCCTCTGCATCTTCTTCATCCTTCAGAAATTCG 1556
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Db      1  AAAATCAGCCTCTGCATCTTCTTCATCCTTCAGAAATTCG 41

RESULT 2
BI523344/c      1099 bp      mRNA      linear      EST 29-AUG-2001
LOCUS      6031759381 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240216 3',
DEFINITION      mRNA sequence.
ACCESSION      BI523344
VERSION      BI523344.1 GI:15348136
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE      1 (bases 1 to 1099)
AUTHORS      NIH-MGC http://mgc.ncl.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: c9apbs-remail.nih.gov
              Tissue Procurement: Life Technologies, Inc.
              cDNA Library Preparation: Life Technologies, Inc.
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/MLN at:
              http://image.llnl.gov
              Plate: L14M11605 row: 1 column: 09
              High quality sequence start: 40
              High quality sequence stop: 727.
              Location/Qualifiers
                1. .1099
                  /organism="Homo sapiens"
                  /db_xref="taxon:9606"
                  /clone="IMAGE:5240216"
                  /clone_1id="NIH_MGC_121"
                  /lab_host="DH10B"
                  /note="Organ: brain; Vector: pcmv-SpOrf6; Site_1: NotI;
                  Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                  fetal brains, female age 20 weeks, female age 24 weeks,
                  and male age 26 weeks. Library is oligo-dT primed and
                  directionally cloned (EcoRV site is destroyed upon
                  cloning). Average insert size 1.7 kb, insert size range
                  0.7-3.5 kb. Library is normalized and enriched for
                  full-length clones and was constructed by C. Gruber
                  (Invitrogen). Research Genetics tracking code 017. Note:
                  this is a NIH_MGC Library."

```

| | | | | | |
|-----------------------|---|---------------|-----------|---------|-----------------|
| BASE COUNT | 359 a | 244 c | 218 g | 276 t | 2 others |
| ORIGIN | | | | | |
| Query Match | 2.5%; Score 40; DB 13; Length 1099; | | | | |
| Best Local Similarity | 100.0%; Pred. No. 3,8e-09; | | | | |
| Matches | 40; Conservative | 0; Mismatches | 0; Indels | 0; Gaps | 0; |
| Oy | 1517 AATCAAGCTTCGACTACTTCTTGATCGTTGCACAAATTCC | 1556 | | | |
| Dn | 524 AAATCAAGCTTCGACTACTTCTTGATCGTTGCACAAATTCC | 485 | | | |
| RESULT 3 | | | | | |
| AIO50362 | | | | | |
| LOCUS | AIO50362 | 589 bp | mRNA | linear | EST 09-JUL-1998 |
| DEFINITION | ub30a07.1 Soares_thymus_2NBMT Mus musculus cDNA clone IMAGE:1379220 5' similar to gb:M55291 INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (HUMAN); gb:M86572 Mus musculus interleukin 12 p35 subunit, complete cds (MOUSE); mRNA sequence. | | | | |
| ACCESSION | AIO50362 | | | | |
| VERSION | AIO50362.1 | GI:3299479 | | | |
| KEYWORDS | EST. | | | | |
| SOURCE | house mouse. | | | | |
| ORGANISM | Mus musculus. | | | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 589) | | | | |
| AUTHORS | Marra,M., Hallier,L., Allen,M., Bowles,M., Dietrich,N., Dubouque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,D., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theisinger,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R. | | | | |
| TITLE | The Mashu-HMI Mouse EST Project | | | | |
| JOURNAL | Unpublished (1996) | | | | |
| COMMENT | Contact: Marra M/Mouse EST Project Mashu-HMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (infoimage.llnl.gov) for further information. MGI:901888 Seq primer: -28m13 rev2 ET from Amershams High quality sequence stop: 60. | | | | |
| FEATURES | Location/Qualifiers | | | | |
| SOURCE | 1..589 | | | | |
| | /organism="Mus musculus" | | | | |
| | /strain="C57BL/6J" | | | | |
| | /db_xref="taxon:10090" | | | | |
| | /clone_image="IMAGE:1379220" | | | | |
| | /clone_lib="Soares_thymus_2NBMT" | | | | |
| | /sex="male" | | | | |
| | /tissue_type="Thymus" | | | | |
| | /dev_stage="4 weeks" | | | | |
| | /lab_host="DH10B" | | | | |
| | /note="Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTCAAGTGGAGCGGCCGTCTTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3D vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Fatima Bernaldo." | | | | |
| BASE COUNT | 162 a | 159 c | 142 g | 126 t | |
| ORIGIN | | | | | |
| Query Match | 1.9%; Score 31; DB 9; Length 589; | | | | |
| Best Local Similarity | 100.0%; Pred. No. 0.00016; | | | | |
| Matches | 31; Conservative | 0; Mismatches | 0; Indels | 0; Gaps | 0; |

OY 1318 AGCATCTATGAGACTTGAGATGTACCAGA 1348
 DB 324 AGCATCTATGAGACTTGAGATGTACCAGA 354

RESULT 4
 BF552757
 LOCUS
 DEFINITION UI-R-CO-12-d-02-0-UI-R1 UI-R-C0 Rattus norvegicus cDNA clone
 UI-R-CO-12-d-02-0-UI 5', mRNA sequence.
 BF552757
 BF552757.1 GI:11662487
 EST.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1 (bases 1 to 373)
 AUTHORS Ronaldo M.F., Lennon, G. and Soares, M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 COMMENT Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: msoares@blue.weeg.uiowa.edu
 CDNA Library Preparation: M.B. Soares Lab Clone distribution:
 Clones will be available through Research Genetics (www.resgen.com)
 This clone is also available through the I.M.A.G.E. Consortium at
 LNL (info@image.llnl.gov). IMAGE ID= 1782759
 Seq primer: M13 Forward.

FEATURES
 source
 1..373
 Location/Qualifiers
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-CO-12-d-02-0-UI"
 /clone_lib="UI-R-C0"
 /lab_host="adult"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C0 library is a subtracted library derived from the UI-R-A1 and UI-R-E1 libraries. The UI-R-A1 library consisted of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, and muscle. The UI-R-E1 library consisted of a mixture of individually tagged normalized libraries constructed from 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-C0) was constructed as follows: PCR amplified cDNA inserts from a pool of UI-R-A1 and UI-R-E1 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the pooled UI-R-A1 and UI-R-E1 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-C0 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996)."

BASE COUNT 106 a 93 c 89 g 85 t
 ORIGIN

Query Match 1.9%; Score 30; DB 12; Length 373;
 Best Local Similarity 100.0%; Pred. No. 0.00047;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1318 AGCATCTATGAGACTTGAGATGTACCAGA 1347
 DB 98 AGCATCTATGAGACTTGAGATGTACCAG 127

RESULT 5
 BI523569
 LOCUS
 DEFINITION 603175938P1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240216 5', mRNA sequence.
 BI523569
 BI523569.1 GI:15348361
 EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 832)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 Email: c9abbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLM11605 row: 1 column: 09
 High quality sequence start: 23
 High quality sequence stop: 821.

FEATURES
 source
 1..832
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5240216"
 /clone_lib="NIH_MGC_121"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Intelligen). Research Genetics tracking code 017. Note: this is a NIH_MGC Library."

BASE COUNT 220 a 233 c 200 g 179 t
 ORIGIN

Query Match 1.8%; Score 29; DB 13; Length 832;
 Best Local Similarity 100.0%; Pred. No. 0.002;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1141 GAAGAGATTGATCATGAAGATATCAGAA 1169
 DB 520 GAAGAGATTGATCATGAAGATATCAGAA 548

RESULT 6
 BM257856
 LOCUS
 DEFINITION 521721 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
 ACCESSION BM257856
 VERSION BM257856.1 GI:17893455

BASE COUNT 342 bp mRNA linear EST 17-DEC-2001
 ORIGIN

| | |
|-----------------------|---|
| KEYWORDS | EST. |
| SOURCE | cow. |
| ORGANISM | Bos taurus |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos. |
| AUTHORS | 1 (bases 1 to 342) |
| TITLE | Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,V.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett ,G.L., Heaton,M.P., Laegreid,M.W., Rohrer,G.A., Chitko-Mckown,C.G.,, Perteira,G.,, Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keefe,J.W. |
| JOURNAL | Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle |
| MEDLINE | Genome Res. 11 (4), 626-630 (2001) |
| COMMENT | 21180013 Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options. PCR primers FORWARD: AGGAACAGCTATGACCAT BACKWARD: GTTTTCCACTCAGCAGC Plate: 125 row: E column: 18 Seq primer: ATTGATGACACTATAC. Location/Qualifiers 1..342 /organism="Bos taurus" /db_xref="taxon:9913" /clone_lib="MARC 3BOV" /tissue_type="pooled" /lab_host="DH10B" /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendinosus muscle, and fetal longissimus muscle." |
| FEATURES | |
| SOURCE | |
| BASE COUNT | 67 a 135 c 74 g 66 t |
| ORIGIN | |
| Query Match | 1.6%; Score 26; DB 13; Length 342; |
| Best Local Similarity | 100.0%; Pred. No. 0.057; |
| Matches | 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| QY | 1099 CAGAAAGCCAGACAACTCTGCAATT 1124 |
| Db | 294 CAGAAGCCAGACAACTCTGCAATT 319 |
| RESULT 7 | |
| LOCUS | BC702253 812 bp mRNA linear EST 07-MAY-2001 |
| DEFINITION | 60268345F01 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4816118 5', mRNA sequence. |
| ACCESSION | BC702253 |
| VERSION | BC702253.1 GI:13973409 |
| KEYWORDS | EST. |
| SOURCE | human. |
| ORGANISM | Homo sapiens |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. |
| AUTHORS | 1 (bases 1 to 812) |
| TITLE | NIH-MGC http://mgc.ncl.nih.gov/. |
| JOURNAL | National Institutes of Health, Mammalian Gene Collection (MGC) |
| COMMENT | Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgaabs-remail.nih.gov Tissue Procurement: Miklos Palcovits, M.D., Ph.D. CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki |

Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
http://image.llnl.gov
Plate: LLAM10714 row: e column: 15
High quality sequence stop: 804.

FEATURES
Source
Location/Qualifiers
1..812
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4816118"
/clone_lib="NIH_MGC_95"
/tissue_type="hippocampus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pBluescripter (modified
pBluescript KS+); Site: 1: BamHI; Site 2: SalI-XhoI (gtcgaag
p); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTVN-3',
size-selected for average insert size 2.5 kb and
normalized to R0T 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT
188 a 249 c 226 g 149 t

ORIGIN

Query Match 1.6%; Score 26; DB 12; Length 812;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1099 CAGAGGCCGACAACTCTAGAATT 1124
|||||
Db 573 CAGAGGCCGACAACTCTAGAATT 598
|||||

RESULT 8
B1725614/c

LOCUS
DEFINITION
1031079H11.Y1 C. reinhardtii CC-1690, Stress II (normalized),
lambda zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.

ACCESSION
B1725614
B1725614.1 GI:15701309

VERSION
EST.

KEYWORDS
Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
Eukaryote; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.

ORGANISM

REFERENCE
1 (bases 1 to 529)
Grossman, A., Chang, C. W., Davies, J. J., Harris, E., Hauser, C., Lefebvre,
P., McDermott, J. P., Strager, J., Silflow, C., and Stern, D.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants. Project: 1031

TITLE
Unpublished (2001)

JOURNAL
Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.

COMMENT
Location/Qualifiers
1..529
/organism="Chlamydomonas reinhardtii"
/strain="CC-1690_wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, Stress II (normalized
)_lambda zap II"
/note="Vector: pBluescript II SK-, Site 1: EcoRI; Site 2:
XhoI; Stress condition II library, constructed by John
Davies and Jeffrey McDermott, comblines cDNAs from CC-1690

FEATURES
Source

cells grown to mid-log phase in TAP (NH₄⁺ - containing) and shifted to TAP - NO₃⁻ (24hrs): H2 production conditions (0, 12hr, 24hr) see Mellis et al. (2000) Plant Phys. 122: 127-135; TAP + H2O2 (1, 12, 24 hr); TAP + sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr). PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda Zap II (Stratagene) in the EcoRI (5') and XhoI (3') sites. phiscript II SK- plasmids were excised from the lambda Zap clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome Research 6: 791-806."

BASE COUNT 103 a 226 c 123 g 77 t

Query Match 1.4% Score 22: DB 13: Length 529:
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 22: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 983 GCAGTGTGGCGTGGCGCG 1004
Db 396 GCACTGTGGCGTGGCGCG 375

RESULT 9 642 bp mRNA linear EST 25-FEB-2002
BM600965
LOCUS 17000687067149 A.Gam.ad.cDNA.blood1 Anopheles gambiae cDNA clone
DEFINITION 1600449680120 5', mRNA sequence.

ACCESSION BM600965
VERSION BM600965.1 GI:18899069
KEYWORDS EST.
SOURCE African malaria mosquito.
ORGANISM Anopheles gambiae

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.

REFERENCE 1 (bases 1 to 642)

AUTHORS Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab

TITLE Cclera Anopheles gambiae EST project

JOURNAL Unpublished (2002)

COMMENT Contact: Holt R.A.

Celera Genomics

45 W. Gude Dr., Rockville, MD 20850, USA

Tel: 2404533151

Fax: 2404534580

Email: HoltRA@celera.com

Plate: NU0100481L row: M column: 02

Seq primer: M13 Reverse.

FEATURES Location/Qualifiers

1..642

/organism="Anopheles gambiae"

/strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"

/db_xref="taxon:7165"

/clone_lib="A.Gam.ad.cDNA.blood1"

/dev_stage="Adult"

/lab_host="DH10b"

/note="Vector: pSport1; Site1: SalI; Site2: NotI; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen 24

hours after human blood feeding. cDNA inserts >500 bp

cloned directionally into pSport 1. Not I site is

Clones available through the Malaria Research and

Reference Reagent Resource Center (www.malaria.mr4.org)"

BASE COUNT 135 a 216 g 98 t

ORIGIN

Query Match 1.4% Score 22: DB 13: Length 642:
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 22: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 983 GCAGTGTGGCGTGGCGCG 1004
Db 147 GCACTGTGGCGTGGCGCG 168

RESULT 10 662 bp DNA linear GSS 02-NOV-2001
AG049786
LOCUS Pan troglodytes DNA, clone: PTB-030A07.R, genomic survey sequence.

DEFINITION AG049786
ACCESSION AG049786.1 GI:16586678

VERSION GSS.

KEYWORDS Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male

SOURCE BAC Library clone:PTB-030A07.R.

ORGANISM

REFERENCE Pan troglodytes
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

1

Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,

Totoki,Y., Watanabe,H. and Sakaki,Y.

BAC end sequences of library PTB

Unpublished

2 (bases 1 to 662)

Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,

Totoki,Y., Watanabe,H. and Sakaki,Y.

Direct Submission Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou,Tsukuba-City, Ibaraki, Japan 305-8565, Japan

(E-mail:chimbese@gsr.riken.go.jp, URL:http://hpg.gsc.riken.go.jp/,

Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB. This BAC end

was generated during the R&D process and may have higher chance of

clone tracking errors.

PRIMERS

Sequencing: M13Rev

LIBRARY Vector : pKS145

R.Site 1 : SacI

R.Site 2 : SacI.

Location/Qualifiers

1..662

/organism="Pan troglodytes"

/db_xref="taxon:9598"

/clone="PTB-030A07.R"

/sex="male"

/cell_type="lymphoblast"

/clone_lib="PTB Chimpanzee Male BAC Library"

BASE COUNT 197 a 118 c 140 g 206 t 1 others

ORIGIN

Query Match 1.4% Score 22: DB 17: Length 662:
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 22: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 307 TTGATTTCACAAAGAAGATG 328

Db 345 TTGATTTCACAAAGAAGATG 366

RESULT 11 369 bp DNA linear GSS 05-MAR-2001

AZ884788
LOCUS RPCI-23-182A5.TV RPCI-23 Mus musculus genomic clone RPCI-23-182A5,

DEFINITION DNA sequence.

ACCESSION AZ884788

VERSION AZ884788.1 GI:13203733

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 369)
 AUTHORS Zhao, S., Nierman, W., Feldblum, T., Malek, J., Shatsman, S., Akirret, B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P., and Fraser, C.M.
 TITLE Mouse BAC End Sequences from Library RPCI-23
 JOURNAL Unpublished (1999)
 COMMENT Other_GSSS: RPCI-23-182A5.TU
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (<http://www.chori.org/bacpac/orderingframe.htm>). BAC end page: http://www.tigr.org/cdb/bac_ends/mouse/bac_end_intro.html
 Plate: 182 row: A column: 5
 Seq primer: T7
 Class: BAC ends.

FEATURES
 source Location/Qualifiers
 1..369
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-23-182A5"
 /clone_1lb="RPCI-23"
 /sex="Female"
 /lab_host="DH10B"
 /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

BASE COUNT 97 a 76 c 86 g 110 t

ORIGIN

Query Match 1.3%; Score 21; DB 17; Length 369;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 484 TTCTGTGACCCCAAGGGGTG 504
 ||||||||||||||||||||
 121 TTCTGTGACCCCAAGGGGTG 141

Db

RESULT 12 489 bp DNA linear GSS 06-MAR-1999
 LOCUS CITBI-El-2544N3.TF CITBI-El Homo sapiens genomic clone 2544N3, DNA
 DEFINITION
 accession AQ393691
 version AQ393691.1 GI:4364714
 keywords GSS.
 source human.
 organism Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 489)
 Zhao, S., Adams, M.D., Nierman, W., Malek, J., Shizuya, H., Simon, M. and Venter, J.C.
 Title Use of BAC End Sequences from Caltech Libraries for Sequence-Ready Map Building
 unpublished (1997)
 Other_GSSS: CITBI-El-2544N3.TR
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850

REFERENCE 1 (bases 1 to 552)
 AUTHORS Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Rheising, B., Allen, M., Bowers, Y., Peterson, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Rittler, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
 TITLE Public Soybean EST Project
 JOURNAL Unpublished (1999)
 COMMENT Contact: Shoemaker R./Public soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 This clone is available through: Resgen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact: cov@resgen.com web site: www.resgen.com
 High quality sequence stop: 424.

FEATURES
 source Location/Qualifiers
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 /organism="Glycine max"
 /db_xref="taxon:3847"
 /clone="SOYBEAN CLONE ID: Gm-cl066-4149"
 /clone_1lb="Gm-cl066"
 /tissue_type="Leaf and shoot tip, salt stressed, 2 week

BASE COUNT 148 a 97 c 103 g 140 t 1 others

ORIGIN

Query Match 1.3%; Score 21; DB 17; Length 489;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1220 ATGAGAGTTCCTGCTTCCA 1240
 ||||||||||||||||||||
 441 ATGAGAGTTCCTGCTTCCA 421

Db

RESULT 13 552 bp mRNA linear EST 19-NOV-2001
 LOCUS BM085578
 sa126g11.y1 Gm-cl066 Glycine max cDNA clone SOYBEAN CLONE ID:
 Gm-cl066-4149 5' similar to TR:Q9SE97 Q9SE97 FORMIN-LIKE PROTEIN
 AHFL.: mRNA sequence.
 accession BM085578
 version BM085578.1 GI:16996206
 keywords EST.
 source soybean.
 organism Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseolae;
 Glycine.

old seedling"
/lab_host="DH10B"
/note="Vector: Bluescript II SK+; Site_1: EcoRI; Site_2: XhoI. The cDNA library was constructed from mRNA isolated from unexpanded leaves and the shoot tips of 2 week old seedling from the cultivar Williams. The 2 week old seedlings were salt stressed in a solution of 500mM NaCl for 3 days prior to harvesting. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

BASE COUNT 132 a 144 c 135 g 141 t
ORIGIN

Query Match 1.3%; Score 21; DB 13; Length 552;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 984 CAGTGTGGCGGTGGCGCCG 1004
|||||
Db 89 CAGTGTGGCGGTGGCGCCG 69

RESULT 14
BJ030774 564 bp mRNA linear EST 05-DEC-2001
LOCUS BJ030774 N1BB Mochii normalized Xenopus neurula library Xenopus
DEFINITION laevis cDNA clone XL005C01 5', mRNA sequence.
ACCESSION BJ030774
VERSION BJ030774.1 GI:17377868
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 564)
Kitsayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-I, T. and Kohara, Y.
Expressed genes in X. laevis embryo
Unpublished (2001)
Contact: Tadasu Shin-I
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.
Location/Qualifiers
l. 564
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XL005C01"
/clone_lib="N1BB Mochii normalized Xenopus neurula library"
/tissue_type="whole embryo"
/dev_stage="stage 15"
/note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs were oligo-dT primed and directionally cloned. Staging according to Nieuwkoop and Faber. Library is substracted and was constructed by N. Garrett and A.M. Zorn. (Wellcome/CRC Institute)."

BASE COUNT 138 a 148 c 136 g 142 t
ORIGIN

Query Match 1.3%; Score 21; DB 13; Length 564;
Best Local Similarity 100.0%; Pred. No. 28;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 GATGCTGGCCAGTATACCTGC 270
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Db 178 GATGCTGGCCAGTATACCTGC 198

RESULT 15
BJ032049 571 bp mRNA linear EST 05-DEC-2001
LOCUS BJ032049 N1BB Mochii normalized Xenopus neurula library Xenopus
DEFINITION laevis cDNA clone XL015h03 5', mRNA sequence.
ACCESSION BJ032049
VERSION BJ032049.1 GI:17375617
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 571)
Kitsayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-I, T. and Kohara, Y.
Expressed genes in X. laevis embryo
Unpublished (2001)
Contact: Tadasu Shin-I
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.
Location/Qualifiers
l. 571
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XL015h03"
/clone_lib="N1BB Mochii normalized Xenopus neurula library"
/tissue_type="whole embryo"
/dev_stage="stage 15"
/note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs were oligo-dT primed and directionally cloned. Staging according to Nieuwkoop and Faber. Library is substracted and was constructed by N. Garrett and A.M. Zorn. (Wellcome/CRC Institute)."

BASE COUNT 142 a 142 c 143 g 144 t
ORIGIN

Query Match 1.3%; Score 21; DB 13; Length 571;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 GATGCTGGCCAGTATACCTGC 270
|||||
Db 140 GATGCTGGCCAGTATACCTGC 160

Search completed: July 16, 2003, 15:58:28
Job time : 2750.57 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: July 16, 2003, 15:58:34 ; Search time 4764.75 Seconds

(Without alignments)

3255.331 Million cell updates/sec

Title: US-09-917-265-62

Perfect score: 2804

Sequence: 1 MHPOQLVISMFLVLASPL.....HAFRIRAVTINRMXYLNSS 533

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 1451402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+pn2.model -DEV=x1h
-O/cgn2.1/USPTO.spool/US09917265/runat_15072003_092106_1601/app_query.fasta.1.3114
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pro -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USRR=US09917265.@CCN_1_11328_4runat_15072003_092106_1601 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGADPOP=10 -XGAPEXT=0.5 -FCADPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
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27: em_sts:*
28: em_un:*

29: em_vi:*
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31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rdd:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|--------------|---------------------|
| 1 | 2443 | 87.1 | 1626 | 12 AF401989 | AF401989 Synthetic |
| 2 | 2393.5 | 85.4 | 1623 | 6 AR091394 | AR091394 Sequence |
| 3 | 2393.5 | 85.4 | 6139 | 6 AR091393 | AR091393 Sequence |
| 4 | 2313.5 | 82.5 | 1560 | 6 AR091395 | AR091395 Sequence |
| 5 | 1764 | 62.9 | 990 | 6 AR151071 | AR151071 Sequence |
| 6 | 1764 | 62.9 | 990 | 6 E15017 | E15017 Canine mRNA |
| 7 | 1751 | 62.4 | 1015 | 4 CFU49100 | U49100 Canis fam1 |
| 8 | 1731 | 61.7 | 990 | 6 AR151061 | AR151061 Sequence |
| 9 | 1697 | 60.5 | 1669 | 12 AF411293 | AF411293 Synthetic |
| 10 | 1658 | 59.1 | 4522 | 6 AX076209 | AX076209 Sequence |
| 11 | 1658 | 59.1 | 4522 | 6 AX076476 | AX076476 Sequence |
| 12 | 1657 | 59.1 | 990 | 6 AX076200 | AX076200 Sequence |
| 13 | 1657 | 59.1 | 990 | 6 AX076482 | AX076482 Sequence |
| 14 | 1655 | 59.0 | 990 | 6 FCU83184 | U83184 Felis catus |
| 15 | 1643 | 58.6 | 1006 | 4 FC1112P40 | Y07762 F. catus MRN |
| 16 | 1567 | 55.9 | 990 | 6 AX154603 | AX154603 Sequence |
| 17 | 1557 | 55.5 | 984 | 6 AX154600 | AX154600 Sequence |
| 18 | 1553 | 55.4 | 1058 | 6 EC1112P40 | Y11129 Equus caball |
| 19 | 1527 | 54.5 | 993 | 4 CEU57752 | U57752 Cervus elap |
| 20 | 1515 | 54.0 | 1012 | 4 BTU11815 | U11815 Bos taurus |
| 21 | 1515 | 54.0 | 1019 | 6 E35794 | E35794 Process for |
| 22 | 1514 | 54.0 | 1389 | 6 AX084106 | AX084106 Sequence |
| 23 | 1512 | 53.9 | 984 | 6 AX154599 | AX154599 Sequence |
| 24 | 1511 | 53.9 | 984 | 4 AF004024 | AF004024 Ovis arie |
| 25 | 1511 | 53.9 | 984 | 4 AF209435 | AF209435 Ovis arie |
| 26 | 1511 | 53.9 | 1012 | 4 AF007576 | AF007576 Capra hir |
| 27 | 1504 | 53.6 | 984 | 6 AX154598 | AX154598 Sequence |
| 28 | 1503.5 | 53.6 | 1870 | 6 A92079 | A92079 Sequence 3 |
| 29 | 1502.5 | 53.6 | 2318 | 9 HUMNKSFP40 | M5290 Human natur |
| 30 | 1501.5 | 53.5 | 987 | 6 AR008950 | AR008950 Sequence |
| 31 | 1501.5 | 53.5 | 987 | 6 AX154633 | AX154633 Sequence |
| 32 | 1501.5 | 53.5 | 987 | 6 BD007070 | BD007070 IL-12 gen |
| 33 | 1501.5 | 53.5 | 987 | 6 BD007076 | BD007076 Gene expr |
| 34 | 1501.5 | 53.5 | 987 | 6 BD007077 | BD007077 Gene expr |
| 35 | 1501.5 | 53.5 | 987 | 6 BD007078 | BD007078 Gene expr |
| 36 | 1501.5 | 53.5 | 987 | 6 128591 | 128591 Sequence 1 |
| 37 | 1501.5 | 53.5 | 1007 | 6 AF180563 | AF180563 Homo sapi |
| 38 | 1501.5 | 53.5 | 1018 | 6 AR052857 | AR052857 Sequence |
| 39 | 1501.5 | 53.5 | 1399 | 6 AR091391 | AR091391 Sequence |
| 40 | 1501.5 | 53.5 | 1399 | 6 HUMCPLP40 | M65272 Human cytot |
| 41 | 1501.5 | 53.5 | 2362 | 6 AR082684 | AR082684 Sequence |
| 42 | 1501.5 | 53.5 | 2362 | 6 AR122960 | AR122960 Sequence |
| 43 | 1501.5 | 53.5 | 2362 | 6 128325 | 128325 Sequence 1 |
| 44 | 1501.5 | 53.5 | 2362 | 6 189770 | 189770 Sequence 1 |
| 45 | 1493.5 | 53.3 | 1080 | 9 MMU19841 | U19841 Macaca muli |

ALIGNMENTS

RESULT 1

AF401989 1626 bp mRNA linear SYN 14-FEB-2002
 DEFINITION Synthetic construct single chain interleukin-12 mRNA, complete cds.
 ACCESSION AF401989
 VERSION AF401989.1 GI:18656516
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
 11770992
 2 (bases 1 to 1626)
 McMonagle, E.L.J., Taylor, S., van Zuijlen, H., Sanders, L.,
 Argyle, D.J., Onions, D.E., Hopkins, C.A., Logan, N.A., Bain, D.,
 Production of biologically active equine interleukin 12 through
 baculovirus expression systems
 Equine Vet. J. 33 (7), 693-698 (2001)
 21626920
 2 (bases 1 to 1626)
 McMonagle, E.L.J., Taylor, S., Keanie, L.J., Hopkins, C.A., Logan, N.A.,
 Argyle, D.J., Onions, D.E., and Nicolson, L.,
 Submitted (24-JUL-2001) Veterinary Pathology, Glasgow Veterinary
 School, Bearsden Rd, Glasgow G61 1QH, UK
 Location/Qualifiers
 1. 1626
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 1. 1626
 /note="derived from Equus caballus: N-terminal p40 subunit
 linked by (Gly4Ser)3 linker to signal peptide deleted p35
 subunit"
 /codon_start=1
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 /db_xref="GI:18656517"
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 GSSDPGVGCAATLSAEVSYDDREIKRYVECGESACPAEESLPIETIVDAVHK
 LKENTTSFTRIDITKDPKNIQLKPKNSROYSEWEPETWSTHSESLTFSI
 QVQGRKKERKDLFMDERTSATVCHKGQILVQARDRYSSSEMAVSQSGGGS
 GGGGGGGSRNLPATPGPMFCILNSQNLRTVSNLTQARQTLFEYSCTSEID
 HEDLKDKSSTVAACLPLEAPNESCLASREISFTTNGSCILPCKASMTLCSSTI
 EDLKMIOVEFKMAKLIDIPQRIEIDNMTTADKIMQALNENSETVPOKPSLEGL
 DEYTKRVKLCILHAFRIRAVTINMGVLNAS"
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 15. 987
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 988..1032
 /note="linker"
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 1033..1611
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 primer_bind
 complement(1612..1626)
 BASE COUNT 429 a 425 c 427 g 345 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 4.38e-214 Length: 1626
 Score: 2443.00 Matches: 463
 Percent Similarity: 91.13% Conservative: 30
 Best Local Similarity: 85.58% Mismatches: 40
 Query Match: 87.13% Indels: 8
 Gaps: 1
 US-09-917-265-62 (1-533) x AF401989 (1-1626)
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 Db 1 ATGGGTACCAACGAGTGGTCTCTCTGTTTCCCTGTTTGGTGGGTCTCCCTC 60

QY 21 MetaLAlleTrpGluLeuGluLysAspValTyrValValGluLeuAspTrpHisProasp 40
 Db 61 ATGGCATATGAGCACTGAGAAAGATGATGATGATGATGATGATGATGATGATGAT 120
 QY 41 AlaProGlyGluMetValValLeuThrCysHisThrProGluGluAspAlaLeuThrTrp 60
 Db 121 GCCCTGGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
 QY 61 ThrSerAlaGlnSerSerGluValLeuGluGlySerGlyValThrLeuThrIleGlnValIys 80
 Db 181 ACCTCGCCCAAGCAATAGAGTCTAGGCTTGGCAAAACCTTACCATTCACATGCAAA 240
 QY 81 GluPheGlyAspAlaGlyGlnTyrThrCysHisLysGlyGlyLysValLeuSerArgSer 100
 Db 241 GAGTTGGAGATGCTGGCTGATACCTGTCACAAAGAGGAGGAGGATCTGACCATCT 300
 QY 101 LeuLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGln 120
 Db 301 CACCTGCTCTTACACAGAGCAATGCAATTTGTCACGATTTTAAAGACCAAG 360
 QY 121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
 Db 361 AAAGATCCAAAATAAGACCTTTCTAAATCTGAGCAAGAAATTATTCGGACGTTTC 420
 QY 141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerArg 160
 Db 421 ACATGCTGTGCTACACAGCAATCAGTACTGATTTGAAATTCAGTCAAAAGACGAGA 480
 QY 161 GlyPheSerAspProGluGlyValTyrThrCysGlyAlaValThrLeuSerAlaGluArgVal 180
 Db 481 GGTCTCTGTGACCCCGAGGGGTGACGTGTGACGACGACGACACTCTCCGACAGAGGCTC 540
 QY 181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
 Db 541 AGCGTGCACGACAGGATATTAAGATGACGAGTGAAGTGAAGTGAAGTGAAGTGAAG 600
 QY 201 ProSerAlaGluGluSerLeuProIleGluValValAlaAspAlaIleHisLysLeuLys 220
 Db 601 CCGCGCGCGAGAGAGCTCCCATTCAGATGCTGATGATGCTGATGATGATGATGATGAT 660
 QY 221 TyrGluAsnTyrTrpSerSerPhePheIleArgAspIleIleLysProAspProThr 240
 Db 661 TATGAAACTACACACAGGCTCTTCTATGAGGACATCATCAACACGACCCGCAAG 720
 QY 241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
 Db 721 AACCTGCAGCTGAAGCATTAAAGAAATTCGCGAGGTGAGTCACTGAGGTGAGTCA 780
 QY 261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGly 280
 Db 781 GAGACCTGGAGACACCCACATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
 QY 281 LysAsnAsnArgGluLysLysAspArgLysCysValAspLysThrSerLysValVal 300
 Db 841 AAGCAACAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 900
 QY 301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerTrp 320
 Db 901 TGCACACAGATGACGATCCGCTGTCACAGGACGAGGACGCTACATCACTGCTGG 960
 QY 321 SerAspTrpAlaSerValSerCysSerGlyGly-----Gly 332
 Db 961 AGCGAATGGCAATCCCTATCTGCACTGATGAGGCTGCTGCTGCTGCTGCTGCTGCTG 1020
 QY 333 GlyGlyGlySerArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeu 352
 Db 1021 GGGGGGGGATCTAAGAACTCCCAACAGCCACAGGCGGAGGATGCTTCCAGTCCCTC 1080
 QY 353 AsnHisSerGlnThrLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThr 372
 Db 1081 AACCAATCCCAAAACCTGCTGAGGACCGTCACAAACAGCCTTCAAGAGGACGAGCA 1140
 QY 373 LeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLys 392

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Db 1141 CTAGAAATTCTACTCCGCACTTCTGAAAGACATGATCATGAGATATCACAAAAGACAG 1200
Qy 393 ThrsrThrValGluValAcylsLeuProLeuGluLeuThrMetAsnGlySerCysLeuAla 412
Db 1201 AGCAGACAGCTGGCGGCTCCCTCCCTCCCTGAACTCCCGGAAAGAGATTGCGTGGCT 1260
Qy 413 SerArgGluLeuSerLeuLeuThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPhe 432
Db 1261 TCACAGACATCTCTTTCATTAATAATGGAGATGGCTTGACCCCGGAAAGGCTTCTTCT 1330
Qy 433 MetThrValLeuCysLeuSerSerLeuTyrgLysAspLeuLysMetTyrgLysGluPhe 452
Db 1321 ATGATGACCGCTGCTGCCCTTACACACATCTATGAGACTTGAAGATGTACACAGTGGAGTTC 1380
Qy 453 LysAlaMetAsnAlaLysLeuLeuMetLysProLysArgGlnLeuPheLeuAspGlnAsn 472
Db 1381 AAGGCGATGATGCCAAGCTGTGATGATGATCTCAGAGCGAGATCTTTCTGATGACAC 1440
Qy 473 MetLeuThrAlaLeuAspGluLeuGlnAlaLeuAsnPheAsnSerValThrValPro 492
Db 1441 ATGCTACAGACCGATTGACAAAGCTGATCCAGCGCTGACTTCAACAGTGGAGACTGTCCA 1500
Qy 493 GlnLysSerSerLeuGluGluProAspPheTyrgLysThrLysIleLysLeuCysIleLeu 512
Db 1501 CAAAGCCCTCCCTTGAGAGACTGATTTTATAAAGCTAAAGTCAAGCTCTGCATCCTT 1560
Qy 513 LeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetLeuSerTyrgLeuAsnSer 532
Db 1561 CTTCATGCGCTTGAGATCCCGCAGTGACCATCAACAGATGATGGCTATCGAATGCT 1620
Qy 533 Ser 533
Db 1621 TCC 1623

RESULT 2
AR091394 AR091394 1623 bp DNA linear PAT 07-SEP-2000
LOCUS Sequence 9 from patent US 5994104.
DEFINITION AR091394
ACCESSION AR091394
VERSION AR091394.1 GI:10018149
KEYWORDS
ORGANISM Unknown.
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 1623)
AUTHORS Anderson, R. James., Prentice, H. Grant. and Macdonald, I. Duncan.
TITLE Interleukin-12 fusion protein
JOURNAL Patent: US 5994104-A 9 30-NOV-1999;
FEATURES
location/Qualifiers
source 1..1623
BASE COUNT 449 a 393 c 408 g 373 t
ORIGIN

Alignment Scores:
Pred. No.: 1,49e-209 length: 1623
Score: 2393.50 Matches: 456
Percent Similarity: 89.46% Conservative: 28
Best Local Similarity: 84.29% Mismatches: 48
Query Match: 85.36% Indels: 9
DB: 6 Gaps: 2

US-09-917-265-62 (1-533) x AR091394 (1-1623)

Qy 1 MethHisProGlnGlnLeuValIleSerTyrgPheSerLeuValLeuLeuAlaSerProLeu 20
Db 1 ATGGGTCCACACAGATGGTGCATCTTGCTTTCCCTGGTGTTCGCGATCTCCCTC 60
Qy 21 MetAlaIleTyrGluLeuGluLysAspValTyrgValValGluLeuLysPheAsp 40
Db 61 GTGGCCATATGGGAACCTGAAGAAGATGTTTATGTCTGAATTTGATGCTCGGAT 120

Qy 41 AlaProGlyLeuMetValValLeuThrCysHisThrProGluGluAspAspIleThrTrp 60
Db 121 GCCCGTGAGAAATGGTGGTCTTACCTGTGACACCCCTGAGAAGATGGATATCACTGG 180
Qy 61 ThrsrAlaGlnSerSerGluValLeuGlySerCylsTyrgLeuThrIleGlnValLys 80
Db 181 ACCTTGACACAGACACTGAGAGCTTGTAGCGTGGCAAAACCCGTGACCATCAAGTCAAA 240
Qy 81 GluPheGlyAspAlaGlyGlnTyrgThrCysHisLysGlyGlyLysValLeuSerArgSer 100
Db 241 GAGTTTGAGATGCTGGCCAGTACCTGTCTACAAAGAGCGAGGTTCATTAAGCATTTGC 300
Qy 101 LeuLeuLeuLeuIleHisLysLysGluAspGlyIleTyrPheThrAspIleLeuLysGluGln 120
Db 301 CTCTGCTGCTTCCAAAAGGAAGATGGATTTGGTCCACTGATATTTAAAGACACAG 360
Qy 121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrgSerGlyArgPhe 140
Db 361 AAAGAACCCAAAATAAGACCTTTCTAAGATGCGAGGCCAAAGAAATTATTCGACGTTTC 420
Qy 141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerArg 160
Db 421 ACCTGCTGGTGGCTGACGACAATCAGTACGATTGACATTCATTCATAAAGCAGAGA 480
Qy 161 GlyPheSerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgVal 180
Db 481 GGCCTCTTGACCCCGCAAGGGGTGACCTGGCGACCTGCTACACTCTGTGAGAGAGATC 540
Qy 181 ArgValAspAsnArgAspTyrgLysTyrgThrValGluCysGlnGluGlySerAlaCys 200
Db 541 AGAGGGGACAAACAGAGATAT---GAGTACTCACTGAGTGAGTCCAGAGACAGAGCTGCG 597
Qy 201 ProSerAlaGluGluSerLeuProIleGluValValAlaAspAlaIleHisLysLeuLys 220
Db 598 CCAAGCTGTGAGAGAGTGTGCCCATTTGAGTGTGATGGCTTCCCAACCTCAAG 657
Qy 221 TyrgLysAsnTyrgThrSerSerPhePheIleArgAspIleIleLysProAspProProThr 240
Db 658 TATGAAACATACACACACACTTCTTATCATGAGCACTCATCAACCTGAGCCGCCAAG 717
Qy 241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTyrgLysTyrgPro 260
Db 718 AACTTGACAGTGAAGCCATTAAAGAAATTTCGCGAGGTGAGGACACTGGAGTACCT 777
Qy 261 AspThrTrpSerThrProHisSerTyrgPheSerLeuThrPheCysIleGlnAlaGlnGly 280
Db 778 GACACCTGGAGTACTCCACATTTCTTCTCTCCCTGACATTCGCTTCAGAGTCCAGGGC 837
Qy 281 LysAsnAsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysVal 300
Db 838 AAGACGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGAGCAAGACCTAGCCACGCTATC 897
Qy 301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrgTyrgSerSerTyrg 320
Db 898 TGCCCGCAAAATGCCACCATTTAGCGTGGCGGCGCAGAGACCGTACATCATCTCATCTGG 957
Qy 321 SerAspTrpAlaSerValSerCysSerGlyGly-----Gly 332
Db 958 AGCGAAATGGGATCTGTGGCTTCAGTGGTGGCGGTGAGACCGCGGTGGCGGAGAGCGGG 1017
Qy 333 GlyGlyGlySerArgAsnLeuProThrProThrProSerProGluMetPheGlnCysLeu 352
Db 1018 GTGGCGCGCAGCAGAAACCTCCCTGGCCACTCCAGACCCAGAGAAATGTTCCCATGCTT 1077
Qy 353 AsnHisSerGlnThrLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThr 372
Db 1078 CACCACATCCCAAAACCTGCTGAGGCGCGCTCAGCAACATGCTCCAGAAAGCGCAGCAAACT 1137
Qy 373 LeuGlnLeuTyrgSerCysThrSerGlnGluIleAspHisGlnLysPheThrLysAspLys 392
Db 1138 CTAGAAATTTATGCTTGCACCTTCTGGAAGATGATCATGATGATATCACAAAGATAAA 1197
Qy 393 ThrsrThrValGluValAcylsLeuProLeuGluLeuThrMetAsnGlnLysCysLeuAla 412

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Db 1198 ACCAGACAGTGGAGCCCTGTTTACATTGGAATTAACCAAGATAGAGTTGCCATAAT 1257
QY 413 SerArgIuIIeserleuIethrasngIysSerCysLeuAlaSerGlyLysAlaSerPhe 432
Db 1258 TCACAGAGACACCTCTTCACTAATATGGAGTGGCTGCTGCCCAAGAAAGACCTCTTTT 1317
QY 433 MetThrValLeuCysLeuSerSerIleTyrgLysPleuLysMetTyrgLysMetGluPhe 452
Db 1318 ATGATGGCCCTGCTGCTAGTATGATTTATGAAGACTTGAAGATGATACCAAGGTGAGTTC 1377
QY 453 LysAlaMetAsnAlaLysLeuMetAsnProLysArgGlnIlePheLeuAspGlnAsn 472
Db 1378 AAGACCATGATGCAAGCTTCGTGATGATCCCAAGAGCAGATCTTTCTAGATCAAAAC 1437
QY 473 MetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValPro 492
Db 1438 ATGTCGGCAGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1497
QY 493 GlnLysSerSerLeuGluLysProAspPheTyrgLysThrLysIleLysLeuCysIleLeu 512
Db 1498 CAAAAATCCCTCCCTTGAAGAACCGGATTTTATAAACTAAATCAAGCTCTGCTATCTT 1557
QY 513 LeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrgLeuAsnSer 532
Db 1558 CTTCATGCTTTCAGAAATCGGCGAGTGCATTTGACAGATGACGAGCTATCTGAAATGCT 1617
QY 533 Ser 533
Db 1618 TTC 1620

RESULT 3
AR091393 6139 bp DNA linear PAT 07-SEP-2000
LOCUS Sequence 7 from patent US 5994104.
DEFINITION AR091393
ACCESSION AR091393
VERSION AR091393.1 GI:10018148
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 6139)
AUTHORS Anderson,R.James., Prentice,H.Grant, and Macdonald,I.Duncan.
TITLE Interleukin-12 fusion protein.
JOURNAL Patent: US 5994104-A 7 30-NOV-1999;
FEATURES
source location/Qualifiers
1..6139
BASE COUNT 1552 a 1538 c 1558 g 1491 t
ORIGIN
Alignment Scores:
Pred. No.: 9..93e-209 Length: 6139
Score: 2393.50 Matches: 456
Percent Similarity: 89.46% Conservative: 28
Best Local Similarity: 84.29% Mismatches: 48
Query Match: 85.36% Indels: 9
DB: 6 Gaps: 2

US-09-917-265-62 (1-533) x AR091393 (1-6139)
QY 1 MetHisProGlnGlnLeuValIleSerTrpPheSerLeuValLeuLeuAlaSerProLeu 20
Db 3222 ATGGGTACACAGAGATGGTGCATCTCTGTTTCCCTGGTTTCTGTCATCTCCCTC 3281
QY 21 MetAlaIleTrpGluLeuGlnLysAspValTyrgValValGluLeuAspTrpPheSerProAsp 40
Db 3282 GTGGCCATATGGGAACATGAAGAAAGATGTTATGTGCTAGAAATGGATGGATTCGGGAT 3341
QY 41 AlaProGlyLysMetValValLeuThrCysHisThrProGlnGlnLysAspTrpIleThrTrp 60
Db 3342 GCCCCTGGAGAAATGTTGCTCCTCACCTGACACACCCCTGAAGAAAGATGTTATCACCTGG 3401

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QY 61 ThrSerAlaGlnSerSerGluValLeuGlnLysGlyLysThrLeuThrIleGlnValLys 80
Db 3402 ACCTTGGACACAGAGAGTGTAGCTCTGACCTGCGCAAAACCTGACCATCCAACTCAAA 3461
QY 81 GluPheGlnLysAlaGlyLysThrCysHisLysGlyLysValLeuSerArgSer 100
Db 3462 GAGTTTGGAGATGCTGGCCAGTACACTTTCACAAAGGAGGAGGAGTTTAAGCCATTGCG 3521
QY 101 LeuLeuLeuIleHisLysLysGlnLysAspGlyIleTrpSerThrAspIleLeuLysGlnGln 120
Db 3522 CTCCTGCTGCTTCACAAAAGAGAGATGGAATTTGGTCCACATGATTTTAAAGGACGAG 3581
QY 121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrgSerLysArgPhe 140
Db 3582 AAAGAACCCAAAATAAGACCTCTTAAATCATCGAGGCCCAAAATTAATTCGTGAGCTTTC 3641
QY 141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArg 160
Db 3642 ACTCTGCTGGCTGACGCAATCACTACTGATTTGACATTTGACGTCAAAAGCAGCAGA 3701
QY 161 GlyPheSerAspProGlnGlnValThrCysGlyAlaValThrLeuSerAlaGlnArgVal 180
Db 3702 GGCTCTTTCAGACCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAAGAGAGTTC 3761
QY 181 ArgValAspAsnArgAspTyrgLysTyrgThrValGluCysGlnGlnLysArgLys 200
Db 3762 AGAGGGGACACAAAGAGATAT--GAGTACTGAGTGAATGTCACAGAGAGAGAGTCCCTGC 3818
QY 201 ProSerAlaGlnGlnLysLeuProIleGlnValAlaValAspAlaIleHisLysLeuLys 220
Db 3819 CCAGCTGTGAGAGAGTGTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3878
QY 221 TyrgLysAsnTyrgThrSerSerPhePheIleArgAspIleIleLysProAspProThr 240
Db 3879 TATGAATACTACACACGACGCTTCTCATCAGGACGATCATCAAACTGACCCACCAAG 3938
QY 241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGlnValSerTrpLeuTyrgPro 260
Db 3939 AACTTGCACCTGAAGCATTAAGAAATTTCTGCGAGGTGAGTGCAGCTGGAGATACCTT 3998
QY 261 AspThrTrpSerThrProHisSerTyrgPheSerLeuThrPheCysIleGlnAlaGlnLys 280
Db 3999 GACACCTGAGTACATCCATTCCTACTCTCTGCTGACATTTCTGCTGATGATGATGATGATGATGAT 4058
QY 281 LysAsnAsnArgGlnLysLysAspArgLeuCysValAspLysThrSerAlaLysValVal 300
Db 4059 AAGAGCAGAGAGAGAAAGAAAGATAGACTTTCACAGCAGACCAACCTCACCCGCTCATC 4118
QY 301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrgTrpSerSerSerTrp 320
Db 4119 TGCCGCAAAATGCGCAGCATTAAGCTGCGGCGCCAGGACGCTACTATAGCTCATCTTTGG 4178
QY 321 SerAspTrpAlaSerValSerCysSerGlyGly-----Gly 332
Db 4179 ACGGAATGGGCATCTGTGCGCCGTCGACGTGTGCGGAGTGGAGGCGGCGTGGCGGAAGCGGC 4238
QY 333 GlyGlyGlySerArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeu 352
Db 4239 GGTGGCGCAGCAGAAACCTCCCGCGCCACTCCAGACCCAGAAATGTTCCCATGCTCTT 4298
QY 353 AsnHisSerGlnThrLeuLeuArgAlaValIleSerAsnThrLeuGlnLysAlaArgIleThr 372
Db 4299 CACCACTCCCAAAACCTGCTGAGGGCGCTGACCAACATCTCTCCAGAAAGCCGACAAACT 4358
QY 373 LeuGluLeuTyrgSerCysThrSerGlnGlnIleAsnHisGlnAspIleThrLysAspLys 392
Db 4359 CTAGAAATTTTACCTTGCCTTCTGACAGATTTGATCATGAAGATATGCAAAAGATATAA 4418
QY 393 ThrSerThrValGlnAlaCysLeuProLeuGlnLeuThrMetAsnGlnLysSerCysLeuAla 412
Db 4419 ACCAGACAGTGGAGCGCTGTTTACCATGTGAATTAACCAAGATAGAGAGTGGCTTAAT 4478
QY 413 SerArgIuIIeserleuIethrasngIysSerCysLeuAlaSerGlyLysAlaSerPhe 432

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Db 4479 TCCAGAGACCTCTTCATTAAGTGAAGTGGCTGGCCCTCCAGAAAGACCTCTTT 4538
Oy 433 MetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPhe 452
Db 4539 ATGATGGCCCTGTCCTTACTAGATTATTAAGACCTGGAAGATTCTACAGCTGAGCTTC 4598
Oy 453 LysAlaMetAsnAlaLysLeuLeuMetAsnProLysArgGlnIlePheLeuAspGlnAsn 472
Db 4559 AAGACCATGAATGCCAAACCTTGATGATGATCTTAAGAGCCAGATCTTCTGATCAAAAC 4658
Oy 473 MetLeuThrAlaIleAspGluLeuGlnAlaLeuAsnPheAsnSerValThrValPro 492
Db 4659 ATGCTGCAGATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4718
Oy 493 GlnLysSerSerLeuGluGluProAspPheTyrThrLysIleLysLeuGlnIleLeu 512
Db 4719 CAAAATCTCTCTTGAAGAACCGATTATTAATAAACTAAATCAACCTCTGCATCTT 4778
Oy 513 LeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnSer 532
Db 4779 CTTCATGCTTTCAACAATTCGGGCACTGACTATTGACAGAGTGACAGCTATCTGAATCT 4838
Oy 533 Ser 533
Db 4839 TCC 4841

RESULT 4
AR091395
LOCUS AR091395 1560 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 11 from patent US 5994104.
ACCESSION AR091395
VERSION AR091395.1 GI:10018150
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1560)
AUTHORS Anderson, R.James., Prentice, H.Grant, and Macdonald, I.Duncan.
TITLE Interleukin-12 fusion protein
JOURNAL Patent: US 5994104-A 11 30-NOV-1999;
FEATUERS Location/Qualifiers
source 1..1560
BASE COUNT 443 a 375 c 393 g 349 t
ORIGIN

Alignment Scores:
Pred. No.: 3e-202 Length: 1560
Score: 2313.50 Matches: 439
Percent Similarity: 89.62% Conservat: 27
Best Local Similarity: 84.42% Mismatches: 45
Query Match: 82.51% Indels: 9
Gaps: 2

US-09-917-265-62 (1-533) x AR091395 (1-1560)
Oy 22 AlaIleTrrpGluLeuGluLysAspValTyrValValGluLeuAspTrrpHisProAspAla 41
Db 1 GCCATTATGGGAACGGAAGAGATGTTATGCTAGATTGATTGCTATCCGATGCC 60
Oy 42 ProGluGluMetValIleuLeuThrCysHisThrProGluGluAspAspIleThrTrrpThr 61
Db 61 CCTGGAAGAATCGTGCTCTCTACCTGTGACACCCCTGGAAGAGATGATATACCTGGAGCC 120
Oy 62 SerAlaGlnSerSerGluValLeuGluLysSerGlySerGlyThrLeuThrIleGlnValLysGlu 81
Db 121 TTGAGACCAAGCACTGAGGTCTTAGGCTCTGCAAAACCCGACATCCAGTCAAAAG 180
Oy 82 PheGlyAspAlaGlnIleTrrpThrCysHisLysGlyLysValLeuSerArgSerLeu 101
Db 181 TTTCAGATGCTGGCCAGTACACTGCTGCACAAAGAGCGAGGTTCCTAAGCCATTCCGCTC 240

Oy 102 LeuLeuIleHisLysLysGluAspGlyIleTrrpSerThrAspIleLeuLysGluGlnLys 121
Db 241 CTGCTGCTTTCACAAAAGGAAGATGGAATTTTGCTCACTGATATTTTAAAGACCAAGAAA 300
Oy 122 GluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThr 141
Db 301 CAACCCAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTAATTCGACGCTTTCACC 360
Oy 142 CysTrrpTrrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGly 161
Db 361 TGTCTGTGCTGACACATCATGACTATTGACATTCAGTGTCAAAAGACGCGAGGC 420
Oy 162 PheSerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArg 181
Db 421 TCTTCTGACCCCAAGGGGTGACGTGCGGAGCTGTACACTCTTCTCCAGAGAGTCCAGA 480
Oy 182 ValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysPro 201
Db 481 GGGGACAAACAGAGATAT--GAGTACACAGTGGAGTGCCAGAGAGACAGTCCCTGCCCA 537
Oy 202 SerAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyr 221
Db 538 GCTGCTGAGGAGAGCTGCCCATGAGGATGATGATGATGATGATGATGATGATGATGAT 597
Oy 222 GluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProThrAsn 241
Db 598 GAAACCTACACCAGAGCTTCTTCATCAGGAGCATCATCAAACTGACCCACCAAGAAC 657
Oy 242 LeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrrpGluTrrpProAsp 261
Db 658 TTGAGCTGGAAGCCATTAAAGATTCTCGGCGAGTGGAGTGCAGCTGGAGTAACCTGAC 717
Oy 262 ThrTrrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnLys 281
Db 718 ACCTGGAGTACTCCACATTCCTTACTTCCCTCGAGATTCTGCTTCAGTCCAGTCCAGGGCAAG 777
Oy 282 AsnAsnArgGluLysLysAspArgLeuGlyValAspLysThrSerAlaLysValValLys 301
Db 778 ACCAAGACAGAAAGAAAGATAGAGTCTTTCACAGGACAAAGACTTCAGCCAGCTCATCTGC 837
Oy 302 HisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTrrpSerSerTrrpSer 321
Db 838 CGCAAAATGCCAGCATTAAGCTGGCGGCCGACGAGCCGCTACTATAGCTCATCTTGAGAC 897
Oy 322 AspTrrpAlaSerValSerCysSerGlyLys-----GlyGly 333
Db 898 GAATGGGATCTGCTCCCTGCGAGTGTGCGGTGGAAGCGCGGTGGCGGAAGCGCGGT 957
Oy 334 GlyGlySerArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsn 353
Db 958 GCGGCGACAGAAACCTCCCTGGCCACTCCAGACCCAGAGATGTTCCCATGCTTTCAC 1017
Oy 354 HisSerGlnThrLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeu 373
Db 1018 CACTCCCAAAACCTGCTGAGGGCGTCCAGCAACATGCTCCAGAAAGCCAGCAAAACCTCTA 1077
Oy 374 GluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThr 393
Db 1078 GAATTTTACCTTTCGACTTTCGAAGAGATTGATCTGAAGATATCCAAAGAGATAAAACC 1137
Oy 394 SerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGlnSerCysLeuAlaSer 413
Db 1138 AGCAGAGCGAGGCGCTGTTTACCATTTGAATTAACCAAGATGAGAGTGGCTTAATTC 1197
Oy 414 ArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMet 433
Db 1198 AGAGAGACCTCTTCATTAACATAATGGAGTGGCTCGGCTCCAGAAAGACCTCTTTATG 1257
Oy 434 ThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLys 453
Db 1258 ATGCGCTGTGCTTACTAGATTATTAAGAAGATTGAAGATGTACAGGTGCTCAAG 1317
Oy 454 AlaMetAsnAlaLysLeuLeuMetAsnProLysArgGlnIlePheLeuAspGlnAsnMet 473

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Db 1318 ACCATGAATGCAGAGCTTCGATGATCCCTAGAGAGAGATCTTTCAGATCAAAACATG 1377
Qy 474 LeuThrAlaIleAspGluLeuGlnAlaLeuAsnPhenSerValThrValProGln 493
Db 1378 CTGGCAGATTATTCATGACTGATGACAGCCCTGATTTCAACAGTGAAGTGCACAA 1437
Qy 494 LysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuGlnIleLeu 513
Db 1438 AATTCCTCCCTGAGAACCGGATTTTATATAAATCAAGCTCTGATCTTCTT 1497
Qy 514 HisAlaPheArgIleArgAlaValThrIleAsnArgMetCysTyrIleAsnSer 533
Db 1498 CATGCTTTCAGAAATTCGGGACGATGACATTCAGACAGATGACAGATCTGATGCTCC 1557

RESULT 5
ARI51071
LOCUS ARI51071 990 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 11 from patent US 6231850.
ACCESSION ARI51071
VERSION ARI51071.1 GI:15117121
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 990)
AUTHORS Okano, F., Satoh, M. and Yamada, K.
TITLE Canine interleukin 12
JOURNAL Patent: US 6231850-A 11 15-MAY-2001;
FEATURES
Location/Qualifiers
source 1..990
/organism="unknown"

BASE COUNT 279 a 244 c 249 g 218 t
ORIGIN

Alignment Scores:
Pred. No.: 3,34e-152 Length: 990
Score: 1764.00 Matches: 329
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 62.91% Indels: 0
DB: 6 Gaps: 0

US-09-917-265-62 (1-533) x ARI51071 (1-990)
Qy 1 MethHisProGlnGlnLeuValIleSerTyrPheSerLeuValIleuAsnLaserProLeu 20
Db 1 ATGCATCTCCAGAGAGTTGTCATCTCTGTTTCCCTGTTTCTGCGCTGCCCTC 60
Qy 21 MetAlaIleTrrPgluLeuGluLysAspValTyrValValGluLeuAspTrrHisProAsp 40
Db 61 ATGGCCATATGGGAACTGGAGAAAGATGTTATGTGTGAGAGTTGAGTGGACACCTGAT 120
Qy 41 AlaProGluGluMetValValLeuThrCysHisThrProGluGluAspIleThrTrp 60
Db 121 GCCCCCGGAGAAATGTTGCTCTCCCTCCATACCCCGAGAGAGATGACATCACTTGG 180
Qy 61 ThrSerAlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
Db 181 ACCTGAGCGCAGAGAGTGAAGTCCAGTCTCTGTAAGCTCTGACCATCCAGTCAAA 240
Qy 81 GluPheGlyAspAlaGlyIleTyrThrCysHisLysGlyGlyLysValLeuSerArgSer 100
Db 241 GAATTTGGAGATGCTGGCCAGTATACCTCCATAAAGAGAGCAAGGTTCTGAGCCGCTCA 300
Qy 101 LeuLeuLeuIleHisLysLysGluAspGlyIleTrrPserThrAspIleLeuLysGluGln 120
Db 301 CTCTGTTGATTCACAAAAGAGAGATGGAATTTGGTCCAGTATATCTTAAAGGACAG 360
Qy 121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
Db 361 AAGAATCCAAAATAAGATCTTTCGAATATGTGAGGCAAGAAATTTATCTGACGCTTTC 420

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Qy 141 ThrCysTrrPrrLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArg 160
Db 421 ACATGCTGGTGGCTGACGGCAATCAGTACGATTTGAATTCAGTGTCAAAATACAGACA 480
Qy 161 GlyPheSerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgVal 180
Db 481 GGCCTCTGACCCCAAGAGGGGTGACATGAGAGAGTGAACATTTTCACAGAGAGGCTC 540
Qy 181 ArgValAspAsnArgAspTrrLysLysTyrThrValGluGlnGlnGlnGlnSerAlaCys 200
Db 541 AGATGGACACACGGGATTTATAGAGTACACGTGAGTGTAGAGAGGAGGAGGAGTCTGC 600
Qy 201 ProSerAlaGluGluSerLeuProIleGluValValAlaAspAlaIleHisLysLeuLys 220
Db 601 CCTCTCCGAGAGAGAGCTACCCATCAGAGTGTGTGTGATCTTTCACAAAGCTCAAG 660
Qy 221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProThr 240
Db 661 TATGAAAGCTACACCCAGAGCTTCTTCATCAGAGATCATCAAAACAGACCCACACA 720
Qy 241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrrPgluTrrPro 260
Db 721 AACCTCAGCTGAGAGCCATTTGAAAATTTCTCGGACGTGAGGTCAAGTGGAAATACCCC 780
Qy 261 AspThrTrrPserThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGly 280
Db 781 GACACCTGGAGAGACCCACATTCCTACTCTCTCCCTGACATTTTGCATACAGGCCAGGGC 840
Qy 281 LysAsnAsnArgGluLysLysAspArgLeuGlyCysValAspLysThrSerAlaLysVal 300
Db 841 AAGAACAAATAGAGAAAGAAAGATAGACTGTGCTGAGCAAGACCTCACCAAGGTCGTG 900
Qy 301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTrrSerSerSerTrr 320
Db 901 TGCCACAGAGATGCCAAGATCCGCTGCAAGCCGAGACCCGCTACTATATGTTCTCTGG 960
Qy 321 SerAspTrrAlaSerValSerCysSer 329
Db 961 AGCGACTGGGCAATCTGTCTCTGCACT 987

RESULT 6
E15017
LOCUS E15017 990 bp DNA linear PAT 28-JUL-1999
DEFINITION Canine mRNA for interleukin 12 40kDa subunit, complete cds.
ACCESSION E15017
VERSION E15017.1 GI:5709700
KEYWORDS JP 1998036397-A/1.
SOURCE
ORGANISM Canis sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 990)
Okano, F.
CANTINE INTERLEUKIN 12 AND ITS PRODUCTION
Patent: JP 1998036397-A 1 10-FEB-1998.
TORYAI IND INC
OS Canis sp. (dog)
PN JP 1998036397-A/1
PD 10-FEB-1998
PF 08-NOV-1996 JP 1996296789
PR 08-NOV-1995 JP 95P 289729, 23-MAY-1996 JP 96P 128104 PT
OKANO FUMIYOSHI
PC C07K14/54, C07H21/04, C12N5/10, C12N15/09, C12P21/02, (C12N5/10, PC
C12R1:91),
PC (C12P21/02, C12R1:91);
CC strandedness: Double;
CC topology: Linear;
FH Key Location/Qualifiers
FH source 1..990
FT /organism="Canis sp."
FT /tissue="liver"
FT CDS 1..990

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| | | | |
|------------|-------------------------------------|---|-----------------|
| QY | 61 | ThSerAlaGlnSerSerGluValIleuGlySerGlyLysThrLeuThrIleGlnValLys | 80 |
| Db | 181 | ACCTGACCCGACAGCAGTGTGAAGTCTTAGTTCTGGTAAACTCTGCACCATCCAAAGTCAA | 240 |
| QY | 81 | GLuPheG1YAspAlaGlyGlnTyrThrCysHisLysG1YGLYysValIleuSerArgSer | 100 |
| Db | 241 | GAAATTGGAGATCCTCGCCAGTATACCTGCGATTAAGAGAGCAAGGTTCTGCAGCCGTCA | 300 |
| QY | 101 | LeuLeuLeuIleHisLysLysGluAspG1YIleTyrSerThrAspIleLeuLysGluGln | 120 |
| Db | 301 | CTCCTGTGATTCACAAAAAGAAAGATGGAATTGGTCCACATGATATCTTAAAGAAACAC | 360 |
| QY | 121 | LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe | 140 |
| Db | 361 | AAAGATCCAAAAATTAAGATCTTTCGAAATGTCAGCAAGAAATTAATTCGTGACCTTTC | 420 |
| QY | 141 | ThrCysTyrTyrPheThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArg | 160 |
| Db | 421 | ACATGCTGTGGCTGCGCCGCAATCACTACTGATTTGAATTCAGTCTCAAAATATACACA | 480 |
| QY | 161 | GlyPheSerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgVal | 180 |
| Db | 481 | GGCTTCTCTGACCCCCCAAGGGTGACATGAGAGCAGTACACTTTCACACAGAGAGGTC | 540 |
| QY | 181 | ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluLysSerAlaCys | 200 |
| Db | 541 | AAGATGGACAAACAGGATTATTAAGAAGTACACAGTGGAGTGTCCAGGAAGCCAGTGGCTGC | 600 |
| QY | 201 | ProSerAlaGluGluSerLeuProIleGluValIleValAspAlaIleHisLysLeuLys | 220 |
| Db | 601 | CCCTGCGCCGAGAGAGCTACCACATCGAGGTGTGTGTGGATGCTTATTCACAAAGCTCAAG | 660 |
| QY | 221 | TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProThr | 240 |
| Db | 661 | TATGAAAACTACACACAGCAGCTTCTTCATCAAGACATATCAAAACCAAGCCACCCACA | 720 |
| QY | 241 | AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerIrrpGluTyrPro | 260 |
| Db | 721 | AACCTGCACGCTAAGCCATGTGAAAAATTTCTCGGCAAGTGGAGTCAAGCTGGGAATAACCCC | 780 |
| QY | 261 | AspThrTyrPsrThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGly | 280 |
| Db | 781 | GACACCTGTGAGCACCCCACTCATCTTCTCTCGACATTTTGGGTACAGGCCACAGGCC | 840 |
| QY | 281 | LysAsnAsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValVal | 300 |
| Db | 841 | AAGAACAATAGAGAAAGAAAGAAATGACTGTCCGTGGACAAACCTCAGCCAAAGTCTGTG | 900 |
| QY | 301 | CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerIrrp | 320 |
| Db | 901 | TGCCACAAAGATGCCCAAGATCCGCTGCAAGCCCGAGACCGCTACTATATTGTAATCTCTGG | 960 |
| QY | 321 | SerAspTrrPalaservalSerCysSer 329 | |
| Db | 961 | AGCGACTGGCATCTGTCTCTGCAGT 987 | |
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| ACCESSION | AR151061 | | |
| VERSION | AR151061.1 | GI:15117111 | |
| KEYWORDS | | | |
| SOURCE | Unknown. | | |
| ORGANISM | Unknown. | | |
| REFERENCE | 1 (bases 1 to 990) | | |
| AUTHORS | Okano, F., Satoh, M. and Yamada, K. | | |
| TITLE | Canine Interleukin 12 | | |
| JOURNAL | Patent: US 6231850-A 1 15-MAY-2001; | | |
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| Query Match: | 61.73% | Indels: | 0 | | |
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| QY | 4 | GINGILNEUVAIIIESETRPHESERLEUVALLEULENIAISERPROLEUMETALALE | 23 | | |
| DB | 10 | CAGAGATGGGCATCTCTTGTTCCCTCGGTTTCTGCGCTCTCCCTCATGGCCATA | 69 | | |
| QY | 24 | TRPSILEUGIULYSASPAVALTYRVALVAGIULENIAASPTPHISPROSPALAPROGLY | 43 | | |
| DB | 70 | TGGGACCTGGAGAAAGATGTTATGTGTGTAAGATTGACTGGCACCCGTATGCCCGGA | 122 | | |
| QY | 44 | GLUWETVALLEUTHRCYSHISTHPRGILGUAASPAIILETHTRPHISERALA | 63 | | |
| DB | 130 | GAATGTGGTCCCTCACCTCCATACCCTCGAAGAAGATGACATCACTGGACCTCACGC | 189 | | |
| QY | 64 | GINSERCIULVALEUGIYSERGILYTHLEUTHLEGILVALYSLUHPHELY | 83 | | |
| DB | 190 | CAGAGCAGTAGAGTCCTAGTCTTGTTAAACCTTCACATCCAGTCAAGATTTTGA | 244 | | |
| QY | 84 | ASPALAGIULNTRYTHRCYSHISLYSGILYLYSVALLEUSERARGSERLEULEN | 103 | | |
| DB | 250 | GATCTGGCCAGATATACCTGCCATTAAGGAGGCAAGCTTGACGCCCTCATCTCTTG | 309 | | |
| QY | 104 | ILEHISLYSGIULSPGLIETPSPETHASPIILEULEYSGILNLYSGILSER | 122 | | |
| DB | 310 | ATTACAAAAAAGAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGATTC | 369 | | |
| QY | 124 | LYSASNLYSILEPHEULEYSCYGIUALIYALYASNTYSERGILYARGPHETHRCYSTTP | 143 | | |
| DB | 370 | AAAAATAGATCTTTCTGAAATGTGAGCCAAAGAAATATTCTGACGTTTCACATGCTGG | 422 | | |
| QY | 144 | TRPHEUTHALIESETRPHISERLEULEYSESERFARGIYLPHESER | 163 | | |
| DB | 430 | TGCGTAGGCCCATCTGATCTGATTTGAAATTCAGTCTCAAAAAGTAGAGAGGCTTCT | 489 | | |
| QY | 164 | ASPTROGLIYVALTHRCYSGIYALVALTHRIUSERALAGIULARGVALASP | 183 | | |
| DB | 490 | GACCCCAAGGGGTGACATGTGGAGCAGTTCGACACTTTCAGCAGAGAGGTCCAGGTGAC | 544 | | |
| QY | 184 | ASNAARGSPILYILYSLYSTRYTHRVAGIUCYSGINGIULYSERIALACYSPROSERALA | 203 | | |
| DB | 550 | AACAGGGATTAIVAAAGATACACAGTGGAGTTCAGGAGGCGACGCTGCCCTCTGCC | 609 | | |
| QY | 204 | GLUGIUSERLEUPTROLLEGILVALVALYALSPALALEHISLYSELYSTYTYGILASN | 223 | | |
| DB | 610 | GAGAGAGGCTTACCCTTCGAGGCTCGTGGATGCTATTTCACMAAGTAAAGTATGAAAAC | 666 | | |
| QY | 224 | TYRTHSERSERPHEHILEARGSPILLEIYLYSPROASPTROPTROTHASNLEUGLN | 243 | | |
| DB | 670 | TACACACAGAGCTTCTTCATCAGACACATCATCAAAACACAGACCCACCAACCTTCAG | 729 | | |
| QY | 244 | LEULYSPROLEULYASNSERARGHISVALGILVALSERTPGLIUTYRPROASPTHTTP | 263 | | |
| DB | 730 | CTAAGACATTTGGAAATTTCTGGACACGGAGGCTCACCTGGGAATCCCGGACACTGG | 789 | | |
| QY | 264 | SETHTRPHISSELYRPHESERLEUTHRPHCYSLIEGINALAGIULYLSASASH | 283 | | |
| DB | 790 | AGCACCCACATCTTCTACTTCTCCCTGCACATTTTGSCATACAGGCCACGGCCAAACAAAT | 849 | | |
| QY | 284 | ARGIULYLYSASPARGLEUCYSVALASPLYSTRSERIALYVALCYSHISLYS | 303 | | |
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QY 304 Aspa1a1ys1leArGValG1na1aArGspArG1rYrYrSerSerSerTrpSerSptRp 323
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RESULT 9
AF411293
LOCUS AF411293 1669 bp mRNA linear SYN 10-SEP-2001
DEFINITION Synthetic construct bioactive single-chain murine Interleukin 12
mRNA, complete cds.
ACCESSION AF411293
VERSION AF411293.1 GI:15529754
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 1669)
AUTHORS Jiang, C., Magee, D.M. and Cox, R.A.
TITLE Construction of a single-chain interleukin-12-expressing retroviral
vector and its application in cytokine gene therapy against
experimental coccidioidomycosis
JOURNAL Infect. Immun. 67 (6), 2996-3001 (1999)
MEDLINE 99270963
PUBMED 10339510
REFERENCE 2 (bases 1 to 1669)
AUTHORS Jiang, C., Magee, D.M. and Cox, R.A.
TITLE Coadministration of interleukin 12 expression vector with antigen 2
cDNA enhances induction of protective immunity against Coccidioides
immitis
JOURNAL Infect. Immun. 67 (11), 5848-5853 (1999)
MEDLINE 20002565
PUBMED 10531239
REFERENCE 3 (bases 1 to 1669)
AUTHORS Jiang, C., Magee, D.M. and Cox, R.A.
TITLE Direct Submision
JOURNAL Submitted (17-AUG-2001) Microbiology, University of Health Science
Center at San Antonio, 15355 Lambda Drive, San Antonio, TX
78245-3027, USA

FEATURES
source Location/Qualifiers
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BASE COUNT 459 a 429 c 434 g 347 t
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Alignment Scores:
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Score: 1697.00 Matches: 335
Percent Similarity: 73.19% Conservative: 69
Best Local Similarity: 60.69% Mismatches: 120
Query Match: 60.52% Indels: 28

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US-09-917-265-62 (1-533) x AF411293 (1-1669)
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QY 21 Meta1a1eTrpG1nLeuG1nLysAspAlaYrVal1Val1G1nLeuAspTrpHisProasp 40
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QY 61 ThrSerAlaG1nSerSerG1nVal1LeuG1nSerG1nYrThrLeuThr1LeG1nVal1Lys 80
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Db 257 GAGTTCTTAGATGCTGGCCAGTACCTGCCCACAAAGAGGCGAGACTCTGAGCCACTCA 316
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Db 428 ACCTGCTATGCTGCTGCTCAAGAAACATGCGCTTGAAGTTCAACATCAAGACGCTAGC 487
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Db 488 AGTCCCGCCGACTCTGGGAGATGACATGTGAATGGGCTCTGCTGCGAGAGAAGTTC 547
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QY 313 AspaTrpTrpTrpSerSerSerTrpSerAspTrpAlaSerValSerCys----- 328
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 DEFINITION Sequence 10 from Patent WO0104155.
 ACCESSION AX076209
 VERSION AX076209.1 GI:12710834
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE 1 (bases 1 to 4522)
 AUTHORS Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
 TITLE Feline interleukin-12 as an immune stimulant
 JOURNAL Patent: WO 0104155-A 10 18-JAN-2001;
 Molegen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
 Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
 CALIFORNIA (US)
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 DB 781 GACACCTGGAGACACCCACATCTCTACTCTCTTAACATTTGGCGTACAGGTCCACAGGC 840
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 DB 841 AAACAAACACAGAAAAGAAAGACAGACTCTCCGTGACAAAGACCTCAGCAAGGCTGCTG 900
 QY 301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
 DB 901 TGGCACAAGGATCCCAAGATCCCGTGGCAAGCCAGGAGCGCTACTATATACCTCATCTGG 960
 QY 321 SerAspTrpAlaSerValSerCysSer 329
 DB 961 AGCAACTGGGCACTCCGTCTCTGCACT 987
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 AX076482 990 bp DNA linear PAT 06-FEB-2001
 LOCUS AX076482
 DEFINITION Sequence 8 from Patent WO0104280.
 ACCESSION AX076482

VERSION AX076482.1 GI:12711034
 KEYWORDS synthetic construct.
 SOURCE synthetic construct.
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 990)
 AUTHORS Leutenegger, C., Schroff, M., Wiltig, B. and Lutz, H.
 TITLE Vaccine against lentiviral infections, such as the feline immune deficiency virus of the cat
 JOURNAL patent: WO 0104280-A 8 18-JAN-2001;
 Mologen Forschungsbereich, Entwicklungsbereich und Vertriebs GmbH (DE);
 Universitaet zuerich (CH)
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 Score: 1657.00 Matches: 308
 Percent Similarity: 96.66% Conservative: 10
 Best Local Similarity: 93.62% Mismatches: 11
 Query Match: 59.09% Indels: 0
 DB: 6 Gaps: 0
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 QY 21 MetAlaIleTrpGluLeuGluLysAspValTyrValValGluLeuAspTrpHisProAsp 40
 DB 61 ATGGCCATATGGGAACCTGGAGAAAACGTTATATGTGTATAGTTGGAGCTGGACCTCGAT 120
 QY 41 AlaProGluLysMetValValLeuThrCysHisThrProGluLysAspPheTrp 60
 DB 121 GCCCGGGAGAAATGGTGGCTTACCTGCATTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
 QY 61 ThrSerAlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
 DB 181 ACCTCGACCAAGCAGTGAAGTCCATAGCTGTGTAATAAATCTGCACCATCCAAAGTCAA 240
 QY 81 GluPheGlyAspAlaGlnTyrTrpCysHisLysGlyLysValLeuSerArgSer 100
 DB 241 GAATTTGGACATCTGGCCAGTATACCTGTCATTAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
 QY 101 LeuLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGln 120
 DB 301 TTCCTCCTGATACACAAAAGAAAGATGGATTTGGTCCAGTATCTTAAGGAAACAG 360
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 QY 141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArg 160
 DB 421 ACCTGCTGGTGGCTGACGGCAATCAGTACGATTTGAAATTCAGTCAAAACACAGACA 480
 QY 161 GlyPheSerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgVal 180
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 QY 201 ProSerAlaGluLysLeuSerLeuProIleGluValValAlaAspAlaIleHisLysLeuLys 220
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 QY 281 LysAsnAsnArgGluLysLysAspArgLeuLysValAspLysThrSerAlaLysVal 300
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 QY 321 SerAspTrpAlaSerValSerCysSer 329
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 FCU83184 990 bp mRNA linear MAM 16-JUL-1999
 LOCUS FCU83184
 DEFINITION Felis catus interleukin-12 p40 subunit (IL-12) mRNA, complete cds.
 ACCESSION U83184
 VERSION U83184.1 GI:2735050
 KEYWORDS
 SOURCE
 ORGANISM
 Felis catus.
 Felis catus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 1 (bases 1 to 990)
 Fehr, D., Dean, G. A., Huder, J., Fan, Z., Hueltner, S., Higgins, J. W.,
 Pedersen, N. C., and Lutz, H.
 Nucleotide and predicted peptide sequence of feline interleukin-12
 (IL-12)
 JOURNAL DNA Seq. 8 (1-2), 77-82 (1997)
 MEDLINE 98182592
 PUBMED 9522125
 REFERENCE 2 (bases 1 to 990)
 Fehr, D., Dean, G. A., Huder, J., Fan, Z., Hueltner, S., Higgins, J. W.,
 Pedersen, N. C., and Lutz, H.
 Direct Submission
 Submitted (24-DEC-1996) Clinical Laboratory, Department of Internal
 Veterinary Medicine, University of Zurich, Winterthurerstrasse 260,
 Zurich, ZH 8057, Switzerland
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 Score:

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 Best Local Similarity: 93.62% Mismatches: 12
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 DB 241 GAATTTGAGATGCTGGGCACTATACCTGTCATTAAGAGCGCAGGTTCTGACCATTCG 300
 QY 101 LeuLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGln 120
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 DB 421 ACCTGTGCTGCTGTGACGCGCAATCAGTACGATTTGAATTCACCTGTCAAAAGCAGCAGA 480
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 DB 781 GACACCTGGAGACACCCACATTCCTACTTCCTTAACATTGGCGTACAGGTCGACGGGC 840
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 DB 841 AAGAACACACAGAGAAAGAAAGACAGACTCTCCGTGGACAAAGACCTCAGCCAAAGTCTGTG 900
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 DB 961

Db 961 AGCAACTGGGCAATCCGTCTGCTGCACT 987

RESULT 15
LOCUS FCIL12P40 1006 bp mRNA linear MAM 13-MAY-1997
DEFINITION F.catus mRNA for interleukin-12 p40 chain.
VERSION Y07762.1 GI:2102664
KEYWORDS interleukin-12 p40.
SOURCE cat.
ORGANISM Felis catus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE
AUTHORS Schjins,V.E., Wierda,C.M., Vahlenkamp,T.W. and Horzinek,M.C.
TITLE Molecular cloning of cat interleukin-12
JOURNAL Immunogenetics 45 (6), 462-463 (1997)
MEDLINE 97246745
PUBMED 9089110
REFERENCE 2 (bases 1 to 1006)
AUTHORS Schjins,V.E.C.J.
TITLE Direct Submission
JOURNAL Submitted (03-SEP-1996) V.E.C.J. Schjins, Virology Division,
Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL
Utrecht, NETHERLANDS
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BASE COUNT 288 a 258 c 249 g 211 t

ORIGIN

Alignment Scores:
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Percent Similarity: 96.058 Conservative: 10
Best Local Similarity: 93.018 Mismatches: 13
Query Match: 58.59% Indels: 0
Gaps: 0

US-09-917-265-62 (1-533) x FCIL12P40 (1-1006)

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QY 121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerIlyrPhe 140
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Db 361 AAAGAAATCCAAAATAAGATCTTTCTAAATGTGAGGCAAAAAGAAATATCTGGAGCTTC 420
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QY 321 SerAspTrpAlaSerValSerCysSer 329
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Db 961 AGCAACTGGGCAATCCGTCTGCTGCACT 987

Search completed: July 17, 2003, 06:40:54
Job time : 4780.75 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_p2n model

Run on: July 16, 2003, 13:41:48 : Search time 376.833 Seconds

(without alignments)
3185.273 Million cell updates/sec

Title: US-09-917-265-62

Perfect score: 2804

Sequence: 1 MHPOQIVISMFSLVILASPL.....HAFRIRAVTIRRMKSYINSS 533

Scoring table:
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Fgapop 6.0 , Fgapext 7.0
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Searched: 2185239 segs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 2393.5 | 85.4 | 6139 | 21 AA240023 | Interleukin-12 fus |
| 2 | 2392 | 85.3 | 8608 | 24 AAD31548 | PIRES-hb7-1-IL12.2 |
| 3 | 2392 | 85.3 | 8629 | 24 AAD31552 | PIRES-IL12.2-hb7-1 |
| 4 | 2389.5 | 85.2 | 8623 | 24 AAD31547 | PIRES-hb7-1-IL12.3 |
| 5 | 2389.5 | 85.2 | 8644 | 24 AAD31551 | PIRES-IL12.3-hb7-1 |
| 6 | 2387 | 85.1 | 8638 | 24 AAD31549 | PIRES-hb7-1-IL12.4 |
| 7 | 2387 | 85.1 | 8659 | 24 AAD31550 | PIRES-IL12.4-hb7-1 |
| 8 | 2358 | 84.1 | 8578 | 24 AAD31545 | PIRES-hb7-1-IL12.1 |
| 9 | 2358 | 84.1 | 8578 | 24 AAD31546 | PIRES-hb7-1-IL12.0 |
| 10 | 1764 | 62.9 | 990 | 19 AAV13817 | Canine IL-12 p40 s |
| 11 | 1764 | 62.9 | 990 | 20 AAX35625 | Nucleic acid encod |
| 12 | 1764 | 62.9 | 990 | 20 AAX3162 | Nucleic acid encod |
| 13 | 1764 | 62.9 | 990 | 22 AAI64388 | Canine coding sequ |
| 14 | 1735 | 61.9 | 990 | 19 AAV13816 | Canine IL-12 p40 s |
| 15 | 1735 | 61.9 | 990 | 20 AAX35615 | Nucleic acid encod |
| 16 | 1735 | 61.9 | 990 | 20 AAX3152 | Nucleic acid encod |
| 17 | 1735 | 61.9 | 990 | 22 AAI64378 | Canine coding sequ |
| 18 | 1729.5 | 61.7 | 2154 | 20 AAX18176 | Canine full length |
| 19 | 1658 | 59.1 | 4522 | 22 AAF26076 | Feline IL-12p40 en |
| 20 | 1658 | 59.1 | 4522 | 22 AAF26094 | Plasmod PMOI-fil12 |
| 21 | 1657 | 59.1 | 990 | 22 AAF26082 | Feline IL-12p40 en |
| 22 | 1657 | 59.1 | 990 | 22 AAF26085 | Feline IL-12p40 en |
| 23 | 1651 | 58.9 | 2193 | 19 AAV56625 | Feline FLAPp40 cDN |
| 24 | 1618.5 | 57.7 | 924 | 20 AAX18177 | Feline FLAPp40 cDN |
| 25 | 1567 | 55.9 | 990 | 22 AAD15209 | Canine mature CIAP |
| 26 | 1557 | 55.5 | 984 | 22 AAD15206 | Modified human cyt |
| 27 | 1554 | 55.4 | 921 | 19 AAV56626 | Modified human cyt |
| 28 | 1554 | 55.4 | 921 | 19 AAV56627 | Feline FLAPp40 cDN |
| 29 | 1515 | 54.0 | 1019 | 21 AAV07079 | Bovine Interleukin |
| 30 | 1514 | 54.0 | 1389 | 22 AAF6880 | Human p40-IL-2 cod |
| 31 | 1512 | 53.9 | 984 | 22 AAD15205 | Modified human cyt |
| 32 | 1505.5 | 53.7 | 5686 | 20 AAZ40415 | Plasmod PINT143 co |
| 33 | 1504 | 53.6 | 984 | 22 AAD15204 | Modified human cyt |
| 34 | 1502.5 | 53.6 | 987 | 20 AAV83199 | Interleukin (IL)-1 |
| 35 | 1501.5 | 53.5 | 987 | 16 AAO97484 | Human Interleukin- |
| 36 | 1501.5 | 53.5 | 987 | 19 AAV07273 | Human Interleukin- |
| 37 | 1501.5 | 53.5 | 987 | 20 AAV07217 | DNA encoding human |
| 38 | 1501.5 | 53.5 | 987 | 20 AAZ40404 | Human Interleukin |
| 39 | 1501.5 | 53.5 | 987 | 20 AAZ40405 | Human Interleukin |
| 40 | 1501.5 | 53.5 | 987 | 20 AAZ40406 | Human Interleukin |
| 41 | 1501.5 | 53.5 | 987 | 22 AAD15210 | Human cytokine p40 |
| 42 | 1501.5 | 53.5 | 1007 | 22 AAD18585 | Human Interleukin- |
| 43 | 1501.5 | 53.5 | 1018 | 15 AAO67879 | EPV 42 KD promoter |
| 44 | 1501.5 | 53.5 | 1018 | 20 AAZ08510 | EPV 42 kDa/human I |
| 45 | 1501.5 | 53.5 | 1397 | 18 AAV00401 | 40 kDa subunit of |

ALIGNMENTS

RESULT 1
AA240023
ID AA240023 standard: DNA: 6139 BP.
AA240023
AA240023:
14-FEB-2000 (first entry)
Interleukin-12 fusion protein, Flexi-12, coding sequence.
Interleukin-12; IL-12; fusion protein; IL-12 p35 subunit; B7 protein;
IL-12 p40 subunit; gene therapy; tumour; leukaemia; Flexi-12; ss.
Synthetic.
Homo septens.
US5994104-A.

PD 30-NOV-1999.
 XX 08-NOV-1996: 96US-0751767.
 XX 08-NOV-1996: 96US-0751767.
 PR (UNLO) ROYAL FREE HOSPITAL SCHOOL MED.
 PA Anderson RJ, Prentice HG, Macdonald ID:
 PI WPI, 2000-038261/03.
 DR P-PSDB: AAY54921.
 XX Nucleic acid constructs encoding interleukin-12 fusion proteins useful
 PT for treating leukemia and other cancers -
 XX Example: Fig 11: 73pp: English.

XX This sequence encodes the human interleukin-12 fusion protein sequence,
 CC designated Flexi-12. The invention relates to an isolated nucleic acid
 CC construct (I) comprising a region encoding an interleukin-12 (IL-12)
 CC fusion protein (comprising an IL-12 p35 subunit, an IL-12 p40 subunit and
 CC a linker peptide (joining the subunits)) and a region encoding a B7
 CC protein. (I) may be used to produce IL-12 fusion proteins according to
 CC standard recombinant DNA methodologies. The fusion proteins may be
 CC produced either in vitro in a fermentation culture or in vivo as part of
 CC a gene therapy protocol (in this case (I) is used to transform a patient's
 CC cells, which then secrete the functional polypeptide to supplement the
 CC patients own production of IL-12 or to rectify mutations which lead to
 CC the expression of inactive polypeptides). The fusion proteins produced in
 CC this way may be used to treat any disease which responds to IL-12 such as
 CC tumours (both solid and dispersed of the kidney, breast, colon, ovarian
 CC and cervical leukaemia and melanomas) and in particular, tumours of the
 CC blood such as leukaemia. Alternatively, the polypeptides may be used as
 CC antigens in the production of antibodies to IL-12 and to assay for
 CC agonists and antagonists of its activity. The antibodies and antagonists
 CC may be used to inhibit the activity of IL-12. (I) may also be used
 CC diagnostically as a probe which hybridizes to sequences encoding IL-12
 CC and the antibodies may be used to detect the presence of IL-12
 CC polypeptides in samples. They may be used diagnostically to quantitate
 CC the expression of the polypeptide by patients and hence which subjects
 CC may be in need of restorative therapy.

XX Sequence 6139 BP; 1552 A; 1558 C; 1558 G; 1491 T; 0 other;

Alignment Scores:

Pred. No.: 3,14e-202 Length: 6139
 Score: 2393.50 Matches: 456
 Percent Similarity: 89.46% Conservative: 28
 Best Local Similarity: 84.29% Mismatches: 48
 Query Match: 85.36% Indels: 9
 DB: 21 Gaps: 2

US-09-917-265-62 (1-533) x AAY40023 (1-6139)

QY 1 MethisProGIngluInleuValIleSerThrPheSerleuValleuLeuAlaSerProleu 20
 DB 3222 ATGGGTCACACAGATGGTCATCTCTGGTTTCCCTGGTTTCCGATCTCCCTC 3281
 QY 21 MetAlaIleThrProIleuGluIlyAspValTyrValValGluIleuAspThrPheIleu 40
 DB 3282 GTGGCCATATGGGAACGAAAGATGTTATCTCTAATAATTGGATTGGTATCCGGAT 3341
 QY 41 AlProGIngluIleuValIleuThrCysHisThrProIleuGluIlyAspValIleuThr 60
 DB 3342 GCCCCTGGAAATAATGGTCTCTCCTGACGACACCCCTGAAGAAGATGGTATCACCCTG 3401
 QY 61 ThrSerAlaGInSerSerGluValIleuGlySerGlyThrIleuThrIleuValIly 80
 DB 3402 ACCTTGACACAGACAGCTGAGGCTTGTGGCTGGCAAAACCCGACCATCAAGTCAAA 3461
 QY 81 GluPheGlyAspAlaGlyIleuTyrThrCysHisIlySerGlyIlyValIleuSerArgSer 100

DB 3462 GAGTTTGGAGATGTCGGCCAGTACACCTGTGTCAAAAGACGGCGAGTTCTTAAGCATTCG 3521
 QY 101 IleuLeuIleIleHisIlySGluAspGlyIleTyrSerThrAspIleIleuIlySGluIn 120
 DB 3522 CTCCTGCTGCTTCACAAAAAGACATGGAATTGGTCCACTGATATTATTTAAAGACACG 3581
 QY 121 IlySGluSerIlyAsnIlyIlePheIleuIlyCysGluAlaIlyAsnTyrSerGlyIlyrPhe 140
 DB 3582 AAAGAACCCAAAAAATAGACCTTCTAAGATTCGAGGCGCAAAATATATTCGAGGTTTC 3641
 QY 141 ThrCysIleThrIleuThrAlaIleSerThrAspIleuIlyPheSerValIlySerSerArg 160
 DB 3642 ACCCTGCTGTGCTCAACATCACTGATCTGATTGACATTGACATTCGTAAGCAAGCAGCA 3701
 QY 161 GlyPheSerAspProGIngluIlyValIlyThrCysGlyAlaValIlyThrLeuSerAlaGluIlyVal 180
 DB 3702 GGCCTCTTCGACCCCAAGGGGTGACGTCCGAGCTCCGACACCTCTGCAAGAGAGTC 3761
 QY 181 ArgValAspAsnAlaArgAspTyrIlyIlySerTyrThrValGluCysGIngluIlySerAlaCys 200
 DB 3762 ACAGGGGACACAAAGAGATAT--GAGTACTGAGTGAGGTCCAGAGACAGTCCCTGC 3818
 QY 201 ProSerAlaGluIlySerleuProIleGluValIleValAspAlaIleHisIlySerIly 220
 DB 3819 CCAGCTGCTGAGAGAGTGTCCCATTTGACGATGCTGATGATCCCTTCACAGCTCAAG 3878
 QY 221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleIlyAspAspProThr 240
 DB 3879 TATGAAACTACACAGCAGCTTCTTCATCAGCAGCATCATCAACCTGACCACCAAG 3938
 QY 241 AsnIleGluIleuIlySerProleuIlyAsnSerArgHisValGluValSerIleuIlyPro 260
 DB 3939 AACTTCACACTCAAGCATTAAGAAATTCGCGAGGTGAGTCACTGCGGAGTACCT 3998
 QY 261 AspThrTyrSerThrProHisSerTyrPheSerIleuThrPheCysIleGluIlyAsnIly 280
 DB 3999 GACACTGGAGTACTGCATCT 4058
 QY 281 LysAsnAsnArgGluIlyIlyAspArgIleuCysValAspIlyThrSerAlaIlyVal 300
 DB 4059 AAGAGCAAGAGAAAGAAAGATAGAGCTTCCAGCAGCAAGACCTCACCCAGCCAGTAC 4118
 QY 301 CysHisIlyAspAlaIlyIleArgValIleArgAspArgTyrTyrSerSerSerTyr 320
 DB 4119 TGCCGCAAAAATGCCAGATTAACGCTGCGGCGCCAGACCGCTACTATAGCTCATCTTGG 4178
 QY 321 SerAspTyrAlaSerValSerCysSerGlyIly-----Gly 332
 DB 4179 AGCGAATGGGCACTGTGCGCTGCACTGGTGGCGCTGGAAGCGCGGTGCGGAAGCGGC 4238
 QY 333 GlyGlyIlySerArgAsnIleuProThrProThrProSerProGlyIlyMetIleuIly 352
 DB 4239 GTGTGGCGGACGAGAAACCTCCCTGCGCCACTCCAGACCCAGAAATGTTCCTCATGCTT 4298
 QY 353 AsnHisSerGlnThrIleuIleArgAlaValSerAsnThrIleuGluIlyAlaArgIleuThr 372
 DB 4299 CACCACTCCCAAAACCTGCTGAGGCGCGTGAAGAAATGCTCCAGAAAGCCAGACAACT 4358
 QY 373 IleuGluIleuTyrSerCysThrSerGluIlyIleAspHisGluAspIleThrIlyAspIly 392
 DB 4359 CTAGAAATTTTACCTTGCACCTTCTGAAGAATGTGATCATGAAGATATCAAAAGATATA 4418
 QY 393 ThrSerThrValGluIlyAcylSerProleuGluIleuThrMetAsnIlySerCysIleuAla 412
 DB 4419 ACCAGACAGTGGAGCGCTGTTCACATTCGAAATTAACCAAGATAGAGATGGTCCCTAAT 4478
 QY 413 SerArgGluIleSerIleuThrAsnGlyIlySerCysIleuAlaSerGlyIlyAlaSerPhe 432
 DB 4479 TCCAGAGAGACCTCTTTCATTAATGAGAGTGTGCTGCTCCAGAAAGACCTTTT 4538
 QY 433 MetThrValIleuIlySerSerIleTyrGluAspIlyIlyMetIlyrGluIlyPhe 452
 DB 4539 ATGATGGCCCTGTGCTTACTATATTATGAAGACTTGAAGATGTACAGAGTGGAGTTC 4598

| QY | 453 | LysLlaMettsnAlaLysLleuMeLAspProLysArGlnIlePheLleuAspGlnAsn | 472 |
|----------|--------------|--|------|
| Db | 4599 | AAGACCATGATGCAAAACCTTCTATGATCTCTAAGACGCGATCTTCTAGATCAAAAC | 4658 |
| QY | 473 | MetLeuThrAlaIleAspGluLleuGlnAlaLeuAsnPheAsnSerValThrValPro | 492 |
| Db | 4659 | ATGCTGCAGTATTATTCAGACTGATGCGAGCCCTGAAATTCACAGTACGATGTGCCA | 4718 |
| QY | 493 | GlnLysSerSerLeuGluGluProAspPheTyrIleThrLysIleLysLeuCysIleLeu | 512 |
| Db | 4719 | CAAAATTCCTCCCTTGAAGAACCCGATTTTATAACTAAATCAACGCTCTGCATACCTT | 4778 |
| QY | 513 | LeuHISAlaPheArgIleArgAlaValThrIleAsnArgMetSerTyrLeuAsnSer | 532 |
| Db | 4779 | CTTATGCTCTTTCAGAAATTCGGCGACTACTTTCACAGAGTACGAGCTATCTGAATGCT | 4838 |
| QY | 533 | Ser 533 | |
| Db | 4839 | TCC 4841 | |
| RESULT 2 | | | |
| AAD31548 | | | |
| ID | AAD31548 | standard; DNA; 8608 BP. | |
| XX | | | |
| AC | AAD31548; | | |
| XX | | | |
| DT | 18-JUN-2002 | (first entry) | |
| XX | | PIRES-hb7-1-IL12.2 vector DNA. | |
| DE | | | |
| XX | | Expression system; interleukin-12; cancer therapy; cellular vaccine; | |
| KW | | immunotherapeutic response; IL-12.2; chimeric; human; Simian virus 40; | |
| KW | | SV40; cytomegalovirus; CMV; ds. | |
| XX | | | |
| OS | | Chimeric - Cytomegalovirus. | |
| OS | | Chimeric - Bacteriophage T7. | |
| OS | | Chimeric - Homo sapiens. | |
| OS | | Chimeric - Bacteriophage T3. | |
| OS | | Chimeric - Rhesus macaque polyoma virus. | |
| OS | | Chimeric - unidentified. | |
| XX | | | |
| FH | Key | Location/Qualifiers | |
| FT | enhancer | 1..750 | |
| FT | | /tag= a | |
| FT | | /note= "CMV enhancer; Also serves as a promoter" | |
| FT | misc_feature | 890..1002 | |
| FT | | /tag= b | |
| FT | | /note= "intervening sequence" | |
| FT | promoter | 1067..1085 | |
| FT | | /tag= c | |
| FT | | /note= "T7 RNA polymerase promoter" | |
| FT | misc_feature | 1090..1984 | |
| FT | | /tag= d | |
| FT | | /note= "Human B7-1 DNA" | |
| FT | misc_feature | 1090..1956 | |
| FT | | /tag= e | |
| FT | | /note= "Human B7-1 coding region" | |
| FT | RBS | 2013..2593 | |
| FT | | /tag= f | |
| FT | | /note= "IRES sequence" | |
| FT | misc_feature | 2627..4263 | |
| FT | | /tag= g | |
| FT | | /note= "Human IL-12.2 DNA" | |
| FT | CDS | 2640..4253 | |
| FT | | /tag= h | |
| FT | | /product= "Human IL-12.2 protein" | |
| FT | misc_feature | 3606..3676 | |
| FT | | /tag= i | |
| FT | | /note= "flexible linker of human IL-12.2 sequence" | |
| FT | promoter | 4362..4383 | |
| FT | | /tag= j | |
| FT | | /note= "T3 RNA polymerase promoter" | |

| FT | polya_signal | 4393..4614 | /*tag= k |
|--|--|--|----------|
| FT | | /note= "SV40 fragment containing polyadenylation signal" | |
| FT | rep_origin | 4709..5164 | /*tag= 1 |
| FT | | /note= "fl origin of replication" | |
| FT | misc_feature | 5228..6595 | /*tag= m |
| FT | | /note= "Neo r expression cassette" | |
| FT | misc_feature | 7006..7866 | /*tag= n |
| FT | | /note= "Ampicillin resistance" | |
| XX | | | |
| XX | US2002018767-A1. | | |
| XX | | | |
| XX | 14-FEB-2002. | | |
| XX | | | |
| PD | | | |
| PE | 10-APR-2001; 2001US-0828825. | | |
| XX | | | |
| PR | 27-JUL-2000; 2000KR-0043498. | | |
| XX | | | |
| XX | (LEES/) LEE S. | | |
| PA | (KIMH/) KIM H. | | |
| XX | | | |
| PI | Lee S, Kim H; | | |
| XX | | | |
| DR | WPI: 2002-239247/29. | | |
| DR | P-PSDB: AAE19820. | | |
| XX | | | |
| PT | New expression system, useful as vaccine for treating cancer, comprises | | |
| PT | DNA molecule encoding Interleukin-12 and a costimulatory molecule, | | |
| PT | operably linked to promoter that directs the expression of DNA molecule | | |
| XX | | | |
| XX | Example 1; Page 31-36; 76pp; English. | | |
| CC | The invention relates to an expression system which comprises a DNA | | |
| CC | molecule encoding Interleukin (IL)-12 and a costimulatory molecule, | | |
| CC | operably linked to a promoter that directs the expression of the DNA | | |
| CC | molecule. Expression vectors of the invention are useful for in vitro | | |
| CC | generation of genetically modified human cancer cells for cancer | | |
| CC | therapy. These cells share phenotypes of both antigen presenting cells | | |
| CC | and cancer cells and are suitable as a cellular vaccine for certain | | |
| CC | types of cancer. Expression vectors are useful for eliciting an anti | | |
| CC | tumour immune response in a individual. They are useful for activating | | |
| CC | T cells for immunotherapeutic responses against primary or metastatic | | |
| CC | cancers. The present sequence is pIRES-HB7-1-IL12.2 vector DNA. | | |
| CC | This vector comprises cytomegalovirus (CMV) promoter and enhancer, | | |
| CC | bacteriophage T7 RNA polymerase promoter, human B7-1 DNA, IRES sequence, | | |
| CC | human IL-12.2 DNA, bacteriophage T3 RNA polymerase promoter, | | |
| CC | Sinian virus 40 (SV40) fragment containing polyadenylation signal, fl | | |
| CC | origin of replication, Neo r expression cassette and ampicillin | | |
| CC | resistance sequence. | | |
| XX | | | |
| SQ | Sequence 8608 BP; 2180 A; 2126 C; 2138 G; 2164 T; 0 other; | | |
| XX | | | |
| Alignment Scores: | | | |
| Pred. No.: | 6,78e-202 | Length: | 8608 |
| Score: | 2392.00 | Matches: | 456 |
| Percent Similarity: | 90.47% | Conservative: | 28 |
| Best Local Similarity: | 85.23% | Mismatches: | 45 |
| Query Match: | 85.31% | Indels: | 6 |
| DB: | 24 | Gaps: | 3 |
| US-09-917-265-62 (1-533) x AAD31548 (1-8608) | | | |
| QY | 4 GlnGlnLeuValIleSerTrpPheSerLeuValIleuLeuAAsrProLeuMetaIaIle | 23 | |
| DB | 2649 CACGAGTGGGATCCTGGTTTCCCTGGTTTCTGGGATCTCCCGTGGCCATA | 2708 | |
| OY | 24 TrpGlnLeuGlnIuLyAspValTyrValValGlnIuLeuAspTrpPheSProAspAlaProGly | 43 | |
| DB | 2709 TGGGAACTGGAAAGATGTTATGTGCTGAAATTTGATGGTGGATGCGGATGCCCCGGA | 2768 | |

QY 44 GluMetValLeuThrCysHisThrProGluGluAspAspIleThrThrSerAla 63
 DB 2769 GAAATGATGCTCTCACTGACCTGACACCCCTGAAGAAGATGATACACCTGACCTTGAC 2828
 QY 64 GluSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPheGly 83
 DB 2829 CAGAGAGTGTAGGCTTGTAGGCTGTGGCAAAACCTTACCATTCACAGTCAAGGATTGGA 2888
 QY 84 AspAlaGlyGlnIleThrCysHisLysGlyLysValLeuSerArgSerIleLeu 103
 DB 2889 GATGCGGCCAGTACACCTGCTCCAAAGAGGCGAGTCTTAAGCCATTGCTCTGCTG 2948
 QY 104 IleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysSer 123
 DB 2949 CTTCACAAAAGCAAGATGGAATTTGGTCCACATGATTTTAAAGACCAAGAAAGACC 3008
 QY 124 LysAspLysIlePheLeuLysCysGluAlaLysAsnTrpSerGlyArgPheThrCys 143
 DB 3009 AAAAATAGACCTTCTTAAGATGCGAGGCCAAAGAAATTTATTTGAGCTTACCTCTG 3068
 QY 144 TrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPheSer 163
 DB 3069 TGGCTGACGACATCAGTACTGATTTGACATTCAGTCAAAAGCAGCAGAGCTCTTCT 3128
 QY 164 AspProGlnGlyValIleThrCysGlyAlaValThrLeuSerAlaGluArgValAsp 183
 DB 3129 GACCCCAAGGGGTGACGTGCGAGCTGTACACTCTGCAAGAGAGACAGAGGGGAC 3188
 QY 184 AsnArgAspTrpLysLysThrValIleGluCysGlnGluLysSerLacysProSerAla 203
 DB 3189 AACAGAGATAT---GAGTACTCAGTGGAGTGGCCAGAGGACAGCTGCGCCAGCTGCT 3245
 QY 204 GluGluSerLeuProIleGluValValAspAlaIleHisLysLeuLysTrpGluAsn 223
 DB 3246 GAGAGAGTCTGCCCTGAGTGCATGCGATGCGCTTCAACAAGCTCAAGATGAAAC 3305
 QY 224 TyrThrSerSerPheHeIleArgAspIleIleLysProAspProProThrAsnLeuGln 243
 DB 3306 TACACCAGAGCTTCTTCAACAGGACATCAACCAACCTGACCCCAACCTTGACG 3365
 QY 244 LeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTrpProAspThrTrp 263
 DB 3366 CTGAAGCCATTAAAGATTTCTGGCGAGGAGAGTGAAGTGAAGTGAAGTGAAGTGAAG 3425
 QY 264 SerThrProHisSerTrpPheSerLeuThrPheCysIleGlnAlaGlnLysAsnAsn 283
 DB 3426 AGTACTCCACATTCCTACTTCTCCGACATTCCTGCGTTCAGAGTCCAGAGGCAAGACAG 3485
 QY 284 ArgGluLysLysAspArgLeuGlyValAspLysThrSerAlaLysValLysCysHisLys 303
 DB 3486 AGAGAAAGAAAGATAGATCTTCAACCAAGACCTGACCAAGCTCATCTGCGCCAAA 3545
 QY 304 AspAlaLysIleArgValGlnAlaArgAspArgTrpTrpSerSerSerTrpSerAspTrp 323
 DB 3546 AATGCCAGCATTAAGGTGGGGGCCAGAGCCCTACTATAGCTCATCTTGAGACGATG 3605
 QY 324 AlaSerValSerCysSerGlyLys-----GlyGlyGlyLys-----ArgAsn 338
 DB 3606 GCATCTGTGCTGCTGAGTGTGGTGGTGAACCGGTGGGAGGAGCCCATGGAGAAC 3665
 QY 339 LeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeu 358
 DB 3666 CTCGCCGTGGCCACTCCAGACCCAGGAATGTTCCATGCTTACACACCCCAAAACCG 3725
 QY 359 LeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTrpSerCys 378
 DB 3726 CTGAGGCGCGTACGACATGCTCCAGAGGCCAAGCAAACTCTGAATTTTAACTTCC 3785
 QY 379 ThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAla 398
 DB 3786 ACTTCTGAAGAGATGATCATGAAGTATACAAAAGATAAAACAGCAGCACTGAGGCGC 3845

QY 399 CysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgIleLeuSerLeu 418
 DB 3846 TGTTCACATTTGAATTAACCAAGATGAGAGTGGCTTAATTCAGAGAGACCTGCTTC 3905
 QY 419 IleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeuCysLeu 438
 DB 3906 ATAACTAATGGGAGTGGCTGGCCCTCAGAAAAGCCCTTTTATGATGGCCCTGCTTC 3965
 QY 439 SerSerIleTrpLysLysLeuLysMetTrpGlnMetGluPheLysAlaMetAsnAlaLys 458
 DB 3966 AGTAGATTTATTAACACTTGAAGATGTCACAGGTGAGTTCAGACCTTGAATGCAAG 4025
 QY 459 LeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAsp 478
 DB 4026 CTTCATGATGATCTTAAGAGCGAGATCTTTAGATCAAAACATGCTGGCAGTTATGAT 4085
 QY 479 GluLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSerLeuGlu 498
 DB 4086 GAGCTGATGACGCGCTGGAATTTCAACAGTGAAGACGTGCCACAAAATCTCCCTTGA 4145
 QY 499 GluProAspPheTrpLysThrLysIleLysLysCysIleLeuLeuHisAlaPheArgIle 518
 DB 4146 GAACCGGATTTTATTAACCTAAATCAAGCTCTGATATCTTCTCATCTTCAAGATTT 4205
 QY 519 ArgAlaValThrIleAsnArgMetSerTrpLysLeuAsnSerSer 533
 DB 4206 CGGCGAGTGCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 4250
 RESULT 3
 AAD31552
 ID AAD31552 standard; DNA: 8629 BP.
 AC AAD31552;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE pIRES-IL12.2-hb7-1 vector DNA.
 XX
 KW Expression system; Interleukin-12; cancer therapy; cellular vaccine;
 KW immunotherapeutic response; IL-12.2; chimeric; human; Simian virus 40;
 KW SV40; cytomegalovirus; CMV; ds.
 OS Chimeric - Cytomegalovirus.
 OS Chimeric - Bacteriophage T7.
 OS Chimeric - Homo sapiens.
 OS Chimeric - Bacteriophage T3.
 OS Chimeric - Rhesus macaque polyoma virus.
 OS Chimeric - Unidentified.
 XX
 FH Location/Qualifiers
 FT 1..750
 FT enhancer
 FT /tag= a
 FT /note= "CMV enhancer; Also serves as a promoter"
 FT promoter
 FT /tag= b
 FT /note= "T7 RNA polymerase promoter"
 FT misc-feature
 FT /tag= c
 FT /note= "Human IL-12.2 DNA"
 FT CDS
 FT 1103..2716
 FT /tag= d
 FT /product= "Human IL-12.2 protein"
 FT misc-feature
 FT 2087..2116
 FT /tag= e
 FT /note= "Linker of human IL-12.2 sequence"
 FT RBS
 FT 2752..3332
 FT /tag= f
 FT /note= "IRES sequence"
 FT misc-feature
 FT 3369..4263
 FT /tag= g
 FT /note= "Human B7-1 DNA"
 FT promoter
 FT 4383..4404
 FT /tag= h


```

FT      /note= "T3 RNA polymerase promoter"
FT      4414..4635
FT      /*tag= 1
FT      /note= "SV40 fragment containing polyadenylation signal"
FT      rep_origin 4730..5185
FT      /*tag= 3
FT      /note= "f1 origin of replication"
FT      misc_feature 5249..6616
FT      /*tag= k
FT      /note= "Neo r expression cassette"
FT      misc_feature 7027..7887
FT      /*tag= 1
FT      /note= "Ampicillin resistance"
XX
XX      US2002018767-A1.
XX
XX      14-FEB-2002.
XX
XX      10-APR-2001; 2001US-0828925.
XX
XX      27-JUL-2000; 2000KR-0043498.
XX
XX      (LEES/) LEE S.
XX      (KIMH/) KIM H.
XX
XX      Lee S, Kim H;
XX
XX      WPI: 2002-239247/29.
XX      P-PSDB: AAE19824.
XX
XX      New expression system, useful as vaccine for treating cancer, comprises
XX      DNA molecule encoding interleukin-12 and costimulatory molecule,
XX      operably linked to promoter that directs the expression of DNA molecule
XX
XX      Example 1; Page 59-63; 76pp; English.
XX
XX      The invention relates to an expression system which comprises a DNA
XX      molecule encoding interleukin (IL)-12 and a costimulatory molecule,
XX      operably linked to a promoter that directs the expression of the DNA
XX      molecule. Expression vectors of the invention are useful for in vitro
XX      generation of genetically modified human cancer cells for cancer
XX      therapy. These cells share phenotypes of both antigen presenting cells
XX      and cancer cells and are suitable as a cellular vaccine for certain
XX      types of cancer. Expression vectors are useful for eliciting an anti
XX      tumour immune response in an individual. They are useful for activating
XX      T cells for immunotherapeutic responses against primary or metastatic
XX      cancers. The present sequence is pIRES-IL12.2 hb7-1 vector DNA.
XX      This vector comprises cytomegalovirus (CMV) promoter and enhancer,
XX      bacteriophage T7 RNA polymerase promoter, human B7-1 DNA, IRES sequence,
XX      human IL-12.2 DNA, bacteriophage T3 RNA polymerase promoter,
XX      Simian virus 40 (SV40) fragment containing polyadenylation signal, f1
XX      origin of replication, Neo r expression cassette and ampicillin
XX      resistance sequence.
XX
XX      Sequence 8629 BP; 2185 A; 2132 C; 2143 G; 2169 T; 0 other;
XX
XX
XX
XX
XX      Alignment Scores:
XX      Pred. No.: 6, 8e-202
XX      Score: 2392.00
XX      Percent Similarity: 90.47%
XX      Best Local Similarity: 85.23%
XX      Query Match: 85.31%
XX      DB: 24
XX      Gaps: 3
XX
XX      US-09-917-265-62 (1-533) x AAD31552 (1-8629)
XX
XX      4 GlnGlnLeuValIleSerTTPPheserLeuValLeuValaaserProLeuMetaIalle 23
XX      |||||||.....
XX      Db 1112 CAGCAGTTGGATCTCTTGTTCCCTGGTTTTCGCGATCTCCCTGTCGCCATA 1171
XX      24 TTPGLeuGnIuLysAspValTTrValValGlnLeuLeuAspTTPPhisProAspAlaProGly 43
XX      |||||||.....

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| | | | |
|----|------|---|------|
| Db | 1172 | TGGCACTGAAGAAGAAGATGTTTAATGCTGACATTTGGATTGGTATCCGGATGCCCTTGA | 1231 |
| Oy | 44 | GlueEtValValLeuthrCysHsIsthProgluIuaSaspIleThrTrpThrsEral | 63 |
| Db | 1232 | GAATGTGTGTCACCTGTGACACCCCTGAAGAGATGGATACCTGTGACCTGGACCTTGGAC | 1291 |
| Oy | 64 | GlnSerSerGluValLeuglySerGlyIysThrLeuthrIleGlnValLysGluPhely | 83 |
| Db | 1292 | CAGAGCACTGAGGCTTTCAGGCTCTGGCAAAACCCTGACATCCAGCAAGACTTGTGCA | 1351 |
| Oy | 84 | AspIlaGlyGlnTrpThrCysHsIstSylGlyLysValLeuSerArgSerLeuLeuLeu | 103 |
| Db | 1352 | GATCTGGCCAGTACACCTGTGCACAAAGAGGCGAGTTCATAGCCATTCTCTCTGCTG | 1411 |
| Oy | 104 | IleHsIstLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGluSer | 123 |
| Db | 1412 | CTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGACACAAAAAGAACCC | 1471 |
| Oy | 124 | LysAsnLysIlePheLeuLysCysGlnAlaLysAsnTrpSerGlyArgPheThrCysTrp | 143 |
| Db | 1472 | AAAAATAAGACCTTTCTACAGATGCGAGCCCAAGAAATTATCTGGACGTTTCAACGCTGG | 1533 |
| Oy | 144 | TrpLeuthrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPheSer | 163 |
| Db | 1532 | TGGCTGACGACAAATCAGTACGATTGTGCATTTCAGTGCACAAAGGAGGAGGCTCTTCT | 1591 |
| Oy | 164 | AspProGlnGlyValThrCysGlyValAlaValThrLeuSerAlaGluArgValArgValAsp | 183 |
| Db | 1592 | GACCCCCCAAGGGGTACCTGCGGAGACTCTACACTCTTGCAGAGACAGCTCAGAGGGAC | 1651 |
| Oy | 184 | AsnArgAspTrpLysLysTrpThrValGluCysGlnGlnGlySerAlaCysProSerAla | 203 |
| Db | 1652 | AACAAGAGATAT---GACTACTCAGGTGAGTGGCCAGAGAGACAGTGCCTGCCACACTGCT | 1708 |
| Oy | 204 | GluGluSerLeuProIleGluValValAlaAspAlaIleHsIstLysLeuLysTrpGluAsn | 223 |
| Db | 1709 | GAGAGAGATCGCCCATTCAGAGTATGATGGATGGCGCTTCCAAACCTCAAGATGTGAAAAA | 1766 |
| Oy | 224 | TyrTrpSerSerPhePheIleArgAspIleIleLysProAspProThrAsnLeuGln | 243 |
| Db | 1769 | TACACCAACACTTCTTCATAGGACATCATCAAACTGACCCCAACACACTTTCGAG | 1822 |
| Oy | 244 | LeuLysProLeuLysAsnSerArgHsIstValGluValSerTrpGluTrpProAspThrTrp | 263 |
| Db | 1829 | CTGAAGCATTAAAGAAATTCGCGAGGTGAGGTCAGCTGGAGTACCTGCACACCTGG | 1888 |
| Oy | 264 | SerThrProHsIstTrpPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsnAsn | 283 |
| Db | 1889 | AGTACTCCACTTCTTACTTCTCCCTGCATTTCCCTCCAGTCCAGGCGCAAGAGCGACAG | 1948 |
| Oy | 284 | ArgGluLysLysAspArgLeuCysValAspLysTrpSerAlaLysValIstCysHsIstLys | 303 |
| Db | 1949 | AGAGAAAAAGAAATAGAGTCTTCACCGCACAAAGACTTAAGCCAGCGTATATGCCGCAAA | 2006 |
| Oy | 304 | AspAlaLysIleArgValGlnAlaArgAspArgTrpTrpSerSerSerTrpSerAspTrp | 323 |
| Db | 2009 | AATGCAGACATTAAGGTCGGGGCCGAGACCGATACATAGCTCTTGTGAGCGAAATGG | 2066 |
| Oy | 324 | AlaSerValSerCysSerGlyGly-----GlyGlyGlyGlySer-----ArgAsn | 338 |
| Db | 2069 | GCATCTGTGGCCTTCAGTGTGGCGGTGGAACCGGTGGCGGTGGCAAGCCATGCGAAGAAC | 2126 |
| Oy | 339 | LeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHsIstSerGlnThrLeu | 358 |
| Db | 2129 | CTCCCGGCGGCACTCCAGACCCAGGAATTTTCCATCTTCACACTCCCAAAACCTG | 2186 |
| Oy | 359 | LeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuLysSerCys | 378 |
| Db | 2189 | CTGAGGGCGCTCAGACATCTCTCCAGAAAGCCAGACAAACTCTAGATTATTTACCTTGC | 2246 |
| Oy | 379 | ThrSerGluGluIleAspHsIstLysIleThrLysAspLysTrpSerThrValGluAla | 398 |
| Db | 2249 | ACTCTGTGAAGGATTGATCAGAAGATTTCCAAAAAGTTAAACCGAGACAGTGGAGGCC | 2306 |

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QY 399 CysleuProleuGluIleuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeu 418
    |||||||
Db 2309 TGTTTACCATGTGAATTAACCAAGATGAGAGTGGCTTAATTCACAGAGACCTCTTTC 2368
    |||||||
QY 419 IlleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeuCysLeu 438
    |||||||
Db 2369 ATAACTAATGGAGATTCCTGGCTCCAGAAAGACCTCTTTATGATGAGCCCTGTGCTT 2428
    |||||||
QY 439 SerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsnAlaLys 458
    |||||||
Db 2429 AGTAGTATTATGAAAGACTGGAAGATGTACAGAGTGGAGTTCAAGACCATGAATGCAAG 2488
    |||||||
QY 459 LeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAsp 478
    |||||||
Db 2489 CTTCGTATGATCTCTAAGAGCAGATCTTCTAGATCAAAAACATGCTGCGCATTTGAT 2548
    |||||||
QY 479 GluLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSerLeuGlu 498
    |||||||
Db 2549 GAGCTGATGCAGGCCCTGAAATTTTCACAGTGAAGATGTGCCACAAAATCTCCCTTGAA 2608
    |||||||
QY 499 GluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIle 518
    |||||||
Db 2609 GAACCGCATTTTATTAACATAAATCAAGCTGTGCAATCTTCTCATGCTTTCAGAAAT 2668
    |||||||
QY 519 ArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnSerSer 533
    |||||||
Db 2669 CGGCGAGTGAATGATGATGAGTGAAGTGAATGATGATGATGATGATGATGATGATGAT 2713
    |||||||

RESULT 4
ID AAD31547 standard; DNA; 8623 BP.
XX
AC AAD31547;
XX
DT 18-JUN-2002 (first entry)
XX
DE PIREs-hb7-1-IL12.3 vector DNA.
XX
KW Expression system; interleukin-12; cancer therapy; cellular vaccine;
KW immunotherapeutic response; IL-12.3; chimeric; human; Simian virus 40;
KW SV40; cytomegalovirus; CMV; ds.
XX
OS Chimeric - Cytomegalovirus.
OS Chimeric - Bacteriophage T7.
OS Chimeric - Homo sapiens.
OS Chimeric - Bacteriophage T3.
OS Chimeric - Rhesus macaque polyoma virus.
OS Chimeric - Unidentified.
XX
FH Key
FT Location/Qualifiers
FT 1..750
FT /tag= a
FT /note= "CMV enhancer; Also serves as a promoter"
FT misc_feature
FT 890..1002
FT /tag= b
FT /note= "intervening sequence"
FT promoter
FT 1067..1085
FT /tag= c
FT /note= "T7 RNA polymerase promoter"
FT misc_feature
FT 1090..1984
FT /tag= d
FT /note= "Human B7-1 DNA"
FT misc_feature
FT 1090..1956
FT /tag= e
FT /note= "Human B7-1 coding region"
FT RBS
FT 2013..2593
FT /tag= f
FT /note= "IRES sequence"
FT misc_feature
FT 2627..4278
FT /tag= g
FT /note= "Human IL-12.3 DNA"
FT CDS
FT 2640..4268

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FT FT /product= "Human IL-12.3 protein"
FT FT misc_feature
FT FT /tag= i
FT FT /note= "flexible linker of human IL-12.3 sequence"
FT FT promoter
FT FT 4398..4407
FT FT /tag= j
FT FT /note= "T3 RNA polymerase promoter"
FT FT polyA_signal
FT FT 4408..4629
FT FT /tag= k
FT FT rep_origin
FT FT 4724..5179
FT FT /tag= l
FT FT /note= "f1 origin of replication"
FT FT misc_feature
FT FT 5243..6610
FT FT /tag= m
FT FT /note= "Neo r expression cassette"
FT FT misc_feature
FT FT 7021..7881
FT FT /tag= n
FT FT /note= "Ampicillin resistance"

US2002018767-A1.
14-FEB-2002.
10-APR-2001; 2001US-0828825.
27-JUL-2000; 2000KR-0043498.
(PAGE 1) LEE S.
(KIM H.) KIM H.
Lee S, Kim H;
WPI: 2002-239247/29.
P-PDSB: AAE19819.

New expression system, useful as vaccine for treating cancer, comprises
DNA molecule encoding interleukin-12 and costimulatory molecule,
operably linked to promoter that directs the expression of DNA molecule

Example 1; Page 24-29; 76pp; English.
XX
PS The invention relates to an expression system which comprises a DNA
XX molecule encoding interleukin (IL)-12 and a costimulatory molecule,
XX operably linked to a promoter that directs the expression of the DNA
XX molecule. Expression vectors of the invention are useful for in vitro
XX generation of genetically modified human cancer cells for cancer
XX therapy. These cells share phenotypes of both antigen presenting cells
XX and cancer cells and are suitable as a cellular vaccine for certain
XX types of cancer. Expression vectors are useful for eliciting an anti
XX tumour immune response in an individual. They are useful for activating
XX T cells for immunotherapeutic responses against primary or metastatic
XX cancers. The present sequence is PIREs-hb7-1-IL12.3 vector DNA.
XX This vector comprises cytomegalovirus (CMV) promoter and enhancer,
XX bacteriophage T7 RNA polymerase promoter, human B7-1 DNA, IRES sequence,
XX human IL-12.3 DNA, bacteriophage T3 RNA polymerase promoter,
XX Simian virus 40 (SV40) fragment containing polyadenylation signal, f1
XX origin of replication, Neo r expression cassette and ampicillin
XX resistance sequence.
XX
SQ Sequence 8623 BP; 2182 A; 2128 C; 2147 G; 2166 T; 0 other;

Alignment Scores:
Pred. No.: 1,13e-201 Length: 8623
Score: 2389.50 Matches: 456
Percent Similarity: 89.63% Conservative: 28
Best Local Similarity: 84.44% Mismatches: 45
Query Match: 85.22% Indels: 11
DB: 24 Gaps: 3

US-09-917-265-62 (1-533) x AAD31547 (1-8623)

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| | | | |
|----|------|---|------|
| OY | 4 | GlnClnLeuValIIESerTPhSerLeuValLeuLeuAlaSerProLeuMetaIle | 23 |
| Db | 2649 | CAGAGTGTGCATCTCTGGTTTCCCTGGTTTTCGGCATCTCCCTCGTGCATATA | 2708 |
| OY | 24 | TrpGluLeuGlnLysAspValTyrValValGluLeuAspTrpHisProAspAlaProGly | 43 |
| Db | 2709 | TGGCACTGAAGAAGATGTTTATGTCTACAATTGATGTGTAATCCGAGATCCCTCGA | 2768 |
| OY | 44 | GluMetValValLeuThrCysHisIsthrProGluGluAspAlaIleThrTPTrpSerAla | 63 |
| Db | 2769 | GAATTCGTGCTCCACCTGTGCACACCCCTGAACAAGATGTAACCTGGACTTGGAC | 2828 |
| OY | 64 | GlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPheGly | 83 |
| Db | 2829 | CAGAGCATGTAGGCTTAGGCTTCGCCAAACCTGCACATCCAAAGTCAAGATTGGA | 2888 |
| OY | 84 | AspAlaGlyGlnTyrThrCysHisIsthrGlyLysValLeuSerArgSerLeuLeuLeu | 103 |
| Db | 2889 | GATCTGGCCCGTACACCTGTCAACAAGACGACGAGGTCTTAACCATTCCTCTCTCG | 2948 |
| OY | 104 | IleHisLysLysGluAspGlyIleIleTrpSerThrAspIleLeuLysGluGlnLysGluSer | 123 |
| Db | 2949 | CTTCACAAAAGAGAATGAGATTTGGTCCACCTATATTTTAAAGCACACAAAGAACCC | 3008 |
| OY | 124 | LysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrp | 143 |
| Db | 3009 | AAAATTAAGACCTTTTACATGTCGACGCCAAGAATTAATCTGGACGTTTCACCTGCTCG | 3068 |
| OY | 144 | TrpLeuPheAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPheSer | 163 |
| Db | 3069 | TGGCTGACGACAATCAGTACTGATTTTGACATTCAGTGTCAAAACAGACAGGCGCTCT | 3128 |
| OY | 164 | AspProGlnGlyValThrCysGlyValAlaValThrLeuSerAlaGluArgValArgValAsp | 183 |
| Db | 3129 | GACCCCAAGCGGTGACGTCGCGACGTCCTACACTCTCGACAGAGAGTCAGAGGGGAC | 3188 |
| OY | 184 | AsnArgAspPheTyrLysTyrThrValGluCysGlnGluGlySerAlaCysProSerAla | 203 |
| Db | 3189 | AACAAAGAGATTT---GAGTACTCAGTGAGGTGCCAGAGGACAGTGGCTGCCACGCTCT | 3245 |
| OY | 204 | GluGlnSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsn | 223 |
| Db | 3246 | GAGAGACGTCGCCCATTTGAGGTGATGTTGATGCGCTTCACAACTCAAGTATGAAAC | 3305 |
| OY | 224 | TyrThrSerSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeuGln | 243 |
| Db | 3306 | TACACCAAGACCTTCTTCATCAGGACATCATCAACCTGACCACCAACACTTGACG | 3365 |
| OY | 244 | LeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThrTrp | 263 |
| Db | 3366 | CTGAAGCATTTAAGAATTCTCGGACGTGAGGTCACTGGGAGTACCCTGCACACCTGG | 3425 |
| OY | 264 | SerThrProHisSerTyrPheSerLeuThrPheCysIleGlnIleGlnGlyLysAsnAsn | 283 |
| Db | 3426 | AGTACCTCACACTTCTACTTCTCCCTGCATTTCTGCGTTGACGTCACAGGCAAGACAAG | 3485 |
| OY | 284 | ArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValValLysHisLys | 303 |
| Db | 3486 | AGACAAAAGAAAGATAGAGTCTTCACGACCAACACACACACGACGACGATCTCCGCA | 3545 |
| OY | 304 | AspAlaLysIleLeuValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAspTrp | 323 |
| Db | 3546 | AATCCCAACGATTAAGGTGGCGGCCACGACCGCTACATATACATCTTTGGAGCGAATGG | 3605 |
| OY | 324 | AlaSerValSerCysSerGlyGly-----GlyGlyGlyGly | 335 |
| Db | 3606 | GCATCTGTGCCCCCTGCAGTGTGGCGGTGCAAGCGGTGGACACGCTGGCGGTGGA | 3665 |
| OY | 336 | Ser-----ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsn | 353 |
| Db | 3666 | AGGCCATGACGAAACCTCCCGCTGGCACCTTCACACCAACGAGGAATGTTCCATCGCTTCA | 3725 |

| | | | |
|----------|------|--|------|
| QY | 334 | HisSerGlnThrLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeu | 373 |
| Db | 3726 | CACCTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAAGGCCAGCAAACTCTTA | 3785 |
| QY | 374 | GluLeuYrSerCysThrSerGluGluLeuAspHisGluuAspIleThrLysAspLysThr | 393 |
| Db | 3786 | GAATTTTACCCCTTGACCTTCGAAAGAGATTGATCATGAAGATTATCACAAAAGATTAACCC | 3845 |
| OY | 394 | SerThrValGluValAcysLeuProLeuGluLeuThrLysGlnSerCysLeuAlaSer | 413 |
| Db | 3846 | AGCACAGTGGAGGCCCTGTTTACCATTTGAACATTAACACAGATTGAGAGTGGCTTAATTCC | 3905 |
| QY | 414 | ArgGluLeuSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMet | 433 |
| Db | 3906 | AGAGAGACCTCTTTCATTAATAATGGAGTTGCCCTGGCCCTCAGAAAAGACCTCTTTATG | 3965 |
| QY | 434 | ThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLys | 453 |
| Db | 3966 | ATGGCCCTGCTCCCTTAGTAGATTATTTAGAAAGACTTGAAGATGTACACAGCTGGAGTTCAG | 4025 |
| QY | 454 | AlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMet | 473 |
| Db | 4026 | ACCATGAATGCAAAAGCTTCTGATGATCTTAAGAGCGAGATCTTTTGATCAAAACATG | 4085 |
| QY | 474 | LeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGln | 493 |
| Db | 4086 | CTGGCAGATTATTGATGAGCTGATGAGGCCCTGAAATTTCAACAGAGACATCTGCCACA | 4145 |
| QY | 494 | LysSerSerLeuGluGluProAspPheTyrIlyThrLysIleLysLeuCysIleLeuLeu | 513 |
| Db | 4146 | AAATCCTCCTCTTGAAGAACCGGATTTTATTAACATAAACTAAACAGCTCTGCATCTCTT | 4205 |
| QY | 514 | HisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnSerSer | 533 |
| Db | 4206 | CATGCTTTCACAATTTCGGCGACGACTATTGATAGAGTATGACGACTATCTAATGCTTCC | 4265 |
| RESULT 5 | | | |
| AAD31551 | ID | AAD31551 standard; DNA; 8644 BP. | |
| XX | XX | AAD31551; | |
| AC | AC | 18-0UN-2002 (first entry) | |
| XX | XX | PIRES-IL12.3-hb7-1 vector DNA. | |
| DE | DE | | |
| XX | XX | | |
| KM | KM | Expression system: interleukin-12; cancer therapy; cellular vaccine; | |
| KW | KW | Immunotherapeutic response; IL-12.3; chimeric; human; Simian virus 40; | |
| SV40 | SV40 | cytomegalovirus; CMV; ds. | |
| OS | OS | Chimeric - Cytomegalovirus. | |
| OS | OS | Chimeric - Bacteriophage T7. | |
| OS | OS | Chimeric - Homo sapiens. | |
| OS | OS | Chimeric - Bacteriophage T3. | |
| OS | OS | Chimeric - Rhesus macaque polyoma virus. | |
| OS | OS | Chimeric - Unidentified. | |
| XX | XX | | |
| PH | PH | Location/Qualifiers | |
| FT | FT | 1..750 | |
| FT | FT | /*tag= a | |
| FT | FT | /*note= "CMV enhancer; Also serves as a promoter" | |
| FT | FT | 1067..1085 | |
| FT | FT | /*tag= b | |
| FT | FT | /*tag= "T7 RNA polymerase promoter" | |
| FT | FT | 1090..2731 | |
| FT | FT | /*tag= c | |
| FT | FT | /*note= "Human IL-12.3 DNA" | |
| FT | FT | 1103..2731 | |
| FT | FT | /*tag= d | |
| FT | FT | /*product= "Human IL-12.3 protein" | |
| FT | FT | 2087..2131 | |
| FT | FT | /*tag= e | |
| FT | FT | /*note= "Linker of human IL-12.3 sequence" | |

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FT /*tag= l
FT /note= "Ampicillin resistance"
PN US2002018767-A1.
XX 14-FEB-2002.
XX 10-APR-2001; 2001US-0828825.
XX 27-JUL-2000; 2000KR-0043498.
PA (LEES/) LEE S.
PA (KIMH/) KIM H.
PI Lee S, Kim H;
XX
XX WPI: 2002-239247/29.
XX P-PSDB; AAEL9823.
XX
XX New expression system, useful as vaccine for treating cancer, comprises
XX DNA molecule encoding interleukin-12 and costimulatory molecule,
XX operably linked to promoter that directs the expression of DNA molecule
XX
XX Example 1; Page 52-57; 76pp; English.
XX
XX The invention relates to an expression system which comprises a DNA
XX molecule encoding interleukin (IL)-12 and a costimulatory molecule,
XX operably linked to a promoter that directs the expression of the DNA
XX molecule. Expression vectors of the invention are useful for in vitro
XX generation of genetically modified human cancer cells for cancer
XX therapy. These cells share phenotypes of both antigen presenting cells
XX and cancer cells and are suitable as a cellular vaccine for certain
XX types of cancer. Expression vectors are useful for eliciting an anti
XX tumour immune response in a individual. They are useful for activating
XX T cells for immunotherapeutic responses against primary or metastatic
XX cancers. The present sequence is pIRES-IL12.3-hb7-1 vector DNA.
XX This vector comprises cytomegalovirus (CMV) promoter and enhancer,
XX bacteriophage T7 RNA polymerase promoter, human B7-1 DNA, IRES sequence,
XX human IL-12.3 DNA, bacteriophage T3 RNA polymerase promoter,
XX simian virus 40 (SV40) fragment containing polyadenylation signal, f1
XX origin of replication, Neo r expression cassette and ampicillin
XX resistance sequence.
XX
XX Sequence 8644 BP; 2187 A; 2134 C; 2152 G; 2171 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 1 14e-201 Length: 8644
XX Score: 2389.50 Matches: 456
XX Percent Similarity: 89.63% Conservative: 28
XX Best Local Similarity: 84.44% Mismatches: 45
XX Query Match: 85.22% Indels: 11
XX DB: 24 Gaps: 3

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us-09-917-265-62 (1-533) x AADJ1551 (1-8644)
QY 4 GlnGlnLeuValIleSerTrpPheSerLeuValLeuLeuAlaSerProIleuMetAlaIle 23
Db 1112 CAGCAGTGGTCACTCTTGGTTTCTCCGTGTTTCTGGCATCTCCCTCGGGCCANA 1171
QY 24 TrpGluLeuGluAspValTyrValAlaGluLeuAspTrpHisProAspAlaProGly 43
Db 1172 TGGGACGTGACAGAAACATGTTATGTCGTAGAATTGATGATCGGATCGCTGGA 1231
QY 44 GluMetValValLeuThrCysHisThrProGluGluAspPheTrpThrSerAla 63
Db 1232 GAATGATGCTCTCCTACCTGTGACACCCCTGAAGAAGATGATGATCCTGACCTGGAC 1291
QY 64 GlnSerSerGluValLeuGluSerGlyLysThrLeuThrIleGlnValLysGluPheGly 83
Db 1292 CAGAGCAGTGAAGTCTTGAAGCTCTGGCAAAACCTGACATCCAACTCAAAAGATTGGA 1351
QY 84 AspAlaGlyGlnThrCysHisLysGlyLysValLeuSerArgSerLeuLeu 103
Db 1352 GATCGTGGCAGTACACCTGTCACAAAGAGGAGGAGTCTTAAGCATTCGCTCGCTG 1411
QY 104 IleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGluSer 123
Db 1412 CTTCACAAAAGAGAAATGGAATTTGGTCCACTGATATTTTAAAGGACCAAGAAACCC 1471
QY 124 LysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrp 143
Db 1472 AAAAATPAAAGCCTTTTAAAGATGCGAGGCCAAGAAATTTATGTGACGTTTACCTGTGG 1531
QY 144 TrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerArgLysPheSer 163
Db 1532 TGGCTGACGACAAATGACTGATCTGATTCAGATTCAGTGCATAAAGCAGCAGAGCTCTT 1591
QY 164 AspProGlnGlyValIleThrCysGlyAlaValIleThrSerAlaGluArgValAsp 183
Db 1592 GACCCCCAAGGGGTGACGTGCGAGAGTGTCTGACACTCTGACAGAGACTCGAGGGGAC 1651
QY 184 AsnArgAspTyrLysTyrThrValIleCysGlnGluGlySerAlaCysProSerAla 203
Db 1652 AACCAAGAGTAT---CAGTACTCAGTGGAGTGCAGAGACAGACAGTCCGCGCAGGTGCT 1708
QY 204 GluGluSerLeuProIleGluValValAlaAspAlaIleHisLysLeuLysTyrGluAsn 223
Db 1709 GAGGAGAGCTGCGCCATTCAGGTCATGTGGATGCCGTTCCACAAAGCTCAAGTATGAAAC 1768
QY 224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProThrTrpTrp 243
Db 1769 TACACCAGCAGCTTCTTCACTACAGGACATCAACCCGACCACCAACTTGCAG 1828
QY 244 LeuLysProLeuLysAsnSerArgHisValGluValIleSerTrpGluTyrProAspTrp 263
Db 1829 CTGAAAGCATTAAAGATTTCTGCGCAGGTCGAGAGTCAGTGGAGTACCTTACACCTGG 1888
QY 264 SerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnLysAsnAsn 283
Db 1889 AGTACTCCCATTCCTACCTCTCTGACATTCCTGCTTCAAGTCCAGGCGCAAGCAAG 1948
QY 284 ArgGluLysLysAspArgLeuLysValAspLysThrSerAlaLysValValCysHisLys 303
Db 1949 ACGAGAAAGAAAGATGAGTCTTCAACCGCAAGACCTCAGCCAGCCAGTCCGCCGCA 2008
QY 304 AspAlaLysIleArgValGlnAlaIleArgAspArgTyrTyrSerSerSerTrpSerAspTrp 323
Db 2009 AATGCGACAGATTAGCGTGGGGCCAGAGACCGCTACTATAGCTCATCTTGGAGCCAAATGG 2068
QY 324 AlaSerValSerCysSerGlyLys-----GlyGlyGlyGly 335
Db 2069 GCATCTGTCGCTCGCAGTGTGCGCGTGAAGCGGTGGCGGGAAGGCGTGGCGTGA 2128
QY 336 Ser-----ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsn 353
Db 2129 AGCCCATGAGAAACCTCCCTGCGCCACTCCAGACCAAGCAATGTCATGCCATCTTCAAC 2188

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FT      Promoter      1067..1085
FT      /tag= b
FT      /note= "T7 RNA polymerase promoter"
FT      misc_feature  1090..2756
FT      /tag= c
FT      /note= "Human IL-12.4 DNA"
FT      CDS           1103..2746
FT      /tag= d
FT      /product= "Human IL-12.4 protein"
FT      misc_feature  2087..2146
FT      /tag= e
FT      /note= "Linker of human IL-12.4 sequence"
FT      RBS           2782..3362
FT      /tag= f
FT      /note= "IRES sequence"
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FT      /tag= g
FT      /note= "Human B7-1 DNA"
FT      promoter      4413..4434
FT      /tag= h
FT      /note= "T3 RNA polymerase promoter"
FT      polyA_signal  4444..4665
FT      /tag= i
FT      /note= "SV40 fragment containing polyadenylation signal"
FT      rep_origin     4760..5215
FT      /tag= j
FT      /note= "fl origin of replication"
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FT      /tag= k
FT      /note= "Neo r expression cassette"
FT      misc_feature  7057..7917
FT      /tag= l
FT      /note= "Ampicillin resistance"
FT      XX
PM      US2002018767-A1.
PD      14-FEB-2002.
PE      10-APR-2001; 2001US-0828825.
PX      27-JUL-2000; 2000KR-0043498.
PA      (LEES/) LEE S.
PA      (KIMH/) KIM H.
PI      Lee S, Kim H;
XX      WPI: 2002-239247/29.
DR      P-PSDB: AAE19822.
PT      New expression system, useful as vaccine for treating cancer, comprises
PT      DNA molecule encoding interleukin-12 and costimulatory molecule,
PT      operably linked to promoter that directs the expression of DNA molecule
PT      .
XX      Example 1: Page 45-50; 76pp: English.
XX
XX      The invention relates to an expression system which comprises a DNA
CC      molecule encoding interleukin (IL)-12 and a costimulatory molecule,
CC      operably linked to a promoter that directs the expression of the DNA
CC      molecule. Expression vectors of the invention are useful for in vitro
CC      generation of genetically modified human cancer cells for cancer
CC      therapy. These cells share phenotypes of both antigen presenting cells
CC      and cancer cells and are suitable as a cellular vaccine for certain
CC      types of cancer. Expression vectors are useful for eliciting an anti
CC      tumour immune response in a individual. They are useful for activating
CC      T cells for immunotherapeutic responses against primary or metastatic
CC      cancers. The present sequence is pIRES-IL12.4-hB7-1 vector DNA.
CC      This vector comprises cytomegalovirus (CMV) promoter and enhancer,
CC      bacteriophage T7 RNA polymerase promoter, human B7-1 DNA, IRES sequence,
CC      human IL-12.4 DNA, bacteriophage T3 RNA polymerase promoter,
CC      Simian virus 40 (SV40) fragment containing polyadenylation signal, fl
CC      origin of replication, Neo r expression cassette and ampicillin

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CC      resistance sequence.
XX
SQ      Sequence 8659 BP; 2189 A; 2135 C; 2161 G; 2174 T; 0 other;

Alignment Scores:
Pred. No.:      1.9e-201
Score:          2387.00
Percent Similarity: 88.81%
Best local Similarity: 83.67%
Query Match:    85.13%
DB:             24
Gaps:           3

US-09-917-265-62 (1-533) x AAD31550 (1-8659)

QY      4 GlnGlnLeuValIleSerTrpPheSerLeuValIleLeuAlaSerProLeuMetAlaIle 23
DB      1112 CAGCAGTGGTCATCTCTGGGTTTCCCTGGCTTTTCGGCATCTCCCTGGCCATA 1171
QY      24 TrpGluLeuGluLysAspValTyrValValGluLeuAspTrpHisProAspAlaProGly 43
DB      1172 TCGGAACCTGAAGAAAGATGTTATGTCGTAGAAATTGGATTGGTATCCGATCCCTGGA 1231
QY      44 GluMetValIleLeuThrCysHisThrProGluGluAspAspIleThrTrpThrSerAla 63
DB      1232 GAAATGGTGTCCTCACCTGTCACACCCCTGAAGAAGTGTATCACCCTGGACCTGGAC 1291
QY      64 GlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPheGly 83
DB      1292 CAGACCACTGAGCTTACGGCTCTGGCAAAACCCGACCAATCCAGTCAAAAGATTGGCA 1351
QY      84 AspAlaGlyGlnTyrThrCysHisLysGlyLysValLeuSerArgSerLeuLeuLeu 103
DB      1352 GATGCTGGCCACTACACCTGTCACAAAGAGCGAGGTTCTTACGCAATTCGCTCGTG 1411
QY      104 IleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGlnSer 123
DB      1412 CTTCACAAAAAGAGAGATGGAATTGGTCCACTGATATTTTAAAGACACAGAAAGACCC 1471
QY      124 LysAsnLysIlePheLeuLysGlyGlnLysAsnTyrSerGlyArgPheThrCysTrp 143
DB      1472 AAAAATTAAGACCTTCTTAAGATGCGAGCGCAAGAAATTTCTGGACGTTTCACCTGCG 1531
QY      144 TrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPheSer 163
DB      1532 TCGCTGACGACACATAGTACTGATTTGACATTGTCATTCGCAAAAGCAGCAGACGCTTCT 1591
QY      164 AspProGlnGlyValThrCysGlyValIleValThrLeuSerAlaGluArgValArgValAsp 183
DB      1592 GACCCCAAGGGGTGACGTGGCGACCTGCTACACTCTCGAGAGAGATCGAGAGGGGAC 1651
QY      184 AsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProSerAla 203
DB      1652 AACCAAGAGGTAT--GAGTACTCACTGGAGTCCCGAGGACAGTGGCTGGCCACCTGCT 1708
QY      204 GlnGlnSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlnAsn 223
DB      1709 GAGGAGAGCTTCGCCATTGAGGTGCTATGGTGGATGCCGTTCCACACAGCTCAAGATATAAAC 1768
QY      224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeuGln 243
DB      1769 TACACCACGACAGTCTTCATCAGGACATCATCAACCTGAGCCCAACCAACTTTCAG 1828
QY      244 LeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrTrpProAspThrTrp 263
DB      1829 CTGAAGCCATTAAAGAAATTCGCGAGGTGAGGTGACCTGGAGTACCTGGACACCTGG 1888
QY      284 SerTrpHisSerSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 283
DB      1889 ACTACTCCACATCTCTACTTCTCCTGCACTTTCGCTTCAGCTCAGGCGCAGGCAAGAGCAAG 1948
QY      284 ArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValValCysHisLys 303
DB      1949 AGACAAAGAAAGATAGAGTCTTCACCGACAAAGACCTCAGCCAGCATCTGCGCGAAA 2008

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QY 304 AspaAlaIysIleArgValGlnAlaArgAspArgTyrSerSerSerTrpSerAspTrp 323
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QY 324 AlaSerValSerCysSerGlyGly----- 331
Db 2069 GCATCTGTGGCCCTGAGTGTGGCGTGGAAAGCGGTGGCGGTGGAGCGGTGGCGA 2128
QY 332 ---GlyGlyGlyGlySer-----ArgAsnLeuProThrProThrProSerProGlyMet 348
Db 2129 AGCGGTGGCGGTGGAGCGCCATGAGAAACCTCCCGTGGCGCATCTCCAGACCGAGATG 2188
QY 349 PheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaValSerAsnThrLeuGlnLys 368
Db 2189 TTCCCATGCCCTTCACCACTCCCAAAACCTGCTGAGGCGCCGACCAACATCTCCAGAG 2248
QY 369 AlaArgGlnThrLeuGlnLeuTyrSerCysThrSerGlnGlnIleAspHisGlnAspIle 388
Db 2249 GCCAGACAACTCTAGAAATTTTACCTTGACCTTCTAGAGAGATTCATCAGAGATATC 2308
QY 389 ThrLysAspLysThrSerThrValGlnAlaCysLeuProLeuGlnLeuThrMetAsnGln 408
Db 2309 ACAAAAGATAAACACGACAGAGCTGAGGCGCTGTACCATTTGAAATTAACCAAGAAATGAG 2368
QY 409 SerCysLeuAlaSerArgGlnIleSerLeuIleThrAsnGlySerCysLeuAlaSerGly 428
Db 2369 AGTTCCTTAATTCAGAGACACCTCTTCTAATCTAATGAGATGCGCTGCCGCTCCAGA 2428
QY 429 LysAlaSerPheMetThrValLeuCysLeuSerSerIleTyrGlnAspLeuMetLys 448
Db 2429 AAGACCTCTTTTATGATGCGCTGCTGCTTACTGATGATTTTATGAGACTTGAAGATGTAC 2488
QY 449 GlnMetGlnPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePhe 468
Db 2489 CAGGTGAGTTCAAGACCATGAATGCAAGCTTCTGATGATCTCTAAGAGCAGATCTTT 2548
QY 469 LeuAspLysAsnMetLeuThrAlaIleAspGlnLeuLeuGlnAlaLeuAsnPheAsnSer 488
Db 2549 CTAGATCAAAACAGCTGGCAGTATTGATGAGCTGATGCGGCCCTGAATTTCAACAGCT 2608
QY 489 ValThrValProGlnLysSerSerLeuGlnLeuProAspPheTyrLysThrLysIleLys 508
Db 2609 GAGACTGTGCCACAAAATCTCCCTTGAAAGAACCGGATTTTATTAATAAATAAATCAAG 2668
QY 509 LeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSer 528
Db 2669 CTCTGCACTACTTCTTCATGCTTTCAGAAATTCGGCAGTGAATATGAGAGTATGAGC 2728
QY 529 TyrLeuAsnSerSer 533
Db 2729 TATCTGAATGCTTCC 2743

RESULT 8
AAD31545
ID AAD31545 standard; DNA; 8578 BP.
XX AAD31545;
AC AAD31545;
DT 18-JUN-2002 (first entry)
XX
DE pIRES-hb7-1-IL12.1 vector DNA.
XX
KW Expression system; interleukin-12; cancer therapy; cellular vaccine;
KW immunotherapeutic response; IL-12.1; chimeric; human; Simian virus 40;
KW SV40; cytomegalovirus; CMV; ds.
XX
OS Chimeric - Cytomegalovirus.
OS Chimeric - Bacteriophage T7.
OS Chimeric - Homo sapiens.
OS Chimeric - Bacteriophage T3.
OS Chimeric - Rhesus macaque polyoma virus.
OS Chimeric - Unidentified.

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XX Key Location/Qualifiers
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FT /note= "CMV IE"
FT 659..750
FT /tag= b
FT /note= "CMV IE"
FT 1067..1085
FT /tag= c
FT /note= "T7 RNA promoter"
FT 1090..1984
FT /tag= d
FT /note= "Human B7-1 DNA"
FT 1090..1956
FT /tag= e
FT /note= "Human B7-1 coding region"
FT 2013..2593
FT /tag= f
FT /note= "IRES sequence"
FT 2627..4263
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FT /note= "Human IL-12.1 DNA"
FT 2640..4223
FT /tag= h
FT /product= "Human IL-12.1 protein"
FT 3624..3629
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FT /note= "Flexible linker of human IL-12.1 sequence"
FT 4352..4431
FT /tag= j
FT /note= "T3 RNA polymerase promoter"
FT 4362..4583
FT /tag= k
FT /note= "SV40 fragment containing polyadenylation signal"
FT 4678..5133
FT /tag= l
FT /note= "11 origin of replication"
FT 5197..6564
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FT /note= "Neo r expression cassette"
FT 6975..7835
FT /tag= n
FT /note= "Ampicillin resistance"

US2002018767-A1.
14-FEB-2002.
10-APR-2001; 2001US-0828825.
27-JUL-2000; 2000KR-0043498.
(LIENS/) LEE S.
(KIMH/) KIM H.
Lee S, Kim H;
WPI: 2002-239247/29.
P-PSDB; AAL19817.
New expression system, useful as vaccine for treating cancer, comprises
DNA molecule encoding interleukin-12 and costimulatory molecule,
operably linked to promoter that directs the expression of DNA molecule
Example 1; Page 10-15; 76pp; English.
The invention relates to an expression system which comprises a DNA
molecule encoding interleukin (IL)-12 and a costimulatory molecule,
operably linked to a promoter that directs the expression of the DNA
molecule. Expression vectors of the invention are useful for in vitro
generation of genetically modified human cancer cells for cancer

```


CC therapy. These cells share phenotypes of both antigen presenting cells
CC and cancer cells and are suitable as a cellular vaccine for certain
types of cancer. Expression vectors are useful for eliciting an anti
CC tumour immune response in a individual. They are useful for activating
T cells for immunotherapeutic responses against primary or metastatic
cancers. The present sequence is pIRES-hb7-1-IL12.1 vector DNA.
CC This vector comprises cytomegalovirus (CMV) IE promoter and enhancer,
CC bacteriophage T7 RNA promoter, human B7-1 DNA, IRES sequence, human
CC IL-12.1 DNA, bacteriophage T3 RNA polymerase promoter, Simian virus 40
CC (SV40) fragment containing polyadenylation signal, fl origin of
CC replication, Neo r expression cassette and ampicillin resistance
CC sequence.

XX Sequence 8578 BP; 2176 A; 2122 C; 2120 G; 2160 T; 0 other;

Alignment Scores:

| Pred. No.: | Length: | 8578 |
|------------------------|---------|------------------|
| Score: | 2358.00 | 449 |
| Percent Similarity: | 90.00% | Conservative: 28 |
| Best Local Similarity: | 84.72% | Mismatches: 47 |
| Query Match: | 84.09% | Indels: 6 |
| DB: | 24 | Gaps: 2 |

US-09-917-265-62 (1-533) x AAD31545 (1-8578)

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OY 4 GlnGlnLeuValIleSerTrpPheSerLeuValLeuLeuAlaSerProLeuMetAlaIle 23
DB 2649 CAGCAGTGGTCATCTTGGTGTTCCTGCTTTTGGCATGTCCCTGTCGCCATA 2708
OY 24 TrpGlnLeuGlnLysAspValTyrValValGlnLeuAspTrpHisProAspAlaProGly 43
DB 2709 TGGGAACCTGAAGAAAGATGTTATGTCGTAGCAATTGGATTGGATCCGATGCCCTTGA 2768
OY 44 GluMetAlaValLeuThrCysHisThrProGlnLysAspIleThrTrpThrSeraIa 63
DB 2769 GAAATGGTGGTCCCTGACCTGACACCCCTGAAAGAAATGGATACCTGGACCTTGGAC 2828
OY 64 GluSerSerGluValLeuGlnGlySerGlyLysThrLeuThrIleGlnValLysGlnPheGly 83
DB 2829 CAGAGCAGTGAAGCTTGAAGCTCTGGCAAAACCTGACCATCCAGTCACAAAGAGTTTGA 2888
OY 84 AspAlaGlnGlnTyrThrCysHisLysGlyLysValLeuSerArgSerLeuLeu 103
DB 2889 GATCCTGGCCAGTACACCTGTCACAAAGACGCGAGTCTTAAGCCATTGCCCTCCTG 2948
OY 104 IleHisLysLysGlnAspGlyIleTrpSerThrAspIleLeuLysGlnGlnGlySer 123
DB 2949 CTTCACAAAAGCAAGATGGAATTTGGTCCACTGATATTTTAAAGACCCAGAAAGACC 3008
OY 124 LysAsnLysIlePheLeuLysCysGlnAlaLysAsnTyrSerGlyArgPheThrCysTrp 143
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OY 144 TrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPheSer 163
DB 3069 TGGCTGACGACAACTACTAGATTGACATTCAGTGCACAAAGACAGACGCGCTTCT 3128
OY 164 AspProGlnGlyValIleThrCysGlyAlaValThrLeuSerAlaGlnArgValArgValAsp 183
DB 3129 GACCCCAAGCGGTGACGTCGCGAGCTGTACACTCTCTGACAGAGAGTGAAGGGGAC 3188
OY 184 AsnArgAspTyrLysLysTyrThrValGlnCysGlnGlnGlnGlnGlnGlnGlnGlnGln 203
DB 3189 AACAGAGAGTAT---GAGTACTGAGTGCAGTGCAGGACGAGACAGTGCCTGCCGAGCTCCT 3245
OY 204 GluGlnSerLeuProIleGlnValValValAlaAlaIleHisLysLeuLysTyrGlnAsn 223
DB 3246 GAGAGAGTCTGCCCATTTGAGGTGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 3305
OY 224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeuGln 243
DB 3306 TACACGACGAGCTTCTTCATCAGGAGCATCATCAAACTGACCCACCAACACACTTGCAG 3365
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OY 244 LeuLysProLeuLysAsnSerArgHisValGlnValSerTrpGlnTyrProAspThrTrp 263
DB 3366 CTGAAGCCATTAAAGAAATTCTCGGACAGTGAAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 3425
OY 264 SerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlnGlyLysAsnAsn 283
DB 3426 AGTACTCCACATTCCTACTCTCCCTGACATTCGCGCTTCAGGTCAGGGGCAAGGCAAG 3485
OY 284 ArgGlnLysLysAspArgLeuCysValAspLysThrSeraLysValValCysHisLys 303
DB 3486 AGACAAAAGAAAGATAGAGTCTTACCGACACAGACCTCAGCCAGCTCATCTGCCGCAAA 3545
OY 304 AspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTyrSerAspTrp 323
DB 3546 AATGCCAGCATTTACCGCGCGGCGGACAGACCGCTACTATACCTCATCTTGGACGAAATGG 3605
OY 324 AlaSerValSerCysSerGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 343
DB 3606 GCATCTGTGCCCTCAGTCATGCG-----AGAAACCTCCCGTGGCCACT 3650
OY 344 ProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaValSer 363
DB 3651 CCAGACCCAGSAAATGTTCCATGCTTCACCACTCCCAAAACCTGCTGAGGCGCTCAGC 3710
OY 364 AsnThrLeuGlnLysAlaArgGlnThrLeuGlnLeuTyrSerCysThrSerGlnGlnIle 383
DB 3711 AACATGCTCCAGAAAGGCGACAGCAAACTCTAGAAATTTAACCTTGACACTTGAAGAGATT 3770
OY 384 AspHisGlnAspIleThrLysAspLysThrSerThrValGlnAlaCysLeuProLeuGln 403
DB 3771 GATCATGAAAGATACACAAAGATGAAACCCGACAGTGGAGGCTGTTTACCATTTGAA 3830
OY 404 LeuThrMetAlaGlnGlySerCysLeuAlaSerArgGlnIleSerLeuIleThrAsnGlySer 423
DB 3831 TTAACCAAGATGAGAGTGGCTTAATTCAGAGAGACCTTTTCATTAAGTAAAGGAGT 3890
OY 424 CysLeuAlaSerGlyLysAlaSerPheMetThrValLeuCysLeuSerSerIleTyrGln 443
DB 3891 TGCGTGGCGCTCAGAAAGACCTCTTTATGATGGCGCTGCTAGTATGATTTATGAA 3950
OY 444 AspLeuLysMetTyrGlnMetGlnPheLysAlaMetLysAlaLysLeuLeuMetAspPro 463
DB 3951 GACTTGAAGAGTGCACAGCTGAGTTCGAAAGCATGAAATGCAAGCTTCATGATGATCT 4010
OY 464 LysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGlnLeuLeuAla 483
DB 4011 AAGAGCGAGTCTTTAGATCAAAACATGCTGGCAGTTATTGATGACCTGATGCAGGCC 4070
OY 484 LeuAsnPheAsnSerValThrValProGlnLysSerSerLeuGlnGluProAspPheTyr 503
DB 4071 CTGAATTTCAACAGTGAAGACTGTGGCCACAAAATCCCTTGAAGAACCGGATTTTAT 4130
OY 504 LysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIle 523
DB 4131 AAAACTAAATCAAGCTTCGATCTTCATGCTTTCAGAAATTCGGGAGTGCATATT 4190
OY 524 AsnArgMetMetSerTyrLeuAsnSerSer 533
DB 4191 GATAGAGTGAAGTATCTGATATGCTTCC 4220
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RESULT 9
AAD31546
ID AAD31546 standard; DNA: 8578 BP.
XX
AC AAD31546;
XX
DT 18-JUN-2002 (first entry)
XX
DE pIRES-hb7-1-IL12.0 vector DNA.
XX
KW Expression system: interleukin-12; cancer therapy: cellular vaccine;
KW immunotherapeutic response: IL-12; chimERIC; human; Simian virus 40;
KW SV40; cytomegalovirus; CMV; ds.

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XX OS Chimeric - Cytomegalovirus.
OS OS Chimeric - Bacteriophage T7.
OS OS Chimeric - Homo sapiens.
OS OS Chimeric - Bacteriophage T3.
OS OS Chimeric - Rhesus macaque polyoma virus.
XX OS Chimeric - Unidentified.
FH Key Location/Qualifiers
FT enhancer 1..659
FT /tag= a
FT /note= "CMV IE"
FT promoter 659..750
FT /tag= b
FT /note= "CMV IE"
FT misc_feature 890..1002
FT /tag= c
FT /note= "intervening sequence"
FT promoter 1067..1085
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FT /tag= n
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XX US2002018767-A1.
XX PN
XX PD 14-FEB-2002.
XX PR 27-JUL-2000; 2000KR-0043498.
XX PF 10-APR-2001; 2001US-0828825.
XX PA (LEES/) LEE S.
XX PA (KIMH/) KIM H.
XX PI Lee S, Kim H;
XX WPI: 2002-239247/29.
XX P-PSDB; AAE19818.
PT New expression system, useful as vaccine for treating cancer, comprises
PT DNA molecule encoding interleukin-12 and costimulatory molecule,
PT operably linked to promoter that directs the expression of DNA molecule

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PT -
XX -
XX Example 1: Page 17-22; 76pp; English.
XX The invention relates to an expression system which comprises a DNA
CC molecule encoding Interleukin (IL)-12 and a costimulatory molecule,
CC operably linked to a promoter that directs the expression of the DNA
CC molecule. Expression vectors of the invention are useful for in vitro
CC generation of genetically modified human cancer cells for cancer
CC therapy. These cells share phenotypes of both antigen presenting cells
CC and cancer cells and are suitable as a cellular vaccine for certain
CC types of cancer. Expression vectors are useful for eliciting an anti
CC tumour immune response in a individual. They are useful for activating
CC T cells for immunotherapeutic responses against primary or metastatic
CC cancers. The present sequence is PIR5-hb7-1-IL12.0 vector DNA.
CC This vector comprises cytomegalovirus (CMV) IE promoter and enhancer,
CC bacteriophage T7 RNA polymerase promoter, human B7-1 DNA, IRES sequence,
CC human IL-12.0 DNA, bacteriophage T3 RNA polymerase promoter, f1
CC Simian virus 40 (SV40) fragment containing polyadenylation signal, f1
CC origin of replication, Neo r expression cassette and ampicillin
CC resistance sequence.
XX
SQ Sequence 8578 BP; 2176 A; 2122 C; 2120 G; 2160 T; 0 other:
Alignment Scores:
Pred. No.: 7,11e-199 Length: 8578
Score: 2358.00 Matches: 449
Percent Similarity: 90.00% Conservative: 28
Best Local Similarity: 84.72% Mismatches: 47
Query Match: 84.09% Indels: 6
DB: 24 Gaps: 2
US-09-917-265-62 (1-533) x AMD31546 (1-8578)
QY 4 GlnGlnLeuValIleSerTrpPheSerLeuValLeuAlaSerProLeuMetAlaIle 23
DB 2649 CAGCAGTGGTCACTTCCTGGTTCCCTGGTTTCTTGACATCTCCCTCGGCCATA 2708
QY 24 TrpGluLeuGluLysAspValTyrValValGluLeuAspTrpHisProAspAlaProGly 43
DB 2709 TGGCACTGACAGAAAGATGTTATGTCGTAGATTCGATTCGATCGGATCGCCCTGG 2768
QY 44 GluMetValValLeuThrCysHisThrProGluGluAspAspIleThrTrpHisAla 63
DB 2769 GAAATGTCGTCTCTACCTCTGACACCCCTGAAGAAAGATGATCCTGACCTTGGAC 2828
QY 64 GlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPheGly 83
DB 2829 CAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCTGACCATCCAAAGAGTTTGG 2888
QY 84 AspAlaGlyGlnIleThrCysHisLysGlyGlyValLeuSerArgSerLeuLeu 103
DB 2889 GATGCTGGCCAGACACCTGTCTCAAAAGCAGCGAGCTTCATGACCATTCGCTCCGCG 2948
QY 104 IleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGluSer 123
DB 2949 CTTCACAAAAAGGAAATGGAATTTGGTCACATGATTTTAAAGCAGCAAGAAACCC 3008
QY 124 LysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrp 143
DB 3009 AAAAATTAAGACCTTTTAAGATGCGAGGCCAAGAAATTAATTCGAGCTTCACCTCTGG 3068
QY 144 TrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerCeraArgGlyPheSer 163
DB 3069 TGGCTACGACCAATCACTACTGATTGACATTCAGTCTCAAAAGCAGCAGAGCTTCT 3128
QY 164 AspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValAsp 183
DB 3129 GACCCCAAGGGGTGACGTGCGAGAGCTCTGACACTCTGACAGAGAGTACAGAGGAGC 3188
QY 184 AsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerLacysProSerAla 203
DB 3189 AACCAAGGAGTAT--GAGTACTCAGTGGAGTGCACGAGAGACAGTCCCTGCCCCAGCTGCT 3245

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QY 204 GUGLuserLeuProIIleGIuValValAspAlaIleHisIleuLysTYrGIuAsn 223
Db 3246 GAGAGAGTCTGCCATTTGAGGTGATGCTGATGCCCTTACAAAGCTCAAGTATGAAAC 3305
QY 224 TYrThSerSerPhePheIleArGAspIleIeLysFroAspProProthAsnLeuGln 243
Db 3306 TACACGACGAGCTTTCTTCATCAGGAGCATCATCAAACTGACCCACCAACTTTCAG 3365
QY 244 LeuLysProLeuLysAsnSerArGHisValGIuValSerTrpGIuLysTrpProAspThrTrp 263
Db 3366 CTGAACCATTAAGAAATTCGCGAGGTGAGCTGACCGGAGGTACCTGACACTGC 3425
QY 264 SerThProHisSerTrPheSerLeuThrPheCysIleGlnIleGlnIleLysAsnAsn 283
Db 3426 AGTACTCCACATTCCTACTCTCTCCCTGACATTCCTGCTTACAGTCCAGGGCAAGAGCAG 3485
QY 284 ArGGIuLysLysAspArGLeuCysValAspLysThrSerAlaLysValValCysHisLys 303
Db 3486 AGAGAAAGAAAGATAGACTCTTCACCGACAGACCTCACCCACGTCATCTGCCGCAAA 3545
QY 304 AspAlaLysIleArGValGIuAlaArGAspArGTYrTYrSerSerSerTrpSerAspTrp 323
Db 3546 AATGCCAGCATTAAGCTGCGGCCAGGACCGCTACTATGATGATCTTGAGACGAATGC 3605
QY 324 AlaSerValSerCysSerGIyGIyGIyGIyGIySerArGAsnLeuProThrProThr 343
Db 3606 GCATCTGTGCCCTGCAGTCCATG-----AGAAACCTCCCGCTGCCACT 3650
QY 344 ProSerProGIyMetPheGlnCysLeuAsnHisSerGIyThrLeuLeuArGAlaValSer 363
Db 3651 CCAGACCCAGCAATGTTCCCATCTTCACACCTCCCAAAACCTGCTGAGCGCGCTGAGC 3710
QY 364 AsnThLeuGlnLysAlaArGGIyThrLeuGlnLeuTYrSerTYrSerGIyGIyIle 383
Db 3711 AACATCTCCAGAGGCCAGACAACTGAAATTTTACCTTGACCTTGAGAGAAAT 3770
QY 384 AspHisGIyAspIleThrLysAspLysThrSerThrValGIuAlaCysLeuProLeuGIu 403
Db 3771 GATCATGACATGATTCACAAAGATAAACAGCAGCAGCTGAGGCTGTTACCATTTGAA 3830
QY 404 LeuThMetaGlnuSerCysLeuAlaSerArGGIuIleSerLeuIleThrAsnGIySer 423
Db 3831 TTACCCAGAAATGAGGTTGCCCTAAATTTCCAGAGACGCTTTTCATTAATGAGAGT 3890
QY 424 CysLeuAlaSerGIyLysAlaSerPheMetThrValLeuCysLeuSerSerIleTYrGIu 443
Db 3891 TGCCTGCGCTCCGAAAGACCTCTTTATGATGCGCCTGCTAGTATATTATGAA 3950
QY 444 AspLeuLysMetTYrGIyMetGIyPheLysAlaMetAsnAlaLysLeuMetAspPro 463
Db 3951 GATTTCAGATGATGACGAGGTGAGGATTCAGACCATGATCAAAAGCTTCTGATGATCT 4010
QY 464 LysArGGIyIlePheLeuAspGIyAsnMetLeuThrAlaIleAspGIuLeuGlnAla 483
Db 4011 AAGAGGACAGATCTTTAGATCAAAACATGCTGCGACTTATGATGAGTGATGACAGGCC 4070
QY 484 LeuAsnPheAsnSerValThrValProGlnLysSerSerLeuGIuLysProAspPheTYr 503
Db 4071 CTGAATTTCAACGCTGAGACTGTGCCCAAAATCCCTTGAGAGAACGGATTTTAT 4130
QY 504 LysThLysIleLysLeuCysIleLeuLeuHisAlaPheArGIleArGAlaValThrIle 523
Db 4131 AAAACTAATAATCAGCTGCTGATCTCTTCATGCTTTTCAGAAATTCGGGAGTACTATT 4190
QY 524 AsnArGMetCysSerTYrLeuAsnSerSer 533
Db 4191 GATAGAGTATGAGTATCTGAAATGCTTCC 4220

```

RESULT 10
 AAV13817
 ID AAV13817 standard; cDNA to mRNA; 990 BP.
 XX

```

AC AAV13817:
XX
XX 14-MAY-1998 (first entry)
XX
XX Canine IL-12 P40 subunit cDNA.
DE
XX Canine; interleukin-12 P40 subunit; IL-12 P40 subunit; antitumour;
KW antiviral; vaccine adjuvant; ds.
XX
XX Canis sp.
OS
XX
XX Key location/Qualifiers
XX CDS 1..990
XX FT /*tag= a
XX FT /product= interleukin-12_P40_subunit
XX
XX JPI0036397-A.
XX
XX 10-FEB-1998.
XX
XX 08-NOV-1996; 96JP-0296789.
XX
XX 23-MAY-1996; 96JP-0128104.
XX 08-NOV-1995; 95JP-0289729.
XX
XX (TORA ) TORAY IND INC.
XX
XX WPI; 1998-174914/16.
XX
XX P-PSDB; AAW1791.
XX
XX Canine interleukin 12 - comprises P40 and P35 subunits; useful in
XX veterinary medicine, e.g. antitumour, antiviral and vaccine adjuvant
XX activities are expected
XX
XX Claim 10; Pages 10-11; 12pp; Japanese.
XX
XX The present sequence encodes a canine interleukin-12 (IL-12) P40
XX subunit. A canine IL-12 comprising a P40 and P35 subunit is capable
XX of inducing an antiviral activating factor and the expression of
XX class II MHC molecules in canine tumour cells; stimulating
XX proliferation of canine blastogenic lymphocytes and activating
XX canine leukocytes to inhibit canine tumour cells. The canine IL-12
XX can be used in veterinary medicines, e.g. antitumour, antiviral and
XX vaccine adjuvant activities are expected.
XX
XX Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 other:
SQ

```

Alignment Scores:
 Pred. No.: 2,34e-147 Length: 990
 Score: 1764.00 Matches: 329
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 62.91% Indels: 0
 DB: 19 Gaps: 0

US-09-917-265-62 (1-533) x AAV13817 (1-990)

```

QY 1 MethisProGlnGlnLeuValIleSerTrpPheSerLeuValLeuLeuAlaSerProLeu 20
Db 1 ATGCATCTCAGCAGGTGGTCATCTCTGCTTTTCCCTGCTTGGCTGCGCTCCCTC 60
QY 21 MetAlaIleTrpGIuLeuGlnLysAspValTYrValValGIuLeuAspTrpHisProAsp 40
Db 61 ATGGCCATATGGAGACTGGAGAAAGATGTTATATGTTGTAGAGTTGGACTGGACCTGAT 120
QY 41 AlaProGIyGIyMetValValLeuThrCysHisThrProGIuLysAspIleThrTrp 60
Db 121 GCCCCGGAGAAATGGGTGCTTCACCTGCCATACCCCTGAGAGATGACATCAGCTGG 180
QY 61 ThSerAlaGlnSerSerGIyValLeuGlnGlySerGIyLysThrLeuThrIleGlnValLys 80
Db 181 ACCTCAGCGCAGAGCAGTGAAGTCTAGGTTCTGTGTAATAAATCTGACCATCAAGTCAAA 240

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| | | | | |
|------------------|--|---------------------------------|---|-----|
| OY | | 81 | GIUphegiLysAspAlaGlyGlnTrpThrCysSHSLysGlyGlyValLeuSerArgSer | 100 |
| Db | | 241 | GAATTGGAGATGCTGGCCAGTATACCTGCCATAAAGGCGCAAGGTTCAGACCCTCA | 300 |
| OY | | 101 | LeuLeuLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGln | 120 |
| Db | | 301 | CTCCGTGTGATTCACAAAAAAGAAGATGGAATTGGTGCACGTATATCTTTAAAGAAACG | 360 |
| OY | | 121 | LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTrpSerGlyArgphe | 140 |
| Db | | 361 | AAAGAAATCCAAAAAATAGATCTTTCTTGAAATGTGAGGCAAGAAATTAATCTGCACGCTTC | 420 |
| OY | | 141 | ThrcysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerAlaLysSerSerArg | 160 |
| Db | | 421 | ACATCTGCTGTGGCTGACGGCAATCATGACTGATTGAAATTCAGTGTCAAAGTAATACAG | 480 |
| OY | | 161 | GlyPheSerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgval | 180 |
| Db | | 481 | GGCTTCTCTGACCCCCAAGGGGTGCATGTGGAGCAGTGAACACTTCACACAGAGAGGTC | 540 |
| OY | | 181 | ArgValaAspAsnArgAspTrpLysLysTyrrThrValGluCysGlnGluSerAlaCys | 200 |
| Db | | 541 | AGAGTGCACAACAGGGATATTAAGAAATGACACAGTGAAGTGTGACGAGGAGGCACTGC | 600 |
| OY | | 201 | ProSerAlaGluGluSerLeuProIleGluValaValaLysAlaIleHisLysLeuLys | 220 |
| Db | | 601 | CCCTCTGCCGAGAGAACCTTACCCTACGAGGAGTGTGGTGGATGCTATTCACAAGCTCAC | 660 |
| OY | | 221 | TyrGluAsnTyrrThrSerSerPhePheIleArgAspIleIleLysProAspProThr | 240 |
| Db | | 661 | TATGAAAACCTACACCAAGCAGCTTCTTCATCAGAGACATCATCAACCCAGACCCACACA | 720 |
| OY | | 241 | AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValaGluValSerTrpGluTyrrPro | 260 |
| Db | | 721 | AACCTGCAGCTGAAGCATTGAAAAATCTCGCAGCTGAGGTCAGCTGGGAATACCCC | 780 |
| OY | | 261 | AspThrTrpSerThrProHisSerTyrrPheSerLeuThrPheCysIleGlnAlaGlnGly | 280 |
| Db | | 781 | GACACCTGGAGCACCCACATCTCCATCTCTCCCTGCACATTTGTGCATACGAGGCCAGGGCC | 840 |
| OY | | 281 | LysAsnAsnArgGluLysLysAspArgLeuCysValaAspLysThrSerAlaLysVala | 300 |
| Db | | 841 | AAGAACATATAGGAANAAGAAAGATAGACTCTGCTGTGTGACACAACTCTCAGCCAGAGTGTG | 900 |
| OY | | 301 | CysHisLysAspAlaLysIleArgValaGlnAlaArgAspArgTyrrTrpSerSerSerTrp | 320 |
| Db | | 901 | TGCCACAAGAGATGCCAAGATCCGGCGGCAAGGCCGAGACCCGCTACATATAGTTATCTCTG | 960 |
| OY | | 321 | SerAspTrpAlaSerValSerCysSer | 329 |
| Db | | 961 | AGCGACTGGGCATCTGTGTCCTGCAGT | 987 |
| RESULT 11 | | | | |
| AAKX35625 | | | | |
| ID | AAKX35625 | standard; cDNA to mRNA; 990 BP. | | |
| XX | AAKX35625; | | | |
| AC | | | | |
| XX | | | | |
| DT | 09-JUL-1999 | (first entry) | | |
| XX | | | | |
| DE | Nucleic acid encoding canine Interleukin-12 (IL-12). | | | |
| XX | | | | |
| KM | Interleukin-12; IL-12; dog; cat; immune disease; Catil12; heterodimer; | | | |
| KW | tumour; skin disease; infectious disease; allergic disease; ds. | | | |
| XX | | | | |
| OS | Canis sp. | | | |
| XX | | | | |
| FH | Key | Location/Qualifiers | | |
| FT | CDS | 1..990 | | |
| XX | | /*tag= a | | |
| PX | JPI1106350-A. | | | |

| | |
|---|--|
| PD | 20-APR-1999. |
| XX | |
| PR | 15-MAY-1998; 98JP-0133345. |
| XX | |
| PR | 07-AUG-1997; 97JP-0213755. |
| PR | 16-MAY-1997; 97JP-0127690. |
| XX | |
| PA | (TORA) TORAY IND INC. |
| XX | |
| DR | WPI; 1999-308068/26. |
| DR | P-PSDB; AAY02342. |
| XX | |
| PT | A prevention and treating agent containing interleukin 12 (Cali12) - |
| XX | for prevention and treatment of dog and cat immune diseases |
| XX | |
| PS | Claim 1; Page 14-15; 16pp; Japanese. |
| XX | |
| CC | The present sequence encodes canine interleukin-12 (IL-12). The |
| CC | specification describes a method for the prevention and treatment |
| CC | of dog and cat immune diseases. The treatment used an agent comprising |
| CC | dog IL-12 (Cali12) proteins to form a heterodimer. The agent is |
| CC | useful for preventing and treating dog and cat immune diseases, |
| CC | including tumours, skin diseases, infectious diseases and allergic |
| CC | diseases. |
| XX | |
| SQ | Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 other: |
| Alignment Scores: | |
| Pred. No.: | 2,34e-147 Length: 990 |
| Score: | 1764.00 Matches: 329 |
| Percent Similarity: | 100.00% Conservative: 0 |
| Best Local Similarity: | 100.00% Mismatches: 0 |
| Query Match: | 62.91% Indels: 0 |
| DB: | 20 Gaps: 0 |
| US-09-917-265-62 (1-533) x AAX35625 (1-990) | |
| OY | 1 MetHisProGInclnLeuValIleSerTrpPheSerLeuValIleLeuAlaSerProLeu 20 |
| Dd | 1 ATGCATCCACAGCAAGTGGTCATCTCCGTGGTTTCCCGCTTGCGCCTCCCTC 60 |
| OY | 21 MetAlaIlePrGluLeuGlutLysAspValTyValAlaGluLeuAspTrpHisProAsp 40 |
| Dd | 61 ATGGCCATATGGGAAGCTGGAGAAGAAGTGTATTGTTGTAAGATTGGAGCTGCCACTGAT 120 |
| OY | 41 AlaProGluGluMetValValLeuThrCysHisTrpProGluGluAspAlaIleThrTrp 60 |
| Dd | 121 GCCCCCAGAAATAATGGTGTCTCTCATCTGCCATACCCTGAAGAAGATGACATACCTGG 180 |
| OY | 61 ThrSerAlaInSerSerGluValLeuGlySerGlyLysTrpLeuThrIleGlnValLys 80 |
| Dd | 181 ACCTCACGCGAGAGCGTAGTGAAGTCCAGTGTGGTAAACTCTGACCATCCAAGTCAA 240 |
| OY | 81 GluPheGluAspAlaGlyGlnTrpThrCysHisLysGlyLysValLeuSerArgSer 100 |
| Dd | 241 GAATTGTGGAGATCTGCGCCAGTATACCTGCCATTAAGAAGGCGAAGTTCTGAGCGGCTCA 300 |
| OY | 101 LeuLeuLeuLeuHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGln 120 |
| Dd | 301 CTCTCTGTGATTACAAAAAAGAGATGSAATTTGGTCTCAGTATCTTAAAGAACAG 360 |
| OY | 121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTrySerGlyArgPhe 140 |
| Dd | 361 AAAGAATCCAAAATAAGATCTTTTGAAATGTGAGCAAGAAATTAATTCGACGTTTC 420 |
| OY | 141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArg 160 |
| Dd | 421 ACATGCTGGGTGCGTGAAGCAATACGATCATTTGGAATTCACAGTGCAAAAGTAGACA 480 |
| OY | 161 GlyPheSerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgVal 180 |
| Dd | 481 GGCTTCTCTGACCCCAAGGGGTGACATCTGAGACGATGACACCTTTCAGCAGAGGGGTC 540 |

```
QY 181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
Db 541 AGACTGGACAACAGCGATTATTAAGAGACAGCTGGAGTGTCCAGAGGCGAGTCCCTGC 600
QY 201 ProSerAlaGluGluSerLeuProIleGluValValAlaAspAlaIleHisLysLeuLys 220
Db 601 CCCCTCTCCGAGGAGACCTTACCCATCGAGGCTCTGTGTGGATTCTATTCCACMACCTCAAG 660
QY 221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProThr 240
Db 661 TATGCAAAACTACACACAGCAGCTTCTTATCATGAGACATCATCAACACAGCCACCCACA 720
QY 241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTyrGluTyrPro 260
Db 721 AACCTGCAGCTGAAGCCATTGCAAAATTTCTGGCAGCGAGGTGACAGTGGCAATPACCCC 780
QY 261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGly 280
Db 781 GACACCTGGAGACCCCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
QY 281 LysAsnAsnArgGluLysLysAspArgLeuLysValAspLysPhePheAlaLysValVal 300
Db 841 AAGACACATAGACAAAGAAAGATAGACTCTGCTGCAAGACCTCAGCCAAAGTCTGTG 900
QY 301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTyr 320
Db 901 TCCACACAAGATGCCAAGATCCCGCTGCAACGCCGAGACCGCTACTACTACTACTCTCTG 960
QY 321 SerAspTrpAlaSerValSerCysSer 329
Db 961 AGCCACTGGGCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 987

RESULT 12
AA03162
ID AA03162 standard; cDNA to mRNA; 990 BP.
XX
AC AA03162:
XX
DT 30-MAR-1999 (first entry)
XX
DE Nucleic acid encoding canine interleukin 12.
XX
KW Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW skin disease; viral infection; allergic disease; breast tumour;
KW oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW othematoma; pneumoedema; skin soft pedicled soft tumour; anal tumour;
KW otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW feline leukaemia; allergy; pollinosis; ds.
XX
OS Canis sp.
XX
FH key Location/Oualifiers
FT CDS 1..990
FT /*tag= a
FT /product= interleukin_12
FT
FT
FT
PN W09851327-A1.
XX
XX 19-NOV-1998.
XX
XX 07-MAY-1998; 98WO-JP02031.
XX
XX 16-MAY-1997; 97JP-0127690.
XX
XX (TORA ) TORAY IND INC.
XX
XX Okano F, Satoh M, Yamada K:
XX
XX WPI: 1999-070100/06.
XX
XX P-PSDB: AAM84373.
XX
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```
PT New therapeutic and prophylactic agents - comprise
PT genetically-engineered canine interleukin 12, used to treat, e.g.
PT canine and feline immunological diseases
XX
XX Claim 1: Page 30-32; 45pp: Japanese.
XX
CC The present sequence encodes a canine interleukin 12 (IL-12) protein.
CC The IL-12 protein can be used in therapeutic or prophylactic agents.
CC The agents can be used to prevent and treat canine and feline
CC immunological diseases, including dog and cat tumours, skin diseases,
CC viral infections and allergic diseases, especially tumours, breast
CC tumour, oesinophilic granuloma, epidermoid tumour, skin tumour, lipoma,
CC othematoma, pneumoedema, skin soft pedicled soft tumour and anal
CC tumour; skin diseases, otitis externa, dermatitis, eczema, fungal
CC diseases of the skin, pyoderma, allergic dermatitis, nettle rash,
CC traumatic dermatitis and hair loss; infections: dog parvovirus infection
CC and distemper virus, cat plaque virus infection and feline leukaemia, and
CC allergic diseases, e.g. pollinosis.
XX
SQ Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 other:
SQ
Alignment Scores:
Pred. No.: 2,34e-147 Length: 990
Score: 1764.00 Matches: 329
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 62.91% Indels: 0
DB: 20 Gaps: 0
US-09-917-265-62 (1-533) x AA03162 (1-990)
QY 1 MethisPProgInGluLeuValIleSerTyrPheSerLeuValLeuLeuAlaSerProLeu 20
Db 1 ATGCATCTCTCAGCAGTGGTGTATCTCTCTGTTTCCCTCGTTTGGCGCTCTCCCTC 60
QY 21 MetAlaIleTyrGluLeuGluLysAspValTyrValValGluLeuAspTyrPheIleTyr 40
Db 61 ATGCCAATGCGAAGTGGAGAAAGATGTTATGTGTAGAGTGGACTGCACCCATGAT 120
QY 41 AlaProGluGluMetValValLeuThrCysHisThrProGluGluAspAspIleThrTyr 60
Db 121 GCCCCGAGAAATGGTGGTCTCACCCTGCATACCCCTGAAGAAGATGACATACCTTGG 180
QY 61 ThrSerAlaGlnSerSerGluValLeuGlySerLysLysThrLeuThrIleGlnValLys 80
Db 181 ACCTCAGCGCGACAGAGAGTCTAGTCTGTAATAACTGACCATTCACAGTCAAA 240
QY 81 GluPheGlyAspAlaGlyGlnTyrThrCysHisLysGlyGlyValLeuSerArgSer 100
Db 241 GAATTGGAGATGCTGGCCAGTATACCTGCATTAAGAGGCAAGTTCTGACCCCTCA 300
QY 101 LeuLeuLeuIleHisLysLysGluAspGlyIleTyrPheThrAspIleLeuLysGln 120
Db 301 CTCTGTGGATTCCACAAAAGAGATGGAATTTGGTCCACTGATATCTTAAGGACAG 360
QY 121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
Db 361 AAAGATTCCAAAATAAGATCTTCTGAATGTAGGCAAGAAATTAATTCGACGTTTC 420
QY 141 ThrCysTyrTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArg 160
Db 421 ACATGCTGTGGTGGTACGCGCAATCAGTACTGATTTGAATTCACATGTCAAAGATACAGA 480
QY 161 GlyPheSerAspProGlnGlyValThrCysGlyValAlaThrLeuSerAlaGluArgVal 180
Db 481 GGCTTCTGTGACCCCAAGGGGTGACATGTGGACAGGACACTTTCAGCAGAGAGGTC 540
QY 181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
Db 541 AGAGTGCACAACAGGAGTATTAAGACATGACATGTGAGAGGCGAGTCCCTGC 600
QY 201 ProSerAlaGluGluSerLeuProIleGluValValAlaAspAlaIleHisLysLeuLys 220
```

Db 601 CCCTTCGCCGAGAGACCTACCCATCCAGAGCTGCTGCTGATTCATTCACAAAGCTCAG 660
 QY 221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLeuLeuProAspProThr 240
 Db 661 TATGAAACTACACACACACCTTCTTCATCAGAGACATCATCAACACAGCCACCCACA 720
 QY 241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTyrPgluTyrPro 260
 Db 721 AACCTGACCTGAAAGCATTGAAATAATTCGCGACCTGGAGAGTCACTGGGAATACCCC 780
 QY 261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnIleGlnGly 280
 Db 781 GACACCTGGAGACCCACCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
 QY 281 LysAsnAsnArgGlnLysLysAspArgLeuCysValAspLysThrSerAlaLysValVal 300
 Db 841 AAGACATATAGAGAAAGAAAGATAGACTCTGGCTGACAAAGACCTGAGCAAGTCTG 900
 QY 301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTyr 320
 Db 901 TGCACACAGATGCGCAAGATCCGCTGCAAGCCCGAGACCGCTACTACTACTACTCTG 960
 QY 321 SerAspTrpAlaSerValSerCysSer 329
 Db 961 AGCGACTGGGCATCTGTCTCTGCACT 987

RESULT 13

AA164388 standard; DNA: 990 BP.

AA164388;

23-NOV-2001 (first entry)

Canine coding sequence #3.

Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.

Canis familiaris.

Key Location/Qualifiers

FT CDS 1..990

FT sig-peptide 1..66

FT mat-peptide 67..987

FT JP2001161378-A.

19-JUN-2001.

26-SEP-2000: 2000JP-0292946.

01-OCT-1999: 99JP-0281234.

(TORA) TORAY IND INC.

WPI: 2001-592466/67.

P-PSDB: AAG66482.

Preparation of a highly pure protein, interleukin 12, a protein

inhibiting the activity of interleukin 12, and a treating agent and a

treating method for immunopathy of mammalian

Claim 6: Page 16-17: 21pp: Japanese.

The present invention relates to a method for the preparation of a highly
 pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
 the activity of IL12 is contacted to an ion exchanging carrier and/or a
 pigment carrier to get IL12 and/or a protein inhibiting the activity of
 IL12. The protein is used as a preventive agent for dog immunopathy. The

CC present sequence was used in the method of the present invention.
 XX Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 other;

Alignment Scores:

Pred. No.: 2,34e-147 Length: 990
 Score: 1764.00 Matches: 329
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 62.91% Indels: 0
 DB: 22 Gaps: 0

US-09-917-265-62 (1-533) x AA164388 (1-990)

QY 1 MethisProGlnGlnLeuValIleSerTyrPheSerLeuValLeuLeuAlaSerProLeu 20
 Db 1 ATGACATCTCAGACAGTGGTGCATCTCTGTTTCCCTGTTTGGTGGCTCTCCCTC 60
 QY 21 MetAlaIleTyrPgluLeuLysAspValTyrValValGluLeuAspTrpHisProAsp 40
 Db 61 ATGGCCATATGGGAACTGAGAAAGATGTTATGTTGTAGAGTTGGAGCTGGACCTGAT 120
 QY 41 AlaProGlnGlnMetValIleLeuThrCysHisThrProGlnGlnAspIleThrTrp 60
 Db 121 GCCCCGGGAAATGGTGGTCTCCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
 QY 61 ThrSerAlaGlnSerSerGlnValLeuGlnSerGlnLysThrLeuThrIleGlnValLys 80
 Db 181 ACCTCAGCGCAGACAGTGAAGTCTAGTTCGTGTAAGTCTGACCATTCACATGCACAA 240
 QY 81 GluPheGlyAspAlaGlnTyrThrCysHisLysGlyLysValLeuSerArgSer 100
 Db 241 GAATTGGAGATGCTGGCCAGTATACCTCCATAAAGAGGCAAGGTTCTGAGCCGCTCA 300
 QY 101 LeuLeuLeuIleHisLysLysGlnAspGlyIleTyrSerThrAspIleLeuLysGlnGln 120
 Db 301 CTCCTGTGATTCACAAAAAGAGATGGAATTTGGTCCACTATATCTTAAAGAACAG 360
 QY 121 LysGlnSerLysAsnLysIlePheLeuLysCysGlnAlaLysAsnTyrSerGlyArgPhe 140
 Db 361 AAAGATCCCAAAATTAAGATCTTCTGAAATGAGGCAAGATTAATTCGACGCTTTC 420
 QY 141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerArg 160
 Db 421 ACATGCTGGTGGTGGCCAAACACTGCTGATTTAAATTCAGTCAAAAGTACAA 480
 QY 161 GlyPheSerAspProGlnGlnValThrCysGlnAlaValThrLeuSerAlaGlnArgVal 180
 Db 481 GGCTTCTGACCCCAAGGGGTGACATGTGAGACGTACACCTTTCACAGAGAGGTC 540
 QY 181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGlnLysSerAlaCys 200
 Db 541 AGAGTGACACACAGGAGATTATAAGAGTACACAGTGGAGTGCAGAGGGAGTGGCTGC 600
 QY 201 ProSerAlaGlnGlnSerLeuProIleGlnValValValAspAlaIleHisLysLeuLys 220
 Db 601 CCCTCTGCCGAGAGAGCTTACCATCGAGGTGCTGATGCTATTTCACAAAGCTCAAG 660
 QY 221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProThr 240
 Db 661 TATGAAACTACACACACCTTCTTCATCAGAGACATCATCAACACACACCCACCA 720
 QY 241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTyrPgluTyrPro 260
 Db 721 AACCTGACCTGAAAGCATTGAAATAATTCGCGACCTGGAGAGTCACTGGGAATACCCC 780
 QY 261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnIleGlnGly 280
 Db 781 GACACCTGGAGACCCACCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
 QY 281 LysAsnAsnArgGlnLysLysAspArgLeuCysValAspLysThrSerAlaLysValVal 300
 Db 841 AAGACATATAGAGAAAGAAAGATAGACTCTGCTGTCGACAAAGCTCAGCCAAAGTCTG 900

QY 301 CysH1stysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTyr 320
Db 901 TGGCACAAGATGCCAAGATCCGCGTGCAGACCCGAGACCCCTACTAGTTCATCTCTGG 960

QY 321 SerAspTrpAlaSerValSerCysSer 329
Db 961 AGCGACTGGCGATCTGTCTCCTGCAGT 987

RESULT 14
AAV13816
ID AAV13816 standard; cDNA to mRNA; 990 BP.
XX AAV13816:
AC AAV13816:
DT 14-MAY-1998 (first entry)
XX
DE Canine IL-12 P40 subunit cDNA.
KW Canine: interleukin-12 P40 subunit; IL-12 P40 subunit; antitumour;
KM antiviral; vaccine adjuvant; ds.
XX
OS Canis sp.
FH
FH Key Location/Qualifiers
FT CDS 1..990 /*tag= a
FT /product= interleukin-12_P40_subunit
FT

XX JP10036397-A.
XX 10-FEB-1998.
XX
XX 08-NOV-1996; 96JP-0296789.
XX
XX 23-MAY-1996; 96JP-0128104.
XX 08-NOV-1995; 95JP-0289729.
XX
XX (TORA) TORAY IND INC.
XX
XX MPI: 1998-174914/16.
XX
XX P-PSDB: AAM41790.
XX
XX Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT veterinary medicine, e.g. antitumour, antiviral and vaccine adjuvant
PT activities are expected
XX
XX
PS Claim 8; Page 8; 12pp; Japanese.
XX
XX The present sequence encodes a canine interleukin-12 (IL-12) P40
CC subunit. A canine IL-12 comprising a P40 and P35 subunit is capable
CC of inducing an antiviral activating factor and the expression of
CC class II MHC molecules in canine tumour cells, stimulating
CC proliferation of canine blastogenic lymphocytes and activating
CC canine leukocytes to inhibit canine tumour cells. The canine IL-12
CC can be used in veterinary medicines, e.g. antitumour, antiviral and
CC vaccine adjuvant activities are expected.
XX
XX SO Sequence 990 BP: 278 A; 243 C; 251 G; 218 T; 0 other:

Alignment Scores:
Pred. No.: 8.87e-145 Length: 990
Score: 1735.00 Matches: 324
Percent Similarity: 99.69% Conservative: 1
Best Local Similarity: 99.39% Mismatches: 1
Query Match: 61.88% Indels: 0
DB: 19 Gaps: 0

US-09-917-265-62 (1-533) x AAV13816 (1-990)

QY 4 GlnGlnLeuValIleSerTrpPheSerLeuValLeuLeuAlaSerProLeuMetaIle 23
Db 10 CAGCAGTTGGTCAATCTCTGCTTCCCTCGTTTCTGGCGCTCTCCCATGACCATCA 69

QY 24 TrpGlnLeuGlnIuLysAspValTyrValValGlnIuLeuAspTrpPheSerProAspAlaProGly 43
Db 70 TGGGACATGCGAAGAAAGATGTTATCTGTGTAGAGTTGGATGCGACCCCTGATGCCCGCGA 129

QY 44 GlnMetValValLeuThrCysHisThrProGlnIuAspAspIleThrTrpThrSerAla 63
Db 130 GAATGGGTGGTCTCCACCTGGCATACCCCTGAACAGATGACATCACTTGGACCTCAGCG 189

QY 64 GlnSerSerGlnValLeuGlySerGlyLysThrLeuThrIleGlnValLysGlnPheGly 83
Db 190 CAGACAGTGAAGTCTAGGTTCTGTGTAACCTGTGACATCCAAAGTCAAAAGATTGGA 249

QY 84 AspAlaGlnGlnTrpThrCysHisLysGlyLysLysValLeuSerArgSerLeuLeu 103
Db 250 GATGCTGGCCAGTATACCTGCCATGAAGGCAAGGTTCTGGACCCCTCATCTCTGTG 309

QY 104 IleHisLysLysGlnAspGlyIleTrpSerThrAspIleLeuLysGlnGlnLysGlnSer 123
Db 310 ATTCACAAAAAAGAAAGATGGAATTTGGTCCCATGATCTTAAAGAAACAGAAAGATCC 369

QY 124 LysAsnLysIlePheLeuLysCysGlnAlaLysAsnTyrSerGlyArgPheThrCysTrp 143
Db 370 AAAAATGAATCTTCTGAAATGTGAGGCAAGAAATTAATCTGAGCGTTTCACATCGTGG 429

QY 144 TrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPheSer 163
Db 430 TGGCTGACGGCAATCAGTACTGATTTGAATTCAGTGTCAAAATAGACAGAGGCTTCTCT 489

QY 164 AspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgValAsp 183
Db 490 GACCCCAAGGGGTGACATGTGAGCAGTGACATTTTCAGCAGAGAGGTCAGAGTGAG 549

QY 184 AsnArgAspTyrLysLysTyrThrValGlnCysGlnGlnLysSerAlaCysProSerAla 203
Db 550 AACAGGATTAATAAGAGTACACAGTGTGAGGAGTGAGGAGGAGTGTGCTGCGCC 609

QY 204 GlnGlnSerLeuProIleGlnValValValAspAlaIleHisLysLeuLysTyrGlnAsn 223
Db 610 GAGGAGAGCTTACCATGTGAGGTGTGTGTGATGCTATTCCAGAGCTCAAGTATGAAAC 669

QY 224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProTrpAsnLeuGln 243
Db 670 TACACACGACGCTTCTTCATGACAGACATGATCAACACAGACCCACACAACTGTCAG 729

QY 244 LeuLysProLeuLysAsnSerArgHisValGlnValSerTrpGluTyrProAspThrTrp 263
Db 730 CTGAAGCCATTCGAAATTCCTCCGACGTGAGGTGAGTGGGAATACCCCGACACCTGG 789

QY 264 SerTrpProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsnAsn 283
Db 790 AGCACCCCAATTCCT 849

QY 284 ArgGlnLysLysAspArgLeuCysValAspLysThrSerAlaLysValLysCysHisLys 303
Db 850 AGACAAAAGAAAGATACACTGTGCTGACAAAGCCTCAGCAAGTCTGTGTCACAAAG 909

QY 304 AspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAspTrp 323
Db 910 GATCCCAAGATCCCGCTGCAAGCCGAGAGCCGCTACTACTATGTTCTCTGAGAGTGG 969

QY 324 AlaSerValSerCysSer 329
Db 970 GCATCTGTGGCTCTGCAGT 987

RESULT 15
ID AAX35615 standard; cDNA to mRNA; 990 BP.
XX AAX35615
AC AAX35615:
DT 09-JUL-1999 (first entry)
XX

DE Nucleic acid encoding canine Interleukin-12 (IL-12).

XX Interleukin-12; IL-12; dog; cat; immune disease; CatIL2; heterodimer;
 KW tumour; skin disease; infectious disease; allergic disease; ds.

XX Canis sp.

XX Key Location/Qualifiers
 FT CDS 1..990
 FT /+tag= a

XX JP11106350-A.

XX 20-APR-1999.

XX 15-MAY-1998; 98JP-0133345.

XX 07-AUG-1997; 97JP-0213755.

XX 16-MAY-1997; 97JP-0127690.

XX (TORA) TORAY IND INC.

XX WPI; 1999-308068/26.

XX P-PSDB; AAY02339.

XX A prevention and treating agent containing interleukin 12 (CatIL2) -
 PT for prevention and treatment of dog and cat immune diseases

XX Claim 1; Page 12; 16pp; Japanese.

XX The present sequence encodes canine interleukin-12 (IL-12). The
 CC specification describes a method for the prevention and treatment
 CC of dog and cat immune diseases. The treatment used an agent comprising
 CC dog IL-12 (CatIL2) proteins to form a heterodimer. The agent is
 CC useful for preventing and treating dog and cat immune diseases,
 CC including tumours, skin diseases, infectious diseases and allergic
 CC diseases.

XX Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 other;

Alignment Scores:

Pred. NO.: 8.87e-145 Length: 990
 Score: 1735.00 Matches: 324
 Percent Similarity: 99.69% Conservative: 1
 Best Local Similarity: 99.39% Mismatches: 1
 Query Match: 61.88% Indels: 0
 DB: 20 Gaps: 0

US-09-917-265-62 (1-533) x AAX35615 (1-990)

QY 4 GlnGlnLeuValIleSerTrpPheSerLeuValLeuLeuAlaSerProleuMetAlaIle 23
 Db 10 CAGCAGTGTGTCATCTTGTTCCTGTTTGGTGTGGCTCCCTCCATGCGCATFA 69
 QY 24 TrpGlnLeuGlnIleValIleValIleValIleValIleValIleValIleValIle 43
 Db 70 TGGGAAGTGGAGAAAGATGTTATGTTAGAGTTGAGCTGACACCTGATGCCCGGA 129
 QY 44 GluMetValIleLeuTrpCysHisTrpProGlnGluAspSerIleThrTrpIleSerAla 63
 Db 130 GAATGTTGTTCTCCATCTCCATACCCGGAAGAAAGATGATCATCTTGGACCTCAGCG 189
 QY 64 GluSerSerGlnValLeuGlnSerGlnValTrpLeuThrIleGlnValIleValIleValIle 83
 Db 190 CAGAGCAGTAAAGTCTAGTCTGTAAGTCTGACCATCCAGTCAAGCAAGATTTGGA 249
 QY 84 AspAlaGlnIleTrpTrpCysHisLysGlnValIleValIleValIleValIleValIle 103
 Db 250 GATGCTGGCCAGTATACCTCCATAAAGGAGCAAGGTCTGAGCCGCTCAGCTCTGTG 309
 QY 104 IleHisLysLysGlnAspGlyIleTrpSerThrAspIleLeuLysGlnIleLysGlnSer 123
 Db 310 ATTACCAAAAGAAAGATGGAATTTGTTGCTGATATCTTAAAGGAACAGAAATTC 369

QY 124 LysAsnLysIlePheLeuLysCysGlnAlaLysAsnTrpSerGlyArgPheThrCysTrp 143
 Db 370 AAAAATAAATATCTTCTGTAATGTGAGCGCAAGAAATTTATTCGAGCTTTCATGCTG 429
 QY 144 TrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPheSer 163
 Db 430 TGGCTGACCGCATATGATGATTTGAAATTCAGTGTCAAAAGTAGAGAGGCTTCTCT 489
 QY 164 AspProGlnGlnValIleTrpCysGlnValIleThrLeuSerAlaGlnValIleValIleValIle 183
 Db 490 GACCCCAAGGGGTGACATGTGAGCAGTGTTCAGCAGAGAGGTCAGAGTGGAC 549
 QY 184 AsnArgAspTrpLysLysTrpThrValGlnCysGlnGlnGlnSerAlaCysProSerAla 203
 Db 550 AACAGGATTTATAAAGATACACAGTGTGAGAGGTCAGAGAGGTCAGAGGTCAGAGTGGAC 609
 QY 204 GlnGlnSerLeuProIleGlnValIleValIleValIleValIleValIleValIleValIle 223
 Db 610 GAGGAGAGCCATCCATCGAGGTGCTGATGCTATTACACAGCTCAAGTATGAAAC 669
 QY 224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeuGln 243
 Db 670 TACACGACGCTTCTTCTCAGACATATCAAAACAGACCCACCAACCTGACAG 729
 QY 244 LeuLysProLeuLysAsnSerArgHisValGlnValSerTrpGlnTrpProAspThrTrp 263
 Db 730 CTGAAGCCATTGGAATTTCTCGGACGTGAGAGTGTGAGGATATACCCGACACCTGG 789
 QY 264 SerThrProHisSerTrpPheSerLeuThrPheCysIleGlnAlaGlnIleLysAsnAsn 283
 Db 790 AGCACCCCATCTTCTTCTCAGACATATCAAAACAGACCCACCAACCTGACAG 849
 QY 284 ArgGlnLysLysAspArgLeuCysValIleValIleValIleValIleValIleValIleValIle 303
 Db 850 AGGAAAGAAAGATGATGCTGCGTGGCAAGACTCAGCCAGAGTCTGTGCCAAG 909
 QY 304 AspAlaLysIleArgValGlnAlaArgAspArgTrpTrpSerSerSerTrpSerAspTrp 323
 Db 910 GATGCCAAGATCCGCGTGCAGACCCGACCGCTACTATATGATCTTCTGAGCAGCATGG 969
 QY 324 AlaSerValSerCysSer 329
 Db 970 GCATCTGTGCCCTGCACT 987

Search completed: July 16, 2003, 20:24:46
 Job time : 413.833 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 16, 2003, 19:41:51 ; Search time 2535.24 Seconds

(without alignments)

3404.880 Million cell updates/sec

Title: US-09-917-265-62

Perfect score: 2804

Sequence: 1 MHPOQLVISMFLVLLASPL.....HAFIRAVTINRMSTYLNSS 533

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cgn2_1/USPRO.spool/US09917655/runatc_15072003_092107_1610/app-query.fasta.1.3114
-DB=EST -QMT=fastlap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blonsum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09917655 -RCGN_1_1_6304_@runatc_15072003_092107_1610 -KCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_est3:*
12: gb_est4:*
13: gb_est5:*
14: gb_est6:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vit:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------------|---------------------|
| 1 | 566.5 | 20.2 | 475 | 12 BF704417 | BF704417 M1-P-E6-a |
| 2 | 406 | 14.5 | 812 | 12 BG702253 | BG702253 602683459 |
| 3 | 394 | 14.1 | 589 | 9 A1050362 | A1050362 ub30a07.r |
| C 4 | 379 | 13.5 | 1099 | 13 B1523344 | B1523344 603175938 |
| 5 | 354 | 12.6 | 535 | 17 A2441303 | A2441303 1M0232M24 |
| 6 | 340 | 12.1 | 373 | 12 BF552757 | BF552757 UT-R-CO-1 |
| C 7 | 324 | 11.6 | 569 | 17 A2853726 | A2853726 2M0157M01 |
| 8 | 321.5 | 11.5 | 832 | 13 B1523569 | B1523569 603175938 |
| 9 | 172.5 | 6.2 | 342 | 13 BM257856 | BM257856 521721 MA |
| C 10 | 170 | 6.1 | 668 | 17 AG079702 | AG079702 Pan tlog1 |
| 11 | 156 | 5.6 | 509 | 12 BG554242 | BG554242 dab70807. |
| 12 | 153.5 | 5.5 | 875 | 9 AL537375 | AL537375 AL537375 |
| 13 | 152.5 | 5.4 | 882 | 14 BQ223533 | BQ223533 ACENECOURT |
| 14 | 150.5 | 5.4 | 997 | 9 AL528607 | AL528607 AL528607 |
| 15 | 144.5 | 5.2 | 873 | 9 AL518132 | AL518132 AL518132 |
| 16 | 141 | 5.0 | 938 | 12 BE901933 | BE901933 601676878 |
| 17 | 139 | 5.0 | 700 | 14 BQ749057 | BQ749057 UT-M-FB0- |
| 18 | 138.5 | 4.9 | 511 | 12 BG359887 | BG359887 dab8805. |
| 19 | 135.5 | 4.8 | 591 | 14 BM685621 | BM685621 UT-E-C10- |
| C 20 | 134 | 4.8 | 324 | 17 A0981401 | A0981401 RPI-23-3 |
| 21 | 133.5 | 4.8 | 481 | 14 BM710190 | BM710190 UT-E-CO1- |
| 22 | 133.5 | 4.8 | 769 | 14 BM719097 | BM719097 UT-E-EO1- |
| 23 | 129.5 | 4.6 | 683 | 10 AW950312 | AW950312 EST362382 |
| 24 | 127.5 | 4.5 | 912 | 13 B1760931 | B1760931 603043131 |
| 25 | 127 | 4.5 | 1082 | 14 BM919605 | BM919605 ACENECOURT |
| 26 | 126 | 4.5 | 447 | 13 B1824638 | B1824638 603033580 |
| 27 | 124.5 | 4.4 | 361 | 14 T28073 | T28073 EST26562 Hu |
| 28 | 124.5 | 4.4 | 779 | 13 B1333959 | B1333959 602997231 |
| 29 | 123.5 | 4.4 | 421 | 14 D78905 | D78905 HUM526C04B |
| 30 | 123.5 | 4.4 | 502 | 10 BE650170 | BE650170 UT-M-BH3- |
| 31 | 123.5 | 4.4 | 624 | 12 BG713383 | BG713383 p911n.pk0 |
| 32 | 123 | 4.4 | 412 | 9 AL629081 | AL629081 fc09041.y |
| 33 | 123 | 4.4 | 846 | 9 AL525319 | AL525319 AL525319 |
| 34 | 123 | 4.4 | 906 | 12 BG754874 | BG754874 602714263 |
| 35 | 123 | 4.4 | 918 | 9 AL550798 | AL550798 AL550798 |
| 36 | 123 | 4.4 | 927 | 9 AL553060 | AL553060 AL553060 |
| 37 | 123 | 4.4 | 948 | 9 AL545121 | AL545121 AL545121 |
| 38 | 123 | 4.4 | 950 | 9 AL551603 | AL551603 AL551603 |
| 39 | 123 | 4.4 | 973 | 9 AL548148 | AL548148 AL548148 |
| 40 | 122 | 4.4 | 859 | 12 BG434397 | BG434397 602506409 |
| 41 | 121 | 4.3 | 742 | 9 AL549396 | AL549396 AL549396 |
| C 42 | 120 | 4.3 | 916 | 9 AL576559 | AL576559 AL576559 |
| 43 | 119.5 | 4.3 | 666 | 14 BM935910 | BM935910 UT-M-CG0P |
| 44 | 119.5 | 4.3 | 947 | 14 BQ939522 | BQ939522 ACENECOURT |
| 45 | 119 | 4.2 | 675 | 12 BG621100 | BG621100 602616982 |

ALIGNMENTS

RESULT 1
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DEFINITION M1-P-E6-acc-g-09-1-UM sl M1-P-E6 Sus scrofa cDNA clone
ACCESSION BF704417
VERSION BF704417.1 GI:11989825
KEYWORDS EST.
SOURCE Sus scrofa
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 475)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene

JOURNAL
MEDLINE
COMMENT

discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
Contact: Tuggele CK
Molecular Genetics Laboratory, Department of Animal Science
Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
Tel: 5152944252
Fax: 5152942401
Email: cktugge@iastate.edu
Oligo-dr track not found. Not 1 site shown in beginning of sequence
is likely internal to the message. cDNA library preparation: RJ
Woods, JA Green, RS Prather S142 Animal Science Research Center,
Department of Animal Science, University of Missouri-Columbia,
65211 Clone distribution: clones will be available through Research
Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA-NO.

FEATURES
Source

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/strain="crossbreed"
/db_xref="taxon:9823"
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/clone_lib="MI-P-E6"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site 1: Not 1; Site 2: Score: The MI-P-E6
library is derived from fetus at gestational day 20. For
a detailed description of the library from which this
clone was derived, please visit our web site at
http://piglet.genome.iastate.edu/
TAG-SEQ=None found"

BASE COUNT 129 a 120 c 121 g 104 t 1 others
ORIGIN

Alignment Scores:

Pred. No.: 1.98e-52 Length: 475
Score: 566.50 Matches: 107
Percent Similarity: 83.69% Conservative: 11
Best Local Similarity: 75.89% Mismatches: 20
Query Match: 20.20% Indels: 3
Gaps: 1

US-09-917-265-62 (1-533) x BF704417 (1-475)

QY 5 GlnLeuValIleSerTrpPheSerLeuValIleLeuAlaSerProLeuAlaIleTrp 24
Db 58 AACGTACCATCTCCGCTTGGCATCGTTTCTGCTGCTCATGCGCCATGCG 117
QY 25 GluLeuGluLysAspAlaValValGluLeuAspTrpHisProAspAlaProGlyGlu 44
Db 118 GACCTGGAGAAAGACCTTATGTTAGAGGTGAGTGCATGCCATGCCCTCGAGAA 177
QY 45 MetValValLeuThrCysHisThrProGluGluAspIleLeuThrTrpHisAlaGln 64
Db 178 ACAGTAACTCCTCCTGACACGCTGAGAAAGATGACATCAGCTGAGCCAGCAG 237
QY 65 SerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPheGlyAsp 84
Db 238 AGACATGAGTATAGCTCTGGAAGACCTGACATCAGCTCAAGAGTTTCTAGAT 297
QY 85 AlaGlyGlnTrpThrCysHisLysGlyLysValLeuSerArgSerLeuLeuIle 104
Db 298 GGTGGCCAGTACCCGACCAAGAGGCGAGCTGAGCAGTACATCATCTGCTGTC 357
QY 105 HisLysLysGluAspGlyLerTrpSerTrpAspIleLeuGluGlnLysGluSerLys 124
Db 358 CACAAAGAGAAAGAAATTTGCTCAGTAAATTTTA-----AAAAATTTTCAA 408
QY 125 AsnLysIlePheLeuLysCysGluAlaLysAsnTrpSerGlyArgPheThrCysTrpTrp 144
Db 409 AACAAAGACTTCTGAGTGAAGTGAAGACCAATTTACTCGGACGGTTTCAGTCTCATGG 468

QY 145 Leu 145
Db 469 GTG 471

RESULT 2
BG702253
LOCUS
DEFINITION
602683459F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4816118 5',
mRNA sequence.
ACCESSION
BG702253
VERSION
BG702253.1 GI:13973409
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens

REFERENCE
1 (bases 1 to 812)
NIH-MGC http://mgi.nci.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cga@bbsr@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shihaki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10714 row: e column: 15
High quality sequence stop: 804.

FEATURES
Source

1. 812
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/clone="IMAGE:4816118"
/clone_lib="NIH_MGC_95"
/tissue_type="hippocampus"
/lab_host="DH10B"
/note="Organ: Brain; Vector: pBluescript (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag
) Oligo-dr primed using primer 5'-TTTGTGTTTGTGTTTGTGTTT-3',
size-selected for average insert size 2.5 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapped method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC library."

BASE COUNT 188 a 249 c 226 g 149 t

ORIGIN

Alignment Scores:
Pred. No.: 3.39e-34 Length: 812
Score: 406.00 Matches: 107
Percent Similarity: 65.12% Conservative: 5
Best Local Similarity: 62.21% Mismatches: 35
Query Match: 14.48% Indels: 29
Gaps: 4

US-09-917-265-62 (1-533) x BG702253 (1-812)

QY 275 CysIleGlnAlaGlnGlyLysAsnAsnArgGluLysAspArgLeuCysValAspLys 294
Db 373 TGCATCCAG-----CGGCTCGCCCTGTGTGCC 399
QY 295 ThrSerAlaLysValAlaCysHisLysAspAlaLysIleArgValGlnAlaArgAspArg 314
Db 400 TGCAGTCCGCGCTGACGATG-----GTCCAG-----CGC 429
QY 315 TyrTrpSerSerSerTrpSerAspTrpAlaSerValSerCysSerGlyGlyGlyGly 334

| | | | |
|------------|---|---|-----|
| Db | 430 | CCACGCTTCCTTGTGGTACCCTGGTCCCTCGAGCACCCTCA-----GTT | 477 |
| OY | 335 | GlySerA rgsAnLeuProThrP r o ThrProSerProgl yMetPheGlnCysLeuAsnHis | 354 |
| | | ::::::::::::::::::::: | |
| Db | 478 | TG-GCCAGAAACCTCCGCCGTGGCCACTGCACACCAACCAAGGAATGTTCCCATGCTTCACAC | 536 |
| OY | 355 | SerGlnThrLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGlu | 374 |
| | | ::::::::::::::::::::: | |
| Db | 537 | TCCCAAAACCTGGAGGCGGTGACGACAACATGCTCCAGAAGGCGCACCAACCTTGAA | 596 |
| OY | 375 | LeuTrSerCysThrSerGluGlnIleAspHisGluAspIleThrLysAspLysThrSer | 394 |
| | | ::::::::::::::::::::: | |
| Db | 597 | TTTTACCCCTTGACTCTTGAGAGACATCATATAGATATACAAAAAGATAAACACAC | 656 |
| OY | 395 | ThrValGluAlaCysLeuProLeuGlnLeuThrMetAsnGluSerCysLeuAlaSerArg | 414 |
| | | ACATTGGAGGCGCTTTACCATTTGGAATTAACCAAGAATGAGAGTTGCT--AAATCCGA | 714 |
| Db | 657 | ACATTGGAGGCGCTTTACCATTTGGAATTAACCAAGAATGAGAGTTGCT--AAATCCGA | 714 |
| OY | 415 | GluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThr | 434 |
| | | ::::::::::::::::::::: | |
| Db | 715 | GAGACCTCTTTCATACCAATGAGGAGTTGCTGCTCCAGA-AAGACCTCTTTATGATG | 773 |
| OY | 435 | ValLeuSerLeuSerSerIleTygGlnAspLeuLys | 446 |
| | | ::::::::::::::::::::: | |
| Db | 774 | TGCTGTGCTTACTTAGTAT-TATGAGACCTTGAAA | 808 |
| RESULT 3 | | | |
| A1050362 | | | |
| LOCUS | | | |
| DEFINITION | A1050362 | 589 bp mRNA linear EST 09-JUL-1998 | |
| | | ub05a07.f1 Soares_thymus_2NBWf Mus musculus cDNA clone | |
| | | IMAGE:1379220.5' similar to gb:M65291 INTERLEUKIN-12 ALPHA CHAIN | |
| | | PREDUCOR (HUMAN) : gb:M86572 Mus musculus Interleukin 12 p35 | |
| | | subunit, complete cds (MOUSE); , mRNA sequence. | |
| ACCESSION | A1050362 | | |
| VERSION | A1050362.1 | GI:3299479 | |
| KEYWORDS | EST. | | |
| SOURCE | house mouse. | | |
| ORGANISM | Mus musculus | | |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | |
| REFERENCE | 1 (bases 1 to 589) | | |
| AUTHORS | Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,W., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R. | | |
| TITLE | The WashU-HMI Mouse EST Project | | |
| JOURNAL | Unpublished (1996) | | |
| COMMENT | Contact: Marra M/Mouse EST Project WashU-HMI Mouse EST Project Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MG:901688 Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 60. Location/Ounalifiers 1..589 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="IMAGE:1379220" /clone_id="Soares_thymus_2NBWf" /sex="male" /tissue_type="Thymus" /dev_stage="4 weeks" /lab_host="DH10B" /note=Vector: pT73AD-Pac (Pharmacia) with a modified polylinker. Site_1 Not I; Site_2 Eco RI; 1st strand cDNA | | |

was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAGTCGGCGCCGCCTTTTTTTTTTTTTTTTT
3'] : double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pTV7n3 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M.Fátima Bonald.o."

BASE COUNT 162 a 159 C 142 G 126 T

ORIGIN

Alignment Scores:

| | |
|-------------------------------|------------------|
| Pred. No.: 4.31e-33 | Length: 589 |
| Score: 394.00 | Matches: 90 |
| Percent Similarity: 68.90% | Conservative: 23 |
| Best Local Similarity: 54.88% | Mismatches: 43 |
| Query Match: 14.05% | Indels: 8 |
| DB: 9 | Gaps: 3 |

US-09-917-265-62 (1-533) x AI050362 (1-589)

| | | | |
|----|-----|--|-----|
| OY | 368 | LysAlaaArgGlInThrLeuGluLeuTySerCysThrSeriuglIleAspHisGIuaSp | 387 |
| Dd | 108 | CAGGCCAGAGA AAAACTGTAAACATTATTCTCGCACTGCTGAAGCATGATCAAGAAC | 167 |
| OY | 388 | IleThryIasPllyThrSerThrValIGluIlaCysLeuProLeuGluIleThrmEtaSn | 407 |
| Dd | 168 | ATCACACGGAGCAAACACAGCACATVTGAAGACGTGTTACCACATGGAACACTACACAAGAC | 227 |
| OY | 408 | GlusercyLsleualiaserAargLIUleserleuilethrAnsglyserCysleualaSer | 427 |
| Dd | 228 | GAGAGTTOCCCTGGCTACTAGAGAGACTCTTCCACACAAAGAGAGAGCTGCTCCCCA | 287 |
| OY | 428 | GlylsalaserPheMetThrValleucysleuserSerietyrgluaspleuylsMet | 447 |
| Dd | 288 | CAGAAAGACGCTTTGATGATATACCCCTGTGCTTGGTAACATCTATGAGAGACTGAAGATG | 347 |
| OY | 448 | TyrIGmetGluPheLysAlaMetaSnAlaLysleuleuMetaSprolyAsrArgGlnIle | 467 |
| Dd | 348 | TACCAGACAGAGATTCCACAGCCATCACGACACTTAGAATTCACAACCATCACAGATC | 407 |
| OY | 468 | PheleunspgIinasMelIethThralIleaspCluIleuLeuGlnAlalaLeuasPheasn | 487 |
| Dd | 408 | ATTCTAGCAAGAGGCACTCTGGTGGCATGATAGCTGAGTCACTCTGTAATCARPAT | 467 |
| OY | 488 | ServalThrValProGlnLysSerSerleu---GluGluProAspPheTyrlsThrlys | 506 |
| Dd | 468 | GGCGAGACTCTGCCCAAGAACCTCCCTGTGGGAGAGAGCAGACCCCTTACAGAGATGAA | 527 |
| OY | 507 | -----IleLysleuCysIIleleuLeuHIsIalaphearyIleArGla--ValThri | 523 |
| Dd | 528 | AATGAAGCGTCGTGAATCTGTC-----TTTCACGCCCTTTGACAGACCGGCGCTGTACCA | 581 |
| OY | 523 | IeaSnArg 525 | |
| Dd | 582 | TCAACAGG 589 | |

RESULT 4 B1523344/c

LOCUS B1523344 1099 bp mRNA linear EST 29-AUG-2001

DEFINITION 603175938r1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240216 3',

mRNA sequence.

B1523344

ACCESSION B1523344 GI:15348136

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

| | | |
|--|---|--|
| | COMMENT | Contact: Robert Struspeuss, Ph.D. Email: csgaps@femail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov Plate: LLAM1605 row: 1 column: 09 High quality sequence start: 40 High quality sequence stop: 727. Location/Qualifiers |
| | FEATURES | source 1..1099 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:5240216" /lab_host="NIH_MGC_121" /lab_host="DH10B" /note="Organ: brain; Vector: PCMV-SPORT6; Site:1: NotI; Site:2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains; female age 20 weeks; female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH MGC Library." |
| | BASE COUNT | 359 a 244 c 218 g 276 t 2 others |
| | ORIGIN | |
| | Alignment Scores: | |
| | Pred. NO.: | 5.62e-31 Length: 1099 |
| | Score: | 379.00 Matches: 85 |
| | Percent Similarity: | 90.10% Conservative: 6 |
| | Best local Similarity: | 84.16% Mismatches: 7 |
| | Query Match: | 13.52% Indels: 4 |
| | DB: | 13 Gaps: 0 |
| US-09-917-265-62 (1-533) x B1523344 (1-1099) | | |
| OY | 436 | LeucySleuSerSerLleTYrGLAsPleuIsymetTYrGlnMetGLuPhelysAlamEt 455 |
| Dd | 737 | CTGTGCTTTAGTAGTATTATTAACAACACTG-AAAGATGTACCAAGTGGAATTAACAACACTG 679 |
| OY | 456 | AsnaLaTySleu-LeuMeTaSProLYsaRGInIllePhelEuAspGlnasmetLeuTh 475 |
| Dd | 678 | AATGCCAAAGCTTCCTGATGGATCCTTAACAGCACAGATCTTTAGATCAAAACATGCTGC 619 |
| OY | 475 | fAlaIlleAspGlueuEngInAlaleuAsnPhesnseryValThrValProGlnlyse 495 |
| Dd | 618 | AGTTATTGATAGCGATGCAGCGCCCTGAATTTCAACAGTGAAGACTGTGCCAATAATTC 559 |
| OY | 495 | rSerLeugluLuProasp--PheTYrLySThyrLyslLeuCYsIlleLeuLeuIs 514 |
| Dd | 558 | CTCCCTTGAAGAACCAGGATGTTTATATCAAAAACCTGAATCAACAGCTCTCATCTTTCAT 499 |
| OY | 515 | AlapheaRgllleaRgaIalValThrIlleasnArgMetSetTYrTleuAsnSerSer 533 |
| Dd | 498 | GCTTTCAGAAATTGGCGCAGTACGATTAATGATAGAGTGAAGACCTATCTGAAATGCTTCC 442 |
| RESULT 5 | | |
| AZ441303 | | |
| LOCUS | AZ441303 | 535 bp DNA linear GSS 03-OCT-2000 |
| DEFINITION | 100232M24R Mouse 10kb plasmid U08C1M library Mus musculus genomic | |
| ACCESSION | AZ441303 | |
| VERSION | AZ441303.1 | GI:10565316 |
| KEYWORDS | GSS. | |
| SOURCE | house mouse. | |
| ORGANISM | Mus musculus | |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | |

REFERENCE Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus
1 (bases 1 to 535)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamll,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE Unpublished (2000)

JOURNAL Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dduwn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0232 row: M column: 24
Seq primer: CACACAGGAAACACGTATGACC
Class: plasmid ends
High quality sequence stop: 535.

FEATURES
Source
1..535
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U08C1M0232M24"
/clone_lib="Mouse 10kb plasmid U08C1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gii47321149b)AP129072.1) a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 132 a 135 c 130 g 137 t 1 others

ORIGIN

Alignment Scores:
Pred. No.: 1.03e-28 Length: 535
Score: 354.00 Matches: 71
Percent Similarity: 78.00% Conservative: 7
Best Local Similarity: Mismatches: 21
Query Match: 12.62% Indels: 1
DB: 17 Gaps: 0

US-09-917-265-62 (1-533) x AZ441303 (1-535)

Qy 30 ValTyrValValIGulLeuAspTrpHisproksrApAProgiYgiUmetValValLeuThr 49
|||||
Db 86 GTTATGTTGTAAGAGGTGCTGACCTCCCATGCTCCCTGGAGAAACAGTAACCTCACCC 145
|||||

Qy 50 CysHISThr-ProGIuGIuAspAPLeThrTTPTrHserIacInserSerGIuValLe 69
|||||
Db 146 TGTGACACGCTCTGAAGACATGACATCCTGACCTCAACACAGAGACATGGAGTCAT 205
|||||

Qy 69 uGIySerGIyLysThrLeuThrIleGlnValLysGIuLubHeGIuAspAlaGIyIntYrTh 89
:|||||

Db 206 AGGCTTGGAAGACCCCTGACCATCATCTGTCAGAGAGTTTCTAGATGCTGGCCAGATACAC 265
Oy rCysH1stLysGLySLyValLeuSerArgSerLeuLeuLeuH1stLysGLuAs 109
|||||
Db 266 CTGCCACAAAGAGGCGAGCTGTGAGCCACTCATCTGTGCTGCTGACAGAAAGGAAAA 325
Oy 109 pGly1LeTrpSerThrAsp1LeuLysGLuGlnLysGLuSerLysAsnLysIlePhe 128
:|||||
Db 326 TGAATTTGCTGCACCTGAAATTTTAAAGTAATTCATCCCTGACACTATCTTT 383
RESULT 6 373 bp mRNA linear EST 12-DEC-2000
BF552757 UI-R-CO-12-d-02-0-UI.r1 UI-R-CO Rattus norvegicus cDNA clone
LOCUS UI-R-CO-12-d-02-0-UI 5', mRNA sequence.
DEFINITION
ACCESSION BF552757
VERSION BF552757.1 GI:11662487
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 373)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LNL (info@image.llnl.gov). IMAGE ID= 1782759
Seq primer: M13 Forward.
Location/Qualifiers
1..373
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-CO-12-d-02-0-UI"
/clone_lib="UI-R-CO"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pUT3D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; The UI-R-CO
library is a subtracted library derived from the UI-R-AI
and UI-R-EI libraries. The UI-R-AI library consisted of a
mixture of individually tagged normalized libraries
constructed from rat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, and muscle. The UI-R-EI
library consisted of a mixture of individually tagged
normalized libraries constructed from 8, 12 and 18-day
embryo. The tag is a string of 3-5 nucleotides present
between the Not I site and the oligo-dT track which
allows identification of the library of origin of a clone
within the mixture. The subtracted library (UI-R-CO) was
constructed as follows: PCR amplified cDNA inserts from a
pool of UI-R-AI and UI-R-EI clones from which 3' ESTs had
been derived was used as a driver in a hybridization with
the pooled UI-R-AI and UI-R-EI library in the form of
single-stranded circles. The remaining single-stranded
circles (subtracted library) was purified by
hydroxyapatite column chromatography, converted to
double-stranded circles and electroporated into DH10B
bacteria (Life Technologies) to generate the UI-R-CO
library. This procedure has been previously described

(Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
1996) "
BASE COUNT 106 a 93 c 89 g 85 t
ORIGIN
Alignment Scores:
Pred. No.: 2.06e-27 Length: 373
Score: 340.00 Matches: 69
Percent Similarity: 72.13% Conservative: 19
Best Local Similarity: 56.36 Mismatches: 34
Query Match: 12.13% Indels: 0
DB: 12 Caps: 0
US-09-917-265-62 (1-533) x BF552757 (1-373)
Oy 410 CysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLys 429
|||||
Db 8 TGCTGGCTACTAAAGACACTCTTCATTAAGAGGAGGAGCTGCTCCACAAAG 67
Oy 430 AlaSerPheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGln 449
||| |||
Db 68 ACTTCTTGATGATGAGCCCTGTGCTTGTCATCTATGAGCACTTGACATGTACCAG 127
Oy 450 MetGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeu 469
|||||
Db 128 TCAGAGTTCAGAGGCGCATTAATGACAGCACTTCAGAGCCACATCATCAGACATCACTGTG 187
Oy 470 AspGlnAsnMetLeuThrAlaIleAspGluLeuGlnAlaLeuAsnAspAsnSerVal 489
|||||
Db 188 GACAGAAACATGCGTATGCTATGATGAGCTTAATGCGTCTGTAATCAGACGCGCGAG 247
Oy 490 ThrValProGlnLysSerSerLeuGlnGluProAspPheTyrLysThrLysIleLysLeu 509
|||
Db 248 ATTCTGACACCGAAGAGCTCCCATGGAGACACAGATCTTACAGAGTGAAGATGAAGCTC 307
Oy 510 CysIleLeuLeuH1stAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyr 529
|||||
Db 308 TGTATTCGTCGTCATGCTTCAGACACAGCGCTCATGATATCAACAGGCGTATGACTAT 367
Oy 530 LeuAsn 531
|||
Db 368 CTGAGC 373
RESULT 7
A2853726/c 569 bp DNA linear GSS 21-FEB-2001
LOCUS A2853726
DEFINITION 2M0157M01F Mouse 10kb plasmid U06C1M library Mus musculus genomic
clone U06C2M0157M01 F, DNA sequence.
ACCESSION A2853726
A2853726
A2853726.1 GI:13042136
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 569)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamli,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0157 row: M column: 01


```
OY 395 ThrValGlnAlaCysLeuProLeuGlnLeuThr 405
Db 562 ACAAGTGGAGGCGCTGTTTACCATTTGAGATTAAAC 594

RESULT 9
LOCUS BM257856 342 bp mRNA linear EST 17-DEC-2001
DEFINITION 521721 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BM257856
VERSION BM257856.1 GI:17893455
KEYWORDS EST.
SOURCE cDNA.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.

REFERENCE
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,
G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-Mckown,C.G.,
Perteau,G., Holt,I., Karaymicheva,S., Liang,F., Quackenbush,J. and
Keele,J.W.
TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
JOURNAL libraries and construction of a gene index for cattle
MEDLINE Genome Res. 11 (4), 626-630 (2001)
COMMENT 21180013
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt. trimmed with phred
v0.980904.e. Vector identified by cross-match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCAGTCAGCAGC
Plate: 125 row: E column: 18
Seq primer: ATTAGGTGACTATAG.
FEATURES
source
location/Qualifiers
1..342
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."
BASE COUNT 67 a 135 c 74 g 66 t
ORIGIN

Alignment Scores:
Pred. No.: 7.58e-09 Length: 342
Score: 172.50 Matches: 43
Percent Similarity: 73.13% Conservative: 6
Best Local Similarity: 64.18% Mismatches: 14
Query Match: 6.15% Indels: 5
DB: 13 Gaps: 3
US-09-917-265-62 (1-533) x BM257856 (1-342)

OY 317 SerSerSerTyrSerSerTyrP---AlaSerValSerCysSerGlyGlyGlyGlyGly 335
Db 151 TCTCTCTCATATCCACCCCTGTTCTCTCCACCCAGCCGACCTCAGTTTG--- 206

OY 336 SerAraAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSer 355
Db 207 ---AGAGAGCTCTCCACACACACAGCAAGGCCAGGAGG---AGCTGCTCTGCACTACTCC 260

OY 356 GlnThrLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGlnLeu 375
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```
Db 261 CAAAACCTGCGAGCGCTGTCAGACACCGCTACAGAGCGACAACTCTGAGATT 320
OY 376 TyrSerCysThrSerGlnGlu 382
Db 321 TACTCTGACACTTCTGTGAGGAG 341

RESULT 10
LOCUS AG079702/c 668 bp DNA linear GSS 03-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-075107.R, genomic survey sequence.
ACCESSION AG079702
VERSION AG079702.1 GI:16631504
KEYWORDS GSS.
SOURCE Pan troglodytes male lymphoblast DNA, clone_lib: PTB Chimpanzee Male
BAC library clone: PTB-075107.R.
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pan.

REFERENCE
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Tocoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Unpublished
JOURNAL BAC end sequences of library PTB
REFERENCE 2 (bases 1 to 668)
AUTHORS Totoki,Y., Watanabe,H., Toyoda,A., Taylor,T.D., Yada,T.,
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Tocoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsuri-mi-Ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:shimbes@gs.c.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT Clones are derived from the chimpanzee BAC library PTB This BAC end
clones were generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: M13Rev
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
location/Qualifiers
1..668
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-075107.R"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
BASE COUNT 180 a 138 c 137 g 213 t
ORIGIN

Alignment Scores:
Pred. No.: 4.34e-08 Length: 668
Score: 170.00 Matches: 30
Percent Similarity: 82.50% Conservative: 3
Best Local Similarity: 75.00% Mismatches: 7
Query Match: 6.06% Indels: 0
DB: 17 Gaps: 0
US-09-917-265-62 (1-533) x AG079702 (1-668)

OY 122 GlnSerLysAsnLysIlePheLeuLysCysGlnAlaLysAsnTyrSerGlyAraGpneThr 141
Db 542 GAACCCAGACACCTTAACCTTTGTAAGATGGAGACCAAGAAATATTCAGACGCTTCACC 483

OY 142 CysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGly 161
Db 482 TGCTGTGGCTGACGACAAATCACTGATTGACATTTCAGTGTCAAAAGCAGCAGAGG 423

RESULT 11
BG554242
```

| LOCUS | 509 bp | mRNA | linear | EST 09-APR-2001 |
|---|---|--------------------------------------|---|-----------------|
| DEFINITION | BC554242 | dab70a07.y2 NICHD XGC Embd | Xenopus laevis cDNA clone IMAGE:4202388 | |
| ACCESSION | BC554242 | sequence. | | |
| VERSION | BC554242.1 | GI:13566022 | | |
| KEYWORDS | EST. | | | |
| SOURCE | African clawed frog. | | | |
| ORGANISM | Xenopus laevis | | | |
| REFERENCE | Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Xenopus. | | | |
| AUTHORS | NCI-CCGAP | http://www.ncbi.nlm.nih.gov/ncicgap. | | |
| TITLE | National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index | | | |
| JOURNAL | Unpublished (1997) | | | |
| COMMENT | Other-ESTs: dab70a07.x1 Contact: Robert Strausberg, Ph.D. Email: cga@bbs-rrmail.nih.gov Tissue Procurement: Martha Rebert, Steven L. Klein, Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Washington University Genome Sequencing Center clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LNLN at: info@image.lnl.gov Seq primer: -40RP from Glibco High quality sequence stop: 385. Location/Qualifiers | | | |
| FEATURES | 1..509 | | | |
| SOURCE | /organism="Xenopus laevis" /db_xref="taxon:8355" /clone="IMAGE:4202388" /clone_lib="NICHD XGC Embd4" /dev_stage="embryo, stage 31-32" /lab_host="DH10B (phage-resistant)" /note="Organ: whole embryo; Vector: pCMV-Sport6; Site:1; NotI; Site:2; SalI; cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb. Constructed by Life Technologies. Note: This is a Xenopus Gene Collection (XGC) library." | | | |
| BASE COUNT | 111 a 146 c 124 g 128 t | | | |
| ALIGN | | | | |
| Alignment Scores: | 9.99e-07 | Length: 509 | | |
| Pred. NO.: | 156.00 | Matches: 52 | | |
| Score: | 41.03% | Conservative: 28 | | |
| Percent Similarity: | 26.67% | Mismatches: 75 | | |
| Best Local Similarity: | 5.56% | Indels: 40 | | |
| Query Match: | 12 | Gaps: 8 | | |
| US-09-917-265-62 (1-533) x BC554242 (1-509) | | | | |
| 0Y | 86 GLYGNTYRTHCYSHISLYSGLYYSVALLSEURARGSERLEULEULEHIS | 105 | | |
| Db | 6 GGCAACTACACTGCTACAGTCACTCTCGGAGTCTGTAAGATCTGCTCTCTCAGAAATG | 65 | | |
| 0Y | 106 LYSYSGIUAERGLYLIETRPSETRHASPILLEULYSGLIUNLGLUSERLYSASN | 125 | | |
| Db | 66 GGATACCCCGCAGGAGCCCGCTCA----- | 89 | | |
| 0Y | 126 LYSILPELEULYSYSGYLALALASANTYRSERGLYARGPHERHCYSTRTPTPLEU | 145 | | |
| Db | 90 ---GTTTTC-----TGTAGAGCTTCAACACTATAGAG---AACTTTCTGCTTCGCGAAA | 137 | | |
| 0Y | 146 THRALALIESERTHASPILLEULYSHESEERYALLYSSESRATRGGLYPHESERASPRO | 165 | | |
| Db | 138 TCCAGTGCAGACGCTTCCCTCCCTCCAGATTACTGCTTCCCTATCGAGCAGTAATAC | 197 | | |
| 0Y | 166 GLNGLYVALTHRCYSGLYALAVAlTHRIUSESERALAGUATGVALARGVALASPASNARG | 185 | | |
| Db | 198 ATCCGTGGCGTGTGTCTTCAGAACCGCTGGCGGCCCAATATGTGTCTCCGTACGAGAACTCT | 257 | | |

| | | | | |
|------------------------|--|--|---|-----------------|
| Qy | 186 | Aspryr--- | LysLysTyrThrValGlcCysGlnGluLysSerAlaCysProserAlaGlu | 204 |
| | | | | |
| Db | 258 | GAGTTTCGAGACTCCCTACAGATCAACATCACAGAGAAAAA | CCCGCTGGCATCCAGTTTC | 317 |
| Qy | 205 | GluSerLeuProlIleGluValValaValasPalalleHisLysLeuLysTyrGluAsnTyr | | 224 |
| | 318 | CCGCTGCTGCATGTACACGGTG----- | | 338 |
| Qy | 225 | ThrserSerPhepheleatgArspLlelleLysProAsrProPthrAsnLeuGlnLeu | | 244 |
| Db | 339 | ----- | CAGTCAATTGTAAACCGAGACCCTCCAGAGAACCTTGTGTG | 380 |
| Qy | 245 | LysProlLeuLysAnser---- | ArgHisValcGluValserTrgGlyTyrProAsrPThrTirp | 263 |
| | 381 | GAACCAATCCCGTTGCCGCCAGGAGGCTTCMACTCAgTTGGATTAATCCAATCCATTGG | 440 | |
| Qy | 264 | --SetThrProHisSerTyrPheSerLeuThrPheCysIleGln | 277 | |
| Db | 441 | CCCCAAGAAGCTCAT----- | TTCACACTCAAGTTCGCTGTCCAG | 479 |
| RESULT 12 | | | | |
| AL537375 | | 875 bp | mRNA | linear |
| LOCUS | AL537375 | | | EST 13-FEB-2001 |
| DEFINITION | AL537375 lTI_FL013_FBrn1 Homo sapiens cDNA clone CSDF025YJ10 5 | | | |
| ACCESSION | AL537375 | | | |
| VERSION | AL537375.1 | GI:12800868 | | |
| KEYWORDS | EST. | | | |
| SOURCE | human. | | | |
| ORGANISM | Homo sapiens | | | |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| | Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo. | | | |
| REFERENCE | 1 (bases 1 to 875) | | | |
| AUTHORS | Li,W.-B., Gruber,C., Jesse,J., and Polayes,D. | | | |
| TITLE | Full-length cDNA libraries and normalization | | | |
| JOURNAL | Unpublished (2001) | | | |
| COMMENT | Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr. Location/Qualifiers 1. 875 | | | |
| FEATURES | | | | |
| source | /organism="Homo sapiens" /db_xref="taxon:9606" /clone="CSDF025YJ10" /clone_1id="lTI_FL013_FBrn1" /dev_stage="pooled tissue from post conception fetuses (20 week, 24 week and 26 week)" /lab_host="DH10B" /note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville , Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com" | | | |
| BASE COUNT | 166 a | 284 c | 242 g | 182 t |
| ORIGIN | | | | 1 others |
| Alignment Scores: | | | | |
| Pred. NO.: | 4.63e-06 | Length: | | 875 |
| Score: | 153.50 | Matches: | | 64 |
| Percent Similarity: | 37.14% | Conservative: | | 27 |
| Best Local Similarity: | 26.12% | Mismatches: | | 96 |
| Query Match: | 5.47% | Indels: | | 60 |
| Dp: | 9 | Gaps: | | 11 |

DS-09-917-265-62 (1-533) x AL537375 (1-875)


```

Db      489 CCCACTCTGCACTCA-----TCTTCTACAGACTAGGTTTACGCTCAGATAATCGG 542
QY      280 GtlylYsAsnAaArq-----GtlylYsAspArqLeuCySVal 292
      543 GCGAAGCGTCAAGACATTACACATGATGATGTCAGAGACCTCCAGCATCTACTGTGTC 602
Db      293 AsplYstHrSerAlaYsValValCySHsLysAspAlaYsIleArqValGlnAlaArq 312
      603 ATCCAGACGCGCTGAGCGGCTGAGCGAC-----GTGCTGACAGCTTCTGCGCCAG 653
QY      313 AsparYtYrTyrSerSerSerTrpSerAspTrpAlaSerValSerCySserGlyGly 332
      654 GAGGAGTGTGGGCAAGCGGAGTGTGAGGAGTGTG-----ACCC-GGAGGC 697
Db      333 GlylYsGlySerArqAsnLeuProThrProThrProSerProGly 347
      698 CATGGGACGCGCTTGACAGCGCTTCTCTCCACAGACCATCCGGG 742

RESULT 14
AL528607 997 bp mRNA linear EST 13-FEB-2001
LOCUS AL528607 LTL_NFL001_NBC4 Homo sapiens cDNA clone CS0DD001YE13 5
DEFINITION prime, mRNA sequence.
ACCESSION AL528607
VERSION AL528607.1 GI:12792100
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
          Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 997)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
          Genoscope Centre National de Sequencage
          BP 191 91006 Evry cedex - France
          Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1.997
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DD001YE13"
/clone_1b="LTL_NFL001_NBC4"
/sex="male"
/tissue.type="neuroblastoma cells"
/lab.host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by life technologies. Contact: Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifestech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 180 a 331 c 290 g 184 t 12 others
ORIGIN
Alignment Scores:
Pred. No.: 1.24e-05 Length: 997
Score: 150.50 Matches: 67
Percent Similarity: 36.13% Conservative: 32
Best Local Similarity: 24.45% Mismatches: 94
Query Match: 5.37% Indels: 83
DB: 9 Gaps: 12

US-09-917-265-62 (1-533) x AL528607 (1-997)
QY 41 AlaProGlyGluMetValValLeuThrCySHsIleThrProGluGlu----- 55
Db 192 GCCGCCGCCGCGCATTTCTTAAGCCGCCAGARACACAGTCCACAGGAGCGACCCCATGTGCG 251

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QY 56 -----AspAlIleThr-----TrpThrSerAla 63
      252 TAGAGCGCGCTGGGCTCTGACGTGACACATGCGGACAGMAAACTGGATGCTGGC 311
Db 64 GlnSerSerGluValLeuGly-----SerGlyThrLeu 75
      312 GTGACGTGGCGGGTAATGAGACAGCATCGGCCCTGACCTGCTCAACGCTTCAGCTG 371
QY 76 ThrIleGlnValLysGluIuphGlyAspAlaGlyGlnIleThrCySHsLysGlyGly 95
      372 GTGCTTCATGCGCTGGAACCTGGCCACAGTGGCTTACGCTTCCACCGTACTCC 431
Db 96 ValLeuSerArgSerLeuLeuLeuIleHsLysLysGluAspGlyIleTrpSerThrAsp 115
      432 TGGCAGCTGGCGCCACACAGCTCGTGCATGTG-----GCCTTG----- 470
QY 116 IleLeuLysGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsn 135
      471 -----CCGCCGCGGAGCTGTCTCAGCGCGCTCCACACT 509
Db 136 TyrSerGlyArgPheThrCyStrpTrpLeuThrAlaIleSerThrAspLeuLysPheSer 155
      510 TACCCCAAGGCGCTTCTACTGACAGCTGGCATCTGCCACCCACCTACTAT----- 560
QY 156 ValLysSerSerArgGlyPheSerAspProGlnGlyValThrCysGlyAlaValThrLeu 175
      561 -----CCCAAC-----ACCTTCATGATGATGTCG 587
Db 176 SerAlaGlnArgValArgValAspAsnArgAspTyrLysLysTyrThrValGluGln 195
      588 CATGCGCTCCAAATATGTGCTC-----TGCTGA- 613
QY 196 GluGlySerAlaCysProSerAlaGluGlnIuphGlnProIleGluValValAlaAspAla 215
      614 GAAGGA-----CCAGCCCTCAAGAACCGCTGCCACATTCGCTACATGACCTGTT 664
Db 216 IleHsLysLeuLysTyrGlu-----AsnTyr 224
      665 CTCACAC--ATCAGATACAAAGTCTCATAGTGCAGCATGCCCTGGGCCCAATGTC 722
QY 225 ThrSerSerPhePheIleArq---AspIleIleLysProAspProProThrAsnLeuGln 243
      723 ACAGCATATCAGCTTATGACAGATTCACATTTGGAACCTCGACCTCCAAATAATGCGTA 782
Db 244 LeuLysProLeu-----LysAsnSerArgHsValGlnValSerTrpIleuLysProAspThr 262
      783 GCCCGGCGAGTGGCCAGCAACCTCGCGCTGGAGGTACGTGGCAGACCCCTGAGCC 842
QY 263 TrpSerThrProHis-SerTyrPheSerLeuThrPheCys 275
      843 TGGCGTGAACCTGAGTGTCTTCTCTCAAGTCTTCTGCG 882
Db

RESULT 15
AL518132 873 bp mRNA linear EST 13-FEB-2001
LOCUS AL518132 LTL_NFL011_NBC1 Homo sapiens cDNA clone CS0DA001YM20 5
DEFINITION prime, mRNA sequence.
ACCESSION AL518132
VERSION AL518132.1 GI:12781625
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
          Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 873)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
          Genoscope - Centre National de Sequencage
          BP 191 91006 Evry cedex - France
          Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

```


GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: July 16, 2003, 19:43:49 ; Search time 75.1634 Seconds
(without alignments)
2174.711 Million cell updates/sec

Title: US-09-917-265-62
Perfect score: 2804
Sequence: 1 MHPOQLVISMFSLVLLASPL.....HAFRIRAVTINRMSTYLNSS 533

Scoring table: BLOSUM62
Xgapop 10.0 , Ygapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues
Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+.p2n.model -DEV=xlh
-O=/cgn2_1/USP10.spool/US09917265/runat_15072003_092107_1615/app-query.fasta.1.3114
-DB=Issued_Patents_NA -QFMT=fastlap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdl
-LIST=45 -DOCALLIGN=200 -THR.SCORE=PCT -THR.MAX=100 -THR.MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptlo -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USRR=US09917265.@CGN_1_1_119.@runat_15072003_092107_1619 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued_Patents_NA:*
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2: /cgn2_6/plodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/plodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/plodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/plodata/1/ina/PCRTUS_COMB.seq:*
6: /cgn2_6/plodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length DB | ID | Description |
|------------|--------|-------------|-----------|----|-------------------|
| 1 | 2393.5 | 85.4 | 1623 | 2 | US-08-751-767A-9 |
| 2 | 2393.5 | 85.4 | 6139 | 2 | US-08-751-767A-7 |
| 3 | 2313.5 | 82.5 | 1560 | 2 | US-08-751-767A-11 |
| 4 | 1764 | 62.9 | 990 | 4 | US-09-079-984A-11 |
| 5 | 1731 | 61.7 | 990 | 4 | US-09-079-984A-1 |
| 6 | 1503.5 | 53.6 | 1870 | 4 | US-09-310-842-4 |
| 7 | 1502.5 | 53.6 | 987 | 4 | US-08-848-760B-24 |
| 8 | 1502.5 | 53.6 | 2318 | 4 | US-09-851-062-3 |
| 9 | 1501.5 | 53.5 | 987 | 1 | US-08-186-529-1 |
| 10 | 1501.5 | 53.5 | 987 | 1 | US-08-640-386A-1 |
| 11 | 1501.5 | 53.5 | 1018 | 2 | US-08-184-009-194 |
| 12 | 1501.5 | 53.5 | 1018 | 2 | US-08-458-356-194 |

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|----|--------|------|------|---|-------------------|
| 13 | 1501.5 | 53.5 | 1018 | 4 | US-08-460-736-194 |
| 14 | 1501.5 | 53.5 | 1399 | 2 | US-08-751-767A-3 |
| 15 | 1501.5 | 53.5 | 2362 | 1 | US-08-265-087-1 |
| 16 | 1501.5 | 53.5 | 2362 | 1 | US-08-621-483-1 |
| 17 | 1501.5 | 53.5 | 2362 | 2 | US-08-965-688-1 |
| 18 | 1501.5 | 53.5 | 2362 | 4 | US-09-260-173-1 |
| 19 | 1501.5 | 53.5 | 2362 | 2 | US-08-385-335A-13 |
| 20 | 1142.5 | 40.7 | 1061 | 2 | US-08-659-206A-4 |
| 21 | 1132.5 | 40.4 | 6295 | 2 | US-08-659-206A-1 |
| 22 | 970 | 40.4 | 7287 | 2 | US-09-079-984A-12 |
| 23 | 965 | 34.6 | 669 | 4 | US-09-079-984A-2 |
| 24 | 881.5 | 31.4 | 1364 | 1 | US-08-265-087-3 |
| 25 | 881.5 | 31.4 | 1364 | 1 | US-08-621-493-3 |
| 26 | 881.5 | 31.4 | 1364 | 2 | US-08-965-688-3 |
| 27 | 881.5 | 31.4 | 1364 | 4 | US-09-260-173-3 |
| 28 | 878.5 | 31.3 | 762 | 4 | US-08-848-760B-21 |
| 29 | 878.5 | 31.3 | 1316 | 2 | US-08-684-687-3 |
| 30 | 878.5 | 31.3 | 1316 | 4 | US-09-851-520-3 |
| 31 | 878.5 | 31.3 | 1645 | 4 | US-09-310-842-2 |
| 32 | 877 | 31.3 | 660 | 1 | US-08-186-529-3 |
| 33 | 877 | 31.3 | 660 | 1 | US-08-640-386A-3 |
| 34 | 875.5 | 31.2 | 1026 | 2 | US-08-751-767A-1 |
| 35 | 871 | 31.1 | 721 | 2 | US-08-184-009-199 |
| 36 | 871 | 31.1 | 721 | 2 | US-08-458-356-199 |
| 37 | 871 | 31.1 | 721 | 4 | US-08-460-736-199 |
| 38 | 549 | 19.6 | 713 | 2 | US-08-385-335A-10 |
| 39 | 211.5 | 7.5 | 1404 | 6 | 5171840-8 |
| 40 | 211.5 | 7.5 | 1404 | 6 | 5480796-8 |
| 41 | 211.5 | 7.5 | 1486 | 4 | US-08-795-473B-3 |
| 42 | 211.5 | 7.5 | 1486 | 4 | US-09-439-856-3 |
| 43 | 211.5 | 7.5 | 2061 | 6 | 5171840-1 |
| 44 | 211.5 | 7.5 | 2061 | 6 | 5480796-1 |
| 45 | 211.5 | 7.5 | 3319 | 4 | US-08-795-473B-2 |

ALIGNMENTS

RESULT 1
US-08-751-767A-9
Sequence 9, Application US/08751767A
Patent No. 5994104
GENERAL INFORMATION:
APPLICANT: ANDERSON, ROBERT J.
APPLICANT: GRANT, HUGH
APPLICANT: MACDONALD, IAN D.
TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHIE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,767A
FILING DATE: 08-NOV-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B. J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 117-221
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164091
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1623 base pairs

Sequence 194, App
Sequence 3, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 13, Appli
Sequence 4, Appli
Sequence 12, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 21, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 199, App
Sequence 10, App
Patent No. 5171840
Patent No. 5480796
Sequence 3, Appli
Sequence 3, Appli
Patent No. 5171840
Patent No. 5480796
Sequence 2, Appli

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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1620
; US-08-751-767A-9

Alignment Scores:
Score: 2,14e-262 Length: 1623
Percent Similarity: 2393.50 Matches: 456
Best Local Similarity: 89.46% Conservative: 28
Query Match: 84.29% Mismatches: 48
                85.36% Indels: 9
                2 Gaps: 2

US-09-917-265-62 (1-533) x US-08-751-767A-9 (1-1623)

QY 1 MethisProGlnGlnLeuValIleSerThrPheSerLeuValLeuLeuAlaSerProLeu 20
Db 1 ATGGGTCACCCAGAGTGGTGCATCTCTGTTTCCCTGGTTCCTGGCATCTCCCTC 60
QY 21 MetAlaIleThrPheGluLeuGluLysAspValTyrValValGluLeuAspThrPheProasp 40
Db 61 GTGGCCATATGGAACTGAAGAAAGATGTTATGTGTAGTAATGGATGGATCCGGAT 120
QY 41 AlaProGlyGluMetValValLeuThrCysHisThrProGlnGluAspAspIleThrTrp 60
Db 121 GCCCCTGGAATAATGGTGCTCCACCTGTGACACCCCTGAAGAAGTGGTATCACCTGG 180
QY 61 ThrSerAlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
Db 181 ACCTTGACACGAGCGAGTGTGTCTAGGCTCTGCAAAAACCTGACCATCCAAAGTCAAA 240
QY 81 GluPheGlyAspAlaGlnTyrThrCysHisLysGlyValLysValLeuSerArgSer 100
Db 241 GATTTGGAGATCTGCGCCGATACCTGTCCACAAAGAGCGAGGTTCTAAGCCATTCG 300
QY 101 LeuLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGlnGln 120
Db 301 CTCCTGCTGCTTCACAAAAGAAAGATGGATTTGGTCCACTGATTTTAAAGACACG 360
QY 121 LysGlnSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
Db 361 AAAGAACCCCAAAATTAAGACCTTCTAAGATGGAGCCCAAGAAATATCTGACCTTTC 420
QY 141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArg 160
Db 421 ACCTGCTGGTGGCTGACGACAAATCACTGATTTTACATTTCAGTGTCAAAAGCAGACGA 480
QY 161 GlyPheSerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgVal 180
Db 481 GGCTTCTTGACCCCAAGGGGTGAGCTGCGAGTGTACACTCTCTCAGAGAGAGTC 540
QY 181 ArgValAlaAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluLysAlaCys 200
Db 541 AGAGGGGACAAACAGAGATAT--GAGTACTAGTGTGAGTGCAGAGAGACAGTGCCTGC 597
QY 201 ProSerAlaGluGlnSerLeuProIleGlnValValValAspAlaIleHisLysLeuLys 220
Db 598 CCAGCTGCTGAGAGAGTGTGCTCCCATTTGAGTGCATGTGATGCGCTTCAACAGCTCAAG 657
QY 221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProThr 240
Db 658 TATGAAATACACACGACGCTTCTTCATCAGGAGCATCATCAAACTCAACCCACCCAG 717
QY 241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpLysTrpPro 260
Db 718 AACTTGACACTGAAGCATTTAAAGAAATTCCTCGGAGGTGAGAGTCAAGCTGAGTAACT 777
QY 261 AspThrTrpSerThrPheHisSerTyrPheSerLeuThrPheCysIleGlnIleGlnGly 280

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Db 778 GACACCTGGAGTACTCCACATTCCTTCTCCCTGCATCTTCTGCTGACGTCACAGGC 837
QY 281 LysAsnAsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysVal 300
Db 838 AAGAGCAGAGAGAAAAAGAAAGATAGAGTTCACGACAAAGACCCAGCAGGTCATC 897
QY 301 CysHisLysAspAlaLysIleArgValGlnAlaIleArgAspArgTyrThrSerSerSerTrp 320
Db 898 TGCCCGCAAAATGCCACACATTTAGCTGCGGGCCCAAGACCCGCTACTATATGCTATCTTGG 957
QY 321 SerAspTrpAlaSerValSerCysSerGlyLys-----Gly 332
Db 958 AGCGAATGGGCATCTGTGCTCCCTGAGTGGCGGTGAGAGCGCGCGTGGCGGAAGCGGC 1017
QY 333 GlyGlyGlySerArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeu 352
Db 1018 GTGGCGGACGACGAAACCTCCCTGCGCCACTCCAGACCCAGAAATGTTCCCATGCCCTT 1077
QY 353 AsnHisSerGlnThrLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThr 372
Db 1078 CACCACTCCCAAAACCTGCTGAGGGCGCTCAGACAAATGCTCCAGAAGCCAGACAACT 1137
QY 373 LeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLys 392
Db 1138 CTAGAATTTTACCTTGCACCTTCTGAAGAGATTGATCATGAAGATATCAGAAAACATATA 1197
QY 393 ThrSerThrValGlnAlaCysLeuProLeuGluLeuThrMetAsnGlnSerCysLeuAla 412
Db 1198 ACCAGCAGAGTGGAGGCTGTTTACCATTTGAAATTAACAGAAATGAGAGTTCCTAAAT 1257
QY 413 SerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPhe 432
Db 1258 TCCAGAGAGACCTCTTCAATTAATGAGAGTGGCTGCTGCCAGAAAGACCTCTTT 1317
QY 433 MetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetLysIleMetGluPhe 452
Db 1318 ATGATGGCCCTTGCTGATGATGATTTATGAAAGACTTGAAGATTAACAGAGTGGAGTTC 1377
QY 453 LysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsn 472
Db 1378 AAGACATTAATGCAAAAGCTTCTGATGAGTCTCTAAGAGCAATCTTTTAAATCAAAAC 1437
QY 473 MetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValPro 492
Db 1438 ATGCTGGAGTATTGATGATGATGATGACGAGCCCTGAATTTCAACAGTGAAGCTGGCA 1497
QY 493 GlnLysSerSerLeuGlnGluProAspPheTyrLysThrLysIleLysLeuCysIleLeu 512
Db 1498 CAAAATCTCTCCCTTGAAGAACCGGATTTTATTAATAACTAAATCAAGCTGTGCATACTT 1557
QY 513 LeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetLeuSerTyrLeuAsnSer 532
Db 1558 CTTCAATGCTTTGAAATTTGGGAGTGAAGTATTTGACAGAGTGCAGAGCATATCTGAATGCT 1617
QY 533 Ser 533
Db 1618 TCC 1620

RESULT 2
US-08-751-767A-7
; Sequence 7, Application US/08/51767A
; Patent No. 5994104
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, ROBERT J.
; APPLICANT: GRANT, HUGH
; APPLICANT: MACDONALD, IAN D.
; TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VA

```

COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,767A
FILING DATE: 08-NOV-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 117-221
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164091
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 6139 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 3222..4841
US-08-751-767A-7

Alignment Scores:
Pred. No.: 2,05e-261 Length: 6139
Score: 2393.50 Matches: 456
Percent Similarity: 89.46% Conservative: 28
Best Local Similarity: 84.29% Mismatches: 48
Query Match: 85.36% Indels: 9
Gaps: 2
US-09-917-265-62 (1-533) x US-08-751-767A-7 (1-6139)

QY 1 MethisProgluInleuValIleSerTrpPheSerLeuValLeuLeuAlaSerProleu 20
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QY 21 MetAlaIleTrpGluLeuGluLysAspValTyrValValGluLeuAspTrpHisProasp 40
Db 3282 GTGGCCATATGGGAAGTGAAGAGATGTTATGCTAGCAATTGGATTGGTATCCGAT 3341
QY 41 AlaProgluGluMetValIleLeuThrCysHisTrpProgluGluAspAspIleThrTrp 60
Db 3342 GCCCCTGGAATAATGCGTCTCCTCACCTGTGCACCCCTGAGAAGATGATCACCTGG 3401
QY 61 ThrSerAlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
Db 3402 ACCCTGGACCGAGCACTGAGGTCTTAGGCTCTGGCAAAACCCCTGACCATCCAGTCAAA 3461
QY 81 GluPheGlyAspAlaGlyIntyrThrCysHisLysGlyLysValLeuSerArgSer 100
Db 3462 GACTTTGCAATGCTGGCCAGTACCTGTCTACAAAGAGGCGAGGTTCTAAGCCATTGC 3521
QY 101 LeuLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGln 120
Db 3522 CTCCTGCTGCTTCACAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAGCACCCAG 3581
QY 121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
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QY 141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerArg 160
Db 3642 ACCTGCTGGTGGCTGACGACACATAGTACTGATTTGACATTTCAGTGTCAAAAGCAGCA 3701
QY 161 GlyPheSerAspProGlnGlyValThrCysGlyValAlaValThrLeuSerAlaGluArgVal 180

Db 3702 GGCCTCTCTGACCCCAAGGGGTGACGGGAGCTGTGACACTCTCTGCAGAGAGTGC 3761
QY 181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
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QY 201 ProSerAlaGluGluSerLeuProIleGluValValAlaSerAlaIleHisLysLeuLys 220
Db 3819 CCAGCTCTGTGAGGAGCTGTCCCATTTGAGGTCAATGGTGATGCCGTTCCACAAGCTCAAG 3878
QY 221 TyrGluAsnTyrTrpSerSerPhePheIleArgAspIleLysProAspProProThr 240
Db 3879 TATCAAAAACCTACACAGAGCTTCTTCACTGAGGACATCATCAAACTGACCCAGCCAG 3938
QY 241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
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QY 261 AspThrTrpSerTrpProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGly 280
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QY 281 LysAsnAsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValVal 300
Db 4059 AAGAGCAAGAGAGAAAGAAAGATAGAGTCTTCACAGGACAGACCTGACGACGTCATC 4118
QY 301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerTrp 320
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QY 321 SerAspTrpAlaSerValSerCysSerGlyGly-----Gly 332
Db 4179 AGCGAAATGGGATCTGTGCTGCTGAGTGGGCGGTGGAGCGCGCGGTGGCGGAAGCGGC 4238
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QY 353 AsnHisSerGlnThrLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThr 372
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QY 373 LeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLys 392
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QY 393 ThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGlnSerCysLeuAla 412
Db 4419 ACCAGCACAGTGGAGGCGCTGTTACCAATTGGAATTAACCAAGAAATGAGAGTTGCCATAAT 4478
QY 413 SerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPhe 432
Db 4479 TCCAGAGAGACCTTTTCATTAACAAATGGGAGTTGCCCTGCAGAAAGACCTCTTTT 4538
QY 433 MetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlnPhe 452
Db 4539 ATGATGGCCCTGCTCTTAGTAGTATTATTAAGAACCTTGAAGATGTACCAAGGTGAGTTC 4598
QY 453 LysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsn 472
Db 4599 AAGACCATGAATGCAAAAGCTTCTGATGATCTTAAGAGGCGAGATCTTCTGATCAAAAC 4658
QY 473 MetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValPro 492
Db 4659 ATGCTGGCAGTTATTTGATGACCTGATGAGGCGCTGGAATTTTCAACAGAGAGCTGGCA 4718
QY 493 GlnLysSerSerLeuGluGluProAspPheTyrTrpLysIleLysLysCysIleLeu 512
Db 4719 CAAAATATCTCCTTTGAAGAACCGGATTTTATATAAATTAATAATCAACCTCTGCATACTT 4778
QY 513 LeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetSerTyrLeuAsnSer 532

Db 4779 CTTGATGCTTTCAGAAATTCGGGAGAGTACATTGACAGAGTGCAGAGCTATCTGATGCT 4838
QY 533 Ser 533
Db 4839 TCC 4841
RESULT 3
US-08-751-767A-11
Sequence 11, Application US/08751767A
Patent No. 5994104
GENERAL INFORMATION:
APPLICANT: ANDERSON, ROBERT J.
APPLICANT: GRANT, HUGH
APPLICANT: MACDONALD, IAN D.
TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYTE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,767A
FILING DATE: 08-NOV-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 117-221
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164091
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1560 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1557
US-08-751-767A-11
Alignment Scores:
Pred. No.: 2,56e-253 Length: 1560
Score: 233.50 Matches: 439
Percent Similarity: 89.62% Conservative: 27
Best Local Similarity: 84.42% Mismatches: 45
Query Match: 82.51% Indels: 9
Gaps: 2
US-09-917-265-62 (1-533) x US-08-751-767A-11 (1-1560)
QY 22 AAlaIleTTPgluLeuGluLysAspValTyrValValGluLeuAspTTPRHisProAspAla 41
Db 1 GCCATATGAGAACTGAGAAAGATGTTATGTCTAGAAATGATGATGCTATCCGATGCC 60
QY 42 ProGlyGluMetValValLeuThrCysHisThrProGluGluAspAspIleThrTTPThr 61
Db 61 CCTGGAGAAATGGGGCTCCACCTGTGACACCCCTGAGAAAGATGGTATCACCTGGACC 120
QY 62 SerAlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValValGlu 81
Db 121 TTGGACCAAGACAGCTGAGGTCTTAGGCTCTGGCAAAACCTGACCATCAAGTCAAGAG 180

QY 82 PheGlyAspAlaGlyGlnTyrThrCysHisLysGlyGlyLysValLeuSerArSerLeu 101
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QY 102 LeuLeuIleHisLysLysGluAspGlyIleTTPSerThrAspIleLeuLysGluGlnLys 121
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QY 122 GlnSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArpPheThr 141
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QY 142 CysTTPRpleuThrAlaIleSerThrAspLeuLysPheSerValLysSerArGly 161
Db 361 TGCTGTGGCTGAGACATACAGTACTGATTTGACATTCAGTGCACAAAGACAGAGGC 420
QY 162 PheSerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluValArg 181
Db 421 TCTTCGTACCCCAAGGGGTGAGCTGGAGCTGTACACTCTCTGCGAGAGAGTCAGA 480
QY 182 ValAspAsnArGAspTyrLysTyrThrValGluCysGlnGluSerAlaCysPro 201
Db 481 GGGGACACAAAGAGAT---GAGTACTCAGTGGAGTCCAGAGACAGACATGCTGCCCA 537
QY 202 SerAlaGluGlnSerLeuProIleGluValValAspAlaIleHisLysLeuLysTyr 221
Db 538 GCTGCTGAGAGAGATGTCGCCATGAGCATGATGATGATGATCCCTGACAGCTCAAGTAT 597
QY 222 GluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPheThrAsn 241
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QY 242 LeuGlnLeuLysProLeuLysAsnSerArHisValGluValSerTTPGluTyrProAsp 261
Db 658 TTGACGCTGAAGCATTAAGAATTCGCGCAGCTGAGAGTCACTGCGGAGTACCTGAC 717
QY 262 ThrTTPSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnLys 281
Db 718 ACCTGAGTACTCCACATTCCTACTCTCCTGACATTCGCTGACAGGCGCAAG 777
QY 282 AsnAsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValLys 301
Db 778 AGCAAGAGAGAAAGAAAGATAGATCTTCAGGACCAAGCCTCAGCCAGTCATCTGC 837
QY 302 HisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerTTPSer 321
Db 838 CGCAAAATGCCAGCATTTACGCTGCGGCCAGAGACCGCTACTATAGCTATCTTGAGC 897
QY 322 AspTTPAlaSerValSerCysSerGlyGly-----GlyGly 333
Db 898 GAATGGGCAATCTGCTCCCTGACGTGCGCGTGAAGCGCGGTGGCGAAGCGGCGGT 957
QY 334 GlyGlySerArgAsnLeuProThrProThrProSerProGluMetPheGlnCysLeuAsn 353
Db 958 GGGGCGAGCGAAACCTCCCGCCGACCTCCAGACCCAGAGATGTTCCATCCCTTCAC 1017
QY 354 HisSerGlnThrLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeu 373
Db 1018 CACTCCCAAAACCTGTCGAGGCGCGTCAGACATGCTCCAGAAAGCGACACAAACCTGA 1077
QY 374 GluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThr 393
Db 1078 GAATTTTACCTTCCTGATTCGAAAGATGATGATGATGATGATGATGATGATGATGAT 1137
QY 394 SerThrValGluValCysLeuProLeuGluLeuThrMetAsnLysSerLeuAlaSer 413
Db 1138 AGCAGATGAGAGCGCTTTCATTCATTCGAAATTAACCAAGATAGAGATGCTCAAAATTC 1197
QY 414 ArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAspPheMet 433
Db 1198 AGAGAGACCTCTTTCATTAATATGAGAGTGGCTGCTGCCCGCAAGAAAGACCTTTTATG 1257
QY 434 ThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLys 453

Db 1258 ATGGCCCTGCTAGTATTATATGAGACCTGAGATGTAACAGGTGAGTCAAG 1317
OY 454 AlameltsnAlalySleuLeuMetAsProlysaTgGlnIlePheLeuAspGlnAsnMet 473
Db 1318 ACCATGAATGCAAGACTTCTCATGATGCTCTAAGAGCGCAGATCTTCTAGATCAAAACATG 1377
OY 474 LeuThraAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGln 493
Db 1378 CTGGCAGTATTGATGACCTGATGACGCGCTGAAATTTCAACAGTGAAGACTGTGCCACAA 1437
OY 494 LysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeu 513
Db 1438 AAATCTCCCTTGAAAGAACCGGATTTTATAAACTAAATCAAGCTCTGCATCTCTT 1497
OY 514 HisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnSer 533
Db 1498 CATCTTTCAGAAATTCGGCAGTGAATTTGACAGAGTACGAGTATCTGATCTTCC 1557

RESULT 4
US-09-079-984A-11
: Sequence 11, Application US/09079984A
: Patent No. 6231850
: GENERAL INFORMATION:
: APPLICANT: Okano, Fumiyoshi, Satoh, Massahiro,
: APPLICANT: Yamada, Katsushige
: TITLE OF INVENTION: Canine interleukin 12, a production method
: TITLE OF INVENTION: thereof, an immune disease treatment method and preventive
: NUMBER OF INVENTIONS: 16
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Miller & Christenbury Intellectual Property
: ADDRESS: Department of Schneider, Harrison, Segal and Lewis, LLP
: STREET: 1600 Market Street, 39th Floor
: CITY: Philadelphia
: STATE: PA
: COUNTRY: USA
: ZIP: 19103
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy Disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WordPerfect 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/079, 984A
: FILING DATE: 15-MAY-1998
: ATTORNEY/AGENT INFORMATION:
: NAME: Austin R. Miller
: REGISTRATION NUMBER: 16,602
: REFERENCE/DOCKET NUMBER: 1051-98
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215) 563-1810
: TELEFAX: (215) 568-6946
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 990 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: ORIGINAL SOURCE:
: ORGANISM: Canis familiaris
: FEATURE:
: NAME/KEY: Canine IL12
: LOCATION: 1 to 987
: IDENTIFICATION METHOD: Similarity
: US-09-079-984A-11

Alignment Scores:
Pred. No.: 4,27e-191 Length: 990
Score: 1764.00 Matches: 329
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 62.91% Indels: 0
DB: 4 Gaps: 0
US-09-917-265-62 (1-533) x US-09-079-984A-11 (1-990)

OY 1 MethisProGlnGlnLeuValIleSerTrpPheSerLeuValLeuLeuAlaSerProLeu 20
Db 1 ATGCATCTCTACGACATTTGCTCATCTCCGAGTTTCCCTGCTTCTGCTGCTCCCTC 60
OY 21 MetAlaIleTrpGluLeuGluLysAspValIyrValIleGluLeuAspTrpHisProAsp 40
Db 61 ATGCCATATGGAAGAACTGGAAGAAGATTTATGTTAGAGTTGGACTGCCACCCCTGAT 120
OY 41 AlaProGluGluMetValValLeuThrCysHisSerTrpProGluGluAspIleThrTrp 60
Db 121 GCGCCGGAAGAAGTGTGCTCTACCTGCCATACCTCGAAGAAGATGACATCACTTGG 180
OY 61 ThrSerAlaGlnSerSerGluValLeuGlySerGlyLysTrpLeuThrIleGlnValLys 80
Db 181 ACCTCAGCGCAGAGCAGTGAAGTCTCTAGTCTTGSTAAACTCTGACCTCAAGTCAAA 240
OY 81 GluPheGlyAspAlaGlyGlnTyrThrCysHisLysGlyGlyLysValLeuSerArgSer 100
Db 241 GAATTTGAGATGCTGGCCAGTATCTGCCATAAAGAGCAAGCTTCTGAGCCGCTCA 300
OY 101 LeuLeuLeuIleHisLysLysGluAspGlyIleTrpSerTrpAspIleLeuLysGluGln 120
Db 301 CTCTGTGTGATTCACAAAAAAGACATGGAATTTGGTCCCTGATATCTTAAAGGACAG 360
OY 121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
Db 361 AAAGATCCAAAAATAAATCTTTCTGAAATGTGAGCGAAAGAAATTTATCTTGAGAGTTTC 420
OY 141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArg 160
Db 421 ACATGCTGTGTGCTACGCAATCAGTACGATTTGAATTCAGTCTCAAAAGTAGCAGA 480
OY 161 GlyPheSerAspProGlnGlyValIleThrCysGlyAlaValIleThrSerAlaGluArgAl 180
Db 481 GCGTCTCTGACCCCAAGGGGTGACATGTGGAGAGTGAACCTTTCAGCGAGAGGGTTC 540
OY 541 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
Db 541 AGAGTGCACAAACAGGATTTAAAGATACACAGTGGAGTGCAGAGGCGAGTCCCTGC 600
OY 201 ProSerAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
Db 601 CCTCTGCCGAGAGAGCCCTACCATCGAGGTCGTGGATGCTATTCACAAGCTCAAG 660
OY 221 TyrGluAsnTyrTrpThrSerPhePheIleArgAspIleIleLysProAspProProThr 240
Db 661 TATGAAACCTACCCAGGAGCTCTTCTTACAGAGCATCATCAAAACAGACCACCCACA 720
OY 241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValIleSerTrpGluTyrPro 260
Db 721 AACCTGCAGCTGAAGCCATTGAAAATTTCTGGCAGCTGAGAGTCAAGCTGGGAATATCCCC 780
OY 261 AspThrTrpSerTrpProHisSerTyrTrpPheSerLeuThrPheCysIleGlnAlaGlnGly 280
Db 781 GACACCTGAGACACCCCATCTTCTTCCCTCCGACATTTTGCATGACAGCCAGAGGC 840
OY 281 LysAsnAsnArgGluLysLysAspArgLeuGlyValAspLysTrpSerAlaLysValVal 300
Db 841 AAGAACATTAAGAAAAAAGATGACTGTGCGGCAAGACCTCAGCCAAAGCTGTG 900
OY 301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTrpSerSerSerTrp 320
Db 901 TGCCCAAGAGATGCCAAGATCCGCTGCAAGCCGAGACCCGCTACTATAGTTCACTCTGG 960
OY 321 SerAspTrpAlaSerValSerCysSer 329
Db 961 AGCAGCTGGGATCTGTGCTCTGAGT 987

RESULT 5
US-09-917-265-62 (1-533) x US-09-079-984A-1 (1-990)
Sequence 1, Application US/09079984A
Patent No. 6231850
GENERAL INFORMATION:
APPLICANT: Okano, Fumiyoshi, Satoh, Masahiro,
TITLE OF INVENTION: Canine Interleukin 12, a production method
TITLE OF INVENTION: thereof, an immune disease treatment method and preventive
TITLE OF INVENTION: method using it
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Miller & Christenbury Intellectual Property
STREET: 1600 Market Street, 39th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079, 984A
FILING DATE: 15-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Austin R. Miller
REGISTRATION NUMBER: 16,602
REFERENCE/DOCKET NUMBER: 1051-98
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-1810
TELEFAX: (215) 568-6946
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 990 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: Canine IL12
LOCATION: 1 to 987
IDENTIFICATION METHOD: Similarity
US-09-079-984A-1
Alignment Scores:
Pred. No.: 2,44e-187 Length: 990
Score: 1731.00 Matches: 323
Percent Similarity: 99.69% Conservative: 2
Best Local Similarity: 99.08% Mismatches: 1
Query Match: 61.73% Indels: 0
Gaps: 0
US-09-917-265-62 (1-533) x US-09-079-984A-1 (1-990)
QY 4 GlnGlnLeuValIleSerTrpPheSerLeuValLeuLeuAlaSerProLeuMetaIle 23
DB 10 CAGCAGTGTGTCATCTCTGTTTCCCTCGTTTCTGCTGCGCTCCCTCATGCGCATA 69
QY 24 TTPGluLeuGluLysAspValIleValIleGluLeuAspTrpHisProAspIleProGly 43
DB 70 TGGGAACCTGGAGAAATATTTATGTTGAGATTGGAGCTGCACCCCTGATGCCCGGA 129
QY 44 GluMetValIleLeuThrCysHisTrpProGluGluAspIleThrTrpHisSerAla 63
DB 130 GAAATGGTGTCTCTACCTGCGCATACCTGGAAGAAATGACATCTCTGGAGCTAGCG 189
QY 64 GlnSerSerGluValLeuGlySerGlyIleThrLeuThrIleGlnValLysGluPheGly 83

DB 190 CAGACAGTGAAGTCTAGTTCGTGTAACACTGACCATCATCAAGTCAAGAAATTTGGA 249
QY 84 AspAlaGlyGlnTrpThrCysHisLysGlyLysValLeuSerArgSerLeuLeu 103
DB 250 GATGCTGGCCAGTATACCTGCCATTAAGAGGCAAGGTTCTGAGCCGCTACTCTGTG 309
QY 104 IleHisLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGlnSer 123
DB 310 ATTCCAAAAGAAAGATGGAATTTGGTCCACTGATATCTTAAGAGAACAGAAATACC 369
QY 124 LysAsnLysIlePheLeuLysCysGlnAlaLysAsnTrpSerGlyArgPheThrCysTrp 143
DB 370 AAAAATTAAGATCTTCTGAAATGTGAGCAAGAAATTAATTTCTGAGCTTACATGCTGG 429
QY 144 TrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPheSer 163
DB 430 TGGCTGAGCGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGAGAGGCTTCT 489
QY 164 AspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgValAsp 183
DB 490 GACCCCAAGGGGTGACATGTGAGCAGTGAACATTTCCAGCAGAGAGGGTCAGAGTGAC 549
QY 184 AsnArgAspTrpLysLysTrpThrValGluLysGlnGluLysSerAlaCysProSerAla 203
DB 550 AACAGGATTTAAGAACATACACAGTGAAGTGTGAGAGGCGAGTGTGCTGCCCTTSCC 609
QY 204 GlnGlnSerLeuProIleGluValValAlaAlaIleHisLysLeuLysTrpGlnAsn 223
DB 610 GAGGAGACCTTAACCATGAGTGTGCTGATGATCTATTCCAAAGCTCAAGATGAAAC 669
QY 224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProPheThrAsnLeuGln 243
DB 670 TACACACAGAGCTTCTTCATCAGACATCAATCAACCAAGCCACCAAACTGTGAG 729
QY 244 LeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTrpProAspThrTrp 263
DB 730 CTGAAGCCATTGGAAATTTCTGCGACGTGGAGTCACTGGAGTATACCCGACACTGG 789
QY 264 SerThrProHisSerTrpPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsnAsn 283
DB 790 AGCACCACCATTTCTACTTCTCCCTGACATTTGTCATACAGCCGACGCAAGAAAT 849
QY 284 ArgGluLysLysAspArgLeuLysValAspLysTrpSerAlaLysValCysHisLys 303
DB 850 ACAGAAAAGAAAGATGACTCTGCTGCAAGACCTCAGCCAGAGCTGTGTGCCACAG 909
QY 304 AspAlaLysIleArgValGlnAlaArgAspArgTrpTrpSerSerTrpSerAspTrp 323
DB 910 GATGCCAAGATCCGCTGCAGAGCCGAGACCGCTACTATAGTTCACTGAGAGCACTGG 969
QY 324 AlaSerValSerCysSer 329
DB 970 GCATCTGTGCTCCTGCAGT 987
RESULT 6
US-09-310-842-4
Sequence 4, Application US/09310842A
Patent No. 6451593
GENERAL INFORMATION:
APPLICANT: Wiltig, Prof. Burghardt
APPLICANT: Jungmans, Claas
TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Ge
TITLE OF INVENTION: Therapy
FILE REFERENCE: XI 597/99
CURRENT APPLICATION NUMBER: US/09/310, 842A
CURRENT FILING DATE: 1999-05-12
EARLIER APPLICATION NUMBER: DE 196 48 625.4
EARLIER FILING DATE: 1996-11-13
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 1870
TYPE: DNA

ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: gene
LOCATION: (1)..(1870)
OTHER INFORMATION: Interleukin-12 (IL-12, p40-subunit); Oligo DNA Dumbbell
FEATURE:
NAME/KEY: misc-binding
LOCATION: (1)..(2)
OTHER INFORMATION: Intramolecular binding site; the T-nucleotides at position 1 to
OTHER INFORMATION: 2 can be modified with amino or carboxy features
FEATURE:
NAME/KEY: misc-binding
LOCATION: (1869)..(1870)
OTHER INFORMATION: Intramolecular binding site; the T-nucleotides at position 1869
OTHER INFORMATION: to 1870 can be modified with amino or carboxy features
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Strandness: both; nucleic
US-09-310-842-4
Alignment Scores:
Pired. No.: 5,69e-161 Length: 1870
Score: 1503.50 Matches: 284
Percent Similarity: 87.25% Conservative: 24
Best Local Similarity: 80.45% Mismatches: 34
Query Match: 53.62% Indels: 12
DB: 4 Gaps: 2
US-09-917-265-62 (1-533) x US-09-310-842-4 (1-1870)
OY 4 GlnGlnLeuValIleSerTrpPheSerLeuValLeuLeuAlaSerProLeuMetAlaIle 23
Db 642 CAGCAGTGGTGCATCTTGGTTTCCCTGTTTCCGTCATCCCGCTGGCCATA 701
OY 24 TrpGlnLeuGluLysAspValTyrValValGlnLeuLysPheProAspAlaProGly 43
Db 702 TGGGAACCTGAAGAAAGATGTTATGTCCTAGCAATTGATGTCGCGATGCCCTTGA 761
OY 44 GluMetValValLeuTrpCysHisThrProGlnGluAspAspIleThrTrpHisSerAla 63
Db 762 GAATAGTGGTCCCTCACCCTGGACACCCCTGAACAAGATGATCACCCTGGACCTTGGAC 821
OY 64 GlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPheGly 83
Db 822 CAGAGCAGTGAAGCTTGAAGCTTGAAGAAACCTGACATCCAAAGTGAAGAGTTTGA 881
OY 84 AspAlaGlyGlnTrpTrpCysHisLysGlyLysValLeuSerArgSerLeuLeu 103
Db 882 GATGCTGGCCAGTACACCTGTCAAAAGAGCGAGGTTTAAACCATTCCTCCTGCTG 941
OY 104 IleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGlnGlnLysGluSer 123
Db 942 CTCACAAAAAGAGAGATGGAATTTGGTCCACTGATATTTTAAAGACACAGAAAGAACCC 1001
OY 124 LysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrp 143
Db 1002 AAAAATAGACCTTTCTAAGATGCGAGCCCAAGATATTCTGAGCGTTTCACTGCTGCG 1061
OY 144 TrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerArgGlyPheSer 163
Db 1062 TGGCTGACCAATCAGTACTGATTGACATTCAGTCTCAAAACAGACAGAGCTCTTCT 1121
OY 164 AspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgValAsp 183
Db 1122 GACCCCAAGGAGGAGCTGCGAGCTGCTACACTCTCTGAGAGAGAGCTAGAGGGGAC 1181
OY 184 AsnArgAspTyrLysLysTyrThrValGlnCysGlnGlnLysSerAlaCysProSerAla 203
Db 1182 AACAAAGAGTAT---GAGTACTGAGTGGAGTCCAGAGAGACAGTCCCTGCCAGCTGCT 1238
OY 204 GlnGlnSerLeuProIleGlnValValValAspAlaIleHisLysLysLysTyrGlnAsn 223
Db 1239 GAGGAGAGTCTGCCATTGAGGTGATGATGCTGCTTCAACAGCTCAACTATGAAGAAC 1298

OY 224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProThrAsnLeuGln 243
Db 1299 TACACGACGACCTTCTTATCAGGACATCTCAAACTGACCCACCAACCAACTTGGAC 1358
OY 244 LeuLysProLeuLysAsnSerArgHisValGlnValSerTrpGlnTyrProAspThrTrp 263
Db 1359 CTGAAGCCATTAAGAATTTCTGGCAGAGTGAGGTGACCTGGAGTACCTGACACCTGCG 1418
OY 264 SerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 283
Db 1419 AGTACTCCACATTCCTACTCTCCCTGACATTCCTGCGTCCAGGCGCAAGAGCAG 1478
OY 284 ArgGlnLysLysAspArgLeuValAspLysThrSerAlaLysValValCysHisLys 303
Db 1479 AGAGAAAGAAAGATAGAGTCTTACCGACAAAGACCTGACGACGATCTGCCGCAAA 1538
OY 304 AspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAspTrp 323
Db 1539 AATGCCACATTTAGCTGCGGCGGACGAGCGCTACTATGATCATCTTGGAGCGAATGG 1598
OY 324 AlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeu----- 339
Db 1599 GCATCTGCGCCCTGACGTTA-GGAGCTTCATATGACCATACCATCATTTGTAGAGTTT 1657
OY 340 -----ProThrProThrProSerPro 346
Db 1658 ACTTGCCTTAAAAAACCTCCACACCTGCCCTGACCT 1696
RESULT 7
US-08-848-760B-24
Sequence 24, Application US/08848760B
Patent No. 6248721
GENERAL INFORMATION:
APPLICANT: Chang, Lung-Ji
TITLE OF INVENTION: Animal Model For Evaluation Of Vaccines
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESS: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: United States of America
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848,760B
FILING DATE: 25-Jan-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/838,702
FILING DATE: 09-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: PACE, DORAN R.
REGISTRATION NUMBER: 38,261
REFERENCE/DOCKET NUMBER: CNG-100C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5600
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 987 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-08-848-760B-24

| | | | |
|----|-----|--|-----|
| Db | 443 | TGGCGACACACATAGTACTGATTTGACATTCAGTGTGAAAAGCAGCAGAGGCTCTTCT | 502 |
| Oy | 164 | AspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValAsp | 183 |
| Db | 503 | GACCCCAAGGGGTGACGTGCGGAGCTGTACACTCTTGCAGAGAGAGTCAGAGGGGAC | 562 |

| | | | |
|----|-----|--|-----|
| QY | 184 | AsnArgaspTryrLysLysTyrrThyValGluCysGlnGluGlySerAlaCysProSerAla | 203 |
| Db | 563 | AACAAGGAGGTAT--GACTACTCAGGTGAGTCCAGAGACAGTGCCTCCAGCTGCT | 619 |
| QY | 204 | GluGluSerLeuProGluValValAlaAspAlaLeuHisLysLeuTyrrGluAsn | 223 |
| Db | 620 | CAGCAGACTTCGCCCATTTGACGCTCATGGTGGATGCCGTTCCACAAAGCTCAAGTTGAAAC | 679 |
| QY | 224 | TyrThrSerSerPhePheIleArgAspIleIleLysProAspProThrProthraLeuGln | 243 |
| Db | 680 | TACACCAAGACCTTCTTCATCAGGACATCATCAACCTGACCCACCAACTGCAG | 739 |
| QY | 244 | LeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThrTrp | 263 |
| Db | 740 | CTGAAGCCATTAAACAATTTCTGGCAGGAGGAGTGAGTGGGAGTACCTGCACACTGG | 799 |
| QY | 264 | SerThrProHisSerTyrrPheSerLeuThrPheCysIleGluAlaGlnGlyLysAsnAsn | 283 |
| Db | 800 | AGTACTCCACATTCCTACTCTTCCTCGACATTCCTGGTTCAGGTCCAGGCAAGACCAAG | 859 |
| QY | 284 | ArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValValCysHisLys | 303 |
| Db | 860 | AGACAAAAGAAGATAGAGCTCTTCACCGACAGACCTCGCCACGGTCACTTCGCCCAA | 919 |
| QY | 304 | AspAlaLysIleArgValGlnAlaAlaArgAspArgTyrrSerSerSerIrrpSerAspTrp | 323 |
| Db | 920 | AATCCACACATTAGCGTCCGGGCCACGACGCCCTACTATAGCTCATCTTGGAGACCAATGG | 979 |
| QY | 324 | AlaSerValSerCysSer | 329 |
| Db | 980 | GCATCTGTGCGCTCGACT | 997 |

| | ORGANISM: | Homo sapiens |
|--|---|------------------|
| | CELL TYPE: | Lymphoblast |
| | CELL LINE: | RPMI 8866 |
| | FEATURE: | |
| | NAME/KEY: | CDS |
| | LOCATION: | 1..987 |
| | US-08-186-529-1 | |
| Alignment Scores: | | |
| Pred. No.: | 3,25e-161 | 987 |
| Score: | 1501.50 | Matches: 278 |
| Percent Similarity: | 92.02% | Conservative: 22 |
| Best Local Similarity: | 85.28% | Mismatches: 25 |
| Query Match: | 53.55% | Indels: 1 |
| DB: | 1 | Gaps: 1 |
| US-09-917-265-62 (1-533) x US-08-186-529-1 (1-987) | | |
| QY | 4 GInGInLeuValIleSerTrpPheSerLeuValLeuLeuAlaSerProLeuMetaIle | 23 |
| DB | 10 CAGCAGTGGTCATCTCTGGTTTCCCTGGTTTCTTGCGCATCTCCCTCGGGCCATA | 69 |
| QY | 24 TrpGluLeuGluLysAspValTyValValIgluLeuAspTrpHisProAspAlaProGly | 43 |
| DB | 70 TGGGAACATGAAGAAGATGTTATGTGCTAGAAATGGATTGGATTGCGGATGCCCTGA | 129 |
| QY | 44 GumeTValValLeuThrCysHisThrProGluLysAspLleThrTrpTrsAla | 63 |
| DB | 130 GAAATGGTGCTCTCACCTGTACACCCCTGAAGAAGATGCTATCACCCTGGACCTTGAC | 189 |
| QY | 64 GInSerSerGluValLeuGlySerGlyLysTrpLeuThrIleGluValLysGluPheGly | 83 |
| DB | 190 CAGACAGCAGGAGCTCTTAGCGTCTGGCAAAACCCCTGACCATCCAAAGAGTTTGA | 249 |
| QY | 84 AspAlaGlyGlnTrpThrCysHisLysGlyLysValLeuSerArgSerLeuLeu | 103 |
| DB | 250 GATGCTGGCCACTACACCTGTCAAAAGAGGCCAGAGTTCTTAAGCCATTGCTCTGCTG | 309 |
| QY | 104 ILeHISLysGluAspGlyLleTrpSerTrpAspIleLeuLysGluGlnLysGluSer | 123 |
| DB | 310 CTTCACAAAGGAAGATGGAAATTGGTCCACGATATTTTAAAGACCAAGAAAGACC | 369 |
| QY | 124 LysAsnLysIlePheLeuLysCysGluAlaLysAsnTrpSerGlyArgPheThrCysTrp | 143 |
| DB | 370 AAAATTAAGACCTTTCTTAAGATGCCAGGCCAAGAATATTCTGGAGTTTCACTCTCG | 429 |
| QY | 144 TrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPheSer | 163 |
| DB | 430 TGGCTGACGACATAGTACTGATTGTGACATTCAGTGTCAAAAGCCAGACGCTCTTCT | 489 |
| QY | 164 AspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgValAsp | 183 |
| DB | 490 GACCCCAAGGGGTACGTCGCGACGCTGTACACTCTGTGCAGAGAGAGTCAAGGGAC | 549 |
| QY | 184 AsnArgAspTrpLysLysTrpThrValGluCysGlnGluGlySerAlaCysProSerAla | 203 |
| DB | 550 AACAGAGCACTA--GAGTACTCAGTGGAGTCCACAGAGACAGTGCCTGCCACGCTGT | 606 |
| QY | 204 GluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTrpGluAsn | 223 |
| DB | 607 GAGGAGAGCTCCCATTCAGCTCATGCGATGTGCGGTACCAACCTCAAGTATGA AAC | 666 |
| QY | 224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeuGln | 243 |
| DB | 667 TACACCACACGCTTTTCATCAGGACATCAATCAACCCGACCCCAAGAACTTGACG | 726 |
| QY | 244 LeuLysProLeuLysAsnSerArgHisValIgluValSerTrpGluTrpProAspTrpTrp | 263 |
| DB | 727 CTGAAGCCATTAAAGATTCTCGCAGGTGGAGAGTCACTGGGAGTACCTGACACTCG | 786 |
| QY | 264 SerThrProHisSerTrpPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsnAsn | 283 |
| DB | 787 AGTACTCCACATTTCTACTTCTCCGACATTTCTGGTCTGAGGTCCAGGCAAGACCAAG | 846 |

QY 284 ArgGluLysLysAspArgLeuGlyValAspLysThrSerAlaLysValAlaCysHisLys 303
|||||
DB 847 AGAGAAAGAAAGATGAGCTCTTCACGGACCAAGACTGACCGCTCATCTGCCCAAA 906
QY 304 AspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTyrSerAspTTP 323
|||||
DB 907 AATGCCAGCATTAAGCTGGGGCCGACCGCTACTATAGCTTATGAGAGCAATGG 966
QY 324 AlaSerValSerCysSer 329
|||||
DB 967 GCATCTGTGCTCCCTGCAGT 984

RESULT 10

US-08-640-386A-1
; Sequence 1, Application US/08640386A
; Patent No. 5756085
; GENERAL INFORMATION:
; APPLICANT: Sykes, Megan
; APPLICANT: Wolf, Stanley F.
; TITLE OF INVENTION: USE OF INTERLEUKIN-12 TO PREVENT
; TITLE OF INVENTION: GRAFT-VERSUS-HOST DISEASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc., Legal Affairs
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/640,386A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: GI 5225A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-498-8224
; TELEFAX: 617-876-5851
; INFORMATION FOR SEQ. ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 987 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL TYPE: Lymphoblast
; CELL LINE: RPMI 8866
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..987
; US-08-640-386A-1

Alignment Scores:

Score: 3.25e-161
Percent Similarity: 1501.50
Best Local Similarity: 92.028
Query Match: 85.288
53.558

Length: 987
Matches: 278
Conservative: 22
Mismatch: 25
Indels: 1
Gaps: 1

US-09-917-265-62 (1-533) x US-08-640-386A-1 (1-987)

QY 4 GlnGlnLeuValIleSerTyrPheSerLeuValIleLeuAlaSerProIleuMetaIle 23

DB 10 CAGCAGTGGTCATCTCTGGTTTCCCGGCTTTTCTGGCATTCGCCCTCGTGGCAAA 69
QY 24 TTPGluLeuGluLysAspValTyrValValGluLeuAspTTPHisProAspAlaProGly 43
DB 70 TGGAGACTGAGAAAGATGATTTATGCTGAGAAATGGATGGTATCCCGATCCCTGGA 129
QY 44 GluMetValValLeuThrCysHisThrProGluLysAspIleThrTTPHisAla 63
DB 130 GAAATGGTGCTCCTACCTGTCACACCCCTGAAGAAGATGATACCTGACGACTTGGAC 189
QY 64 GlnSerSerGluValLeuGlySerGlyThrLeuThrIleGlnValLysLuhbegly 83
DB 190 CAGAGCAGTGAAGCTTGAAGCTGTCGCAAAACCTGACCATCAAGTCAAAAGATTGGA 249
QY 84 AspAlaGluGlyLysThrCysHisLysGlyLysValLeuSerArgSerLeuLeu 103
DB 250 GATGCTGGCCAGTACCTGTCACAAAGAGCGAGGCTTAAAGCATTCGCTCTG 309
QY 104 IleHisLysLysGluAspGlyIleTTPSerThrAspIleLeuLysGluLysGluSer 123
DB 310 CTTCACAAAAGAGATGGAATTTGCTCAGATATTTTAAAGACCAAGAAAGACC 369
QY 124 LysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrGly 143
DB 370 AAAAATAAGACCTTCTTAAGATGCGAGGCAAGAAATATTCGAGCTTCACTGCTGG 429
QY 144 TTPLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPheSer 163
DB 430 TGGCTGACGACCAATCATCTGATTTGACATTCAGTCAAAAGCAGCAGAGCTTCT 489
QY 164 AspProGluGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgAla 183
DB 490 GACCCCAAGGGGTGACGTCGCGAGCTGCTACACTCTGACAGAGACTCAGAGGGAGAC 549
QY 184 AsnArgAspTyrLysLysTyrThrValGlyCysGlnGluGlySerLacysProSerAla 203
DB 550 AACAAAGAGATAT--GAGTACTGAGTGGAGTGCAGAGAGACAGTCCGACAGCTGCT 606
QY 204 GluLysSerLeuProIleGluValValAlaLysAlaIleHisLysLeuLysTyrGluAsn 223
DB 607 GAGGAGAGTCTGCCCTTATGAGTCAATGAGTGCAGTCCGCTTACACAGCTCAAGTATGAAAC 666
QY 224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeuGln 243
DB 667 TACACCAGCAGCTTCTTCAAGGAGGACATCAATCAAACTGACCCCAAGAACTTGCAG 726
QY 244 LeuLysProLeuLysAsnSerArgHisValGluValSerTTPGluTyrProAspThrTTP 263
DB 727 CTGAAGCCATTAAGATTTCTCGCAGGTGGAGTGAAGTGGAGTGGAGTGGAGTGGAG 786
QY 264 SerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 283
DB 787 AGTACTCCACATTCCTACTTCTCCGACATTCCTGCTTCCAGGTCAGGCAAGACAG 846
QY 284 ArgGluLysLysAspArgLeuGlyValAspLysThrSerAlaLysValAlaCysHisLys 303
DB 847 AGAGAAAGAAAGATGAGCTCTTCACGGACCAAGACTGACCGCTCATCTGCCCAAA 906
QY 304 AspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTyrSerAspTTP 323
DB 907 AATGCCAGCATTAAGCTGGGGCCGACCGCTACTATAGCTTATGAGAGCAATGG 966

RESULT 11

US-08-184-009-194
; Sequence 194, Application US/08184009
; Patent No. 583975
; GENERAL INFORMATION:
; APPLICANT: Paolletti, Enzo

APPLICANT: Tartaglia, James
APPLICANT: Cox, William I.
TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
NUMBER OF SEQUENCES: 217
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtiss, Morris & Safford
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/184, 009
FILING DATE: 19-JAN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEX: 425066CURTHS
INFORMATION FOR SEQ ID NO: 194:
SEQUENCE CHARACTERISTICS:
LENGTH: 1018 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-184-009-194
Alignment Scores:
Pred. No.: 3,42e-161 Length: 1018
Score: 1501.50 Matches: 278
Percent Similarity: 92.02% Conservative: 22
Best Local Similarity: 85.28% Mismatches: 25
Query Match: 53.55% Indels: 1
Gaps: 1
US-09-917-265-62 (1-533) x US-08-184-009-194 (1-1018)
QY 4 GlnGlnLeuValIleSerTrpPheSerLeuValIleuLeuAlaSerProIleuMetAlaIle 23
Db 41 CACGACTGGTCACTCTGCTTCCTGCTTCCCTGCTTCTGCACTCCCTCGTGGCATA 100
QY 24 TrpGlnLeuGlnLysAspValTyrValValGlnLeuAspTrpPheSerProAspAlaProGly 43
Db 101 TGGGAACCTGAGAAACATGTTATGTCGTGAATTGGATGCTATCCGATGCCCTCGGA 160
QY 44 GluMetValIleuThrCysHisThrProGlnGluAspIleThrTrpIleSerAla 63
Db 161 GAAATGCTGCTCTCACCTGTGCACCCCTGAAGAAGATGCTATTCACCTGGACCTGGAC 220
QY 64 GlnSerSerGlnValLeuGlnLysSerGlyLysThrLeuThrIleGlnValLysGluPheGly 83
Db 221 CAGACGACGTAGCTTACGCTCTGCGCAAAACCTGCACATCCAAAGCAAGATTGGA 280
QY 84 AspAlaGlyGlnTyrThrCysHisLysGlyLysValIleuSerAlaGlySerLeuLeu 103
Db 281 GATGCTGGCCAGTACCTCTCTCAAAAGGAGGAGCTTCTAAGCCATTGCTCTGCTG 340
QY 104 IleHisLysLysGlnAspGlyIleTrpSerThrAspIleLeuLysGlnLysGluSer 123
Db 341 CTTCCACAAAAGCAAGATGGAATTTGGTCCACTGATTTTAAAGGACCAAGAAAGACC 400
QY 124 LysAsnLysIlePheLeuLysCysGlnAlaLysAsnTyrSerGlyArpPheThrCysTrp 143
|||||

Db 401 AAAAATAGACTTTCTAAGATGCGAGGCCAAGAAATTATTCGTGACGTTTCACTGCTGG 460
QY 144 TrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerArGlyPheSer 163
Db 461 TGGCTGACGACAAATCACTACTGATTTGACATTCAGTGTCAAAAGCAGAGGCTTCT 520
QY 164 AspProGlnGlyValThrCysGlnAlaValThrLeuSerAlaGluAlaValAsp 183
Db 521 GACCCCAAGAGGGGAGCTGCGAGAGCTGCTACACTCTCTGACAGAGAGTACAGGGGAC 580
QY 184 AsnArgAspTyrLysLysTyrThrValGlnCysGlnGlnLysSerAlaCysProSerAla 203
Db 581 AACAGGAGATAT--GAGTACTGAGTGGAGGCCAGAGAGACAGTGCCTGCCAGCTGCT 637
QY 204 GlnGlnSerLeuProIleGlnValValValAspAlaIleHisLysLeuLysTyrGluAsn 223
Db 638 GAGGAGAGTGTGCCATTGAGGTCATGTGATGCCCTTCAACAAGCTCAAGTATGAAMAC 697
QY 224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProPheAsnLeuGln 243
Db 698 TACACCGACAGCTTCTTATCAGGAGACATATCAACCTGACCCCAAGAACTTCCAG 757
QY 244 LeuLysProLeuLysAsnSerArgHisValGlnValSerTrpGluTyrProAspThrTrp 263
Db 758 CTGAAGCCATTAAAGAAATTCTCGGACAGGTGAGGTGAGTGGAGTACCTGACACCTGG 817
QY 264 SerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsnAsn 283
Db 818 AGTACTCCACATTCCTCTCTCCCTGACATTCGCTGACGGCCAGGCAAGCAAGCAAG 877
QY 284 ArgGlnLysLysAspArgLeuCysValAspLysThrSerAlaLysValLysHisLys 303
Db 878 AGCAAAAGAAAGATAGAGTCTTCAGGACACAAGACCTCAGCCAGGTCATCTGCCGAAA 937
QY 304 AspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAspTrp 323
Db 938 AATGCCAGCATTTAGCGCGGCCGACAGCCGCTACTATGATCATCTTGAGACCAATGG 997
QY 324 AlaSerValSerCysSer 329
Db 998 GCATCTGTGCCCTGCACT 1015
RESULT 12
US-08-458-356-194
Sequence 194, Application US/08458356
Patent No. 5942235
GENERAL INFORMATION:
APPLICANT: Paolelli, Enzo
APPLICANT: Tartaglia, James
APPLICANT: Cox, William I.
TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
NUMBER OF SEQUENCES: 217
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtiss, Morris & Safford
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,356
FILING DATE: 02-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/184,009
FILING DATE: 19-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.

REGISTRATION NUMBER: 25,506
 REFERENCE/DOCKET NUMBER: 454310-2530
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 840-3333
 TELEFAX: (212) 840-0712
 TELEX: 425066CURTMS
 INFORMATION FOR SEQ ID NO: 194:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1018 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-458-356-194

Alignment Scores:

| Pred. No.: | 3,42e-161 | Length: | 1018 |
|------------------------|-----------|---------------|------|
| Score: | 1501.50 | Matches: | 278 |
| Percent Similarity: | 92.02% | Conservative: | 22 |
| Best Local Similarity: | 85.28% | Mismatches: | 25 |
| Query Match: | 53.55% | Indels: | 1 |
| DB: | 2 | Gaps: | 1 |

US-09-917-265-62 (1-533) x US-08-458-356-194 (1-1018)

QY 4 GlnGlnLeuValIleSerTrpPheSerLeuValLeuLeuAlaSerProLeuMetAlaIle 23
 DB 41 CACACAGTGGTCACTCTGCTTCCCTGCTTTCTGTCGATCTCCCGTGGCATTA 100
 QY 24 TrpGlnLeuGlnLysAspValIleValAlaGlnLeuAspTrpHisProAspAlaProGly 43
 DB 101 TGGGAACCTGAAGAAATGTTATGTCGTAGAATTGGATTGGATCCGGATGCCCTTGA 160
 QY 44 GluMetValAlaLeuThrCysHisThrProGlnGluAspAspIleThrTrpTrpSerAla 63
 DB 161 GAATGTGTGCTCTCACTCTGACACCCCTGAAGAAAGATGTCATCAGCTGGACCTTGAC 220
 QY 64 GlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPheGly 83
 DB 221 CAGAGCAGTGAGCTCTTACGCTCTGCAAAACCTGACATCCAAAGTCAAGAGTTTGA 280
 QY 84 AspAlaGlyGlnThrCysHisLysGlyGlyLysValLeuSerArgSerLeuLeu 103
 DB 281 GATGCTGGCCAGTACCTGTCTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 340
 QY 104 IleHisLysLysGlnAspGlyIleTrpSerThrAspIleLeuLysGlnGlnLysGlnSer 123
 DB 341 CTTCAACAAAAGCAATGGAATTTGCTGCACATGATATTTAAAGCAGCAGAAAGAACCC 400
 QY 124 LysAsnLysIlePheLeuLysCysGluAlaLysAsnTrpSerGlyArgPheThrCysTrp 143
 DB 401 AAAAATTAAGACCTTTCTAAGATGCGAGGCCAAGAAATTAATTCGAGCTTACCTGCTGG 460
 QY 144 TrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPheSer 163
 DB 461 TGGCTACGACCAATCTGACTGATGATGATGATGATGATGATGATGATGATGATGATG 520
 QY 164 AspProGlnGlyValIleThrCysGlyAlaValIleThrLeuSerAlaGlnArgValAlaAsp 183
 DB 521 GACCCCAAGGGGTGACGCTGCGAGCTGCTACACTCTCTCCAGAGAGAGTCAAGAGGGGAC 580
 QY 184 AsnArgAspTrpLysLysTrpThrValGluCysGlnGlnGlySerAlaCysProSerAla 203
 DB 581 AACACAGAGATAT---GAGTACTACAGTGGAGTCCAGAGAGCAGTCCCTGCCAGCTGCT 637
 QY 204 GluGlnSerLeuProIleGlnValAlaValAlaAspAlaIleHisLysLeuLysTrpGluAsn 223
 DB 638 GAGCAGAGTCTGCCATTTGAGGTGATGATGATGATGATGATGATGATGATGATGATG 697
 QY 224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeuGln 243
 DB 698 TACACGACGAGCTTCTTCATCAGGAGCAGATCATCAAACTGACCCCAAGAAACTTGCAG 757

QY 244 LeuLysProLeuLysAsnSerArgHisValGlnValSerTrpGluTrpProAspThrTrp 263
 DB 758 CTGAGCCATTAAGATTTCTCGGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAG 817
 QY 264 SerThrProHisSerTrpPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsnAsn 283
 DB 818 AGTACTCACATTCCTACTTCTCTCCCTGACATTCCTGCTTCCAGGTCCAGGGCAGAGCAAG 877
 QY 284 ArgGlnLysLysAspArgLeuCysValAspLysThrSerAlaLysValAlaCysHisLys 303
 DB 878 AGAGAAAGAAAGATAGAGTCTTCACGAGCAAGACCTCAGCAGCAGCTCATCTGCCCAAA 937
 QY 304 AspAlaLysIleArgValGlnAlaArgAspArgTyrTrpSerSerTrpSerAspTrp 323
 DB 938 AATGCCAGCATTTAGCTGGGGGCCAGAGACCGCTACTATAGCTCATCTTGAGCGAATGG 997

RESULT 13

US-08-460-736-194
 ; Sequence 194, Application US/08460736
 ; Patent No. 6265189

GENERAL INFORMATION:

APPLICANT: Paoletti, Enzo
 APPLICANT: Tartaglia, James
 APPLICANT: Cox, William I.
 TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
 NUMBER OF SEQUENCES: 217
 CORRESPONDENCE ADDRESS:
 ADDRESSER: Curtis, Morris & Safford
 STREET: 530 Fifth Avenue
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/460,736
 FILING DATE: 02-JUN-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/184,009
 FILING DATE: 19-JAN-1994

ATTORNEY/AGENT INFORMATION:
 NAME: Frommer, William S.
 REGISTRATION NUMBER: 25,506
 REFERENCE/DOCKET NUMBER: 454310-2530
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 840-3333
 TELEFAX: (212) 840-0712

TELEX: 425066CURTMS
 INFORMATION FOR SEQ ID NO: 194:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1018 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-460-736-194

Alignment Scores:

| Pred. No.: | 3,42e-161 | Length: | 1018 |
|------------------------|-----------|---------------|------|
| Score: | 1501.50 | Matches: | 278 |
| Percent Similarity: | 92.02% | Conservative: | 22 |
| Best Local Similarity: | 85.28% | Mismatches: | 25 |
| Query Match: | 53.55% | Indels: | 1 |
| DB: | 4 | Gaps: | 1 |

US-09-917-265-62 (1-533) x US-08-460-736-194 (1-1018)

QY 4 GlnGlnLeuValIleSerTrpPheSerLeuValLeuLeuAlaSerProLeuMetAlaIle 23
 Db 41 CACAGAGTGGTCACTCTTCTGCTTTTCCCTGGTTTCTGGCATCTCCCTCGTGCCATA 100
 QY 24 TrpGluLeuGluIlyAspValTyrValValGluLeuAspTrpPheIleProAspAlaProGly 43
 Db 101 TGGGAAGTGAAGAAAGATGTTTATGTCGTAGAAATGGATGGTATCCGATGCCCTGGA 160
 QY 44 GluMetValValLeuThrCysHisThrProGluGluAspIleThrTrpThrSerAla 63
 Db 161 GAATGATGGTCTGCTCACCCTGACACCCCTGAAGAACATGGTATCACCCTGGACCTTGAC 220
 QY 64 GlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPheGly 83
 Db 221 CAGAGCAGTGAAGCTTAAAGCTCTGGCAAAACCCTGACCATCCAAAGTCAAGACTTTGGA 280
 QY 84 AspAlaGlyGlnTyrThrCysHisLysGlyLysValLeuSerAspSerLeuLeu 103
 Db 281 GATGCTGGCCAGTACACTCTGCACAAAGAGCGAGGTTCTAAGCCATTGCTCTCTG 340
 QY 104 IleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGluSer 123
 Db 341 CTCACAAAAGAGAGATGAATTTGCTCCACATGATTTTAAAGACCAAGAAAGACC 400
 QY 124 LysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyAspPheThrCysTrp 143
 Db 401 AAAAATAAGACCTTTTCAAGATGCGAGCCAGCAATATTCTGACCTTTTCCACTCTCG 460
 QY 144 TrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPheSer 163
 Db 461 TGGCTGACGACATCACTACTGATTTTACATTCAGTCTCAAAAGACACAGAGCTTCT 520
 QY 164 AspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgValAsp 183
 Db 521 GACCCCAAGCGGTGACGTGCGAGCTGCTACACTCTCTGACAGAGACAGAGGCGAC 580
 QY 184 AsnArgAspTyrIlyLysTyrThrValGluCysGlnGluIlySerAlaCysProSerAla 203
 Db 581 AACAGAGACTAT---GAGTACTAGTGGAGCTGCGAGACACACTGCTGCCCGCAGTCTCT 637
 QY 204 GlnGlnSerLeuProIleGluValValAspAlaIleHisLysLeuLysTyrGluAsn 223
 Db 638 GAGGAGAGTCTGCCCATTTGAGGTCAATGCTGATGCCCTTCAACAAGCTCAAGTATGAAAC 697
 QY 224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspPropThrAsnLeuGln 243
 Db 698 TACACGACGAGCTTCTTCATCAGGACATCATCAACCTGACCCCAAGAACTTGCAG 757
 QY 244 LeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThrTrp 263
 Db 758 CTGAAGCCATTAAAGATTCTCGGACAGTGAAGTCACTGGAGTCACTCCGACACCTCG 817
 QY 264 SerThrProIleSerTrpPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 283
 Db 818 AGTACCTGACATTCCTCTCTCTGCTGACATTTCTGCTTCAAGTCCAGGCAAGACGAC 877
 QY 284 ArgGlnLysLysAspArgLeuCysValAspLysThrSerAlaLysValValCysHisLys 303
 Db 878 AGAGAAAGAAAGATAGACTCTTCACGACAAAGACCTCAGCAGCATCTGCCGCAAA 937
 QY 304 AspAlaLysIleArgValGlnAlaArgAspArgTyrTrpSerSerSerTrpSerAspTrp 323
 Db 938 AATGCGACGATTAAGCGCGCGCCAGGACCGCTACTATAGCTCATCTTGGAGCGAATGG 997
 QY 324 AlaSerValSerCysSer 329
 Db 998 GCATCTGTCCTGCACT 1015

RESULT 14
 US-08-751-767A-3

Sequence 3, Application US/08751767A

Patent No. 5994104

GENERAL INFORMATION:

APPLICANT: ANDERSON, ROBERT J.

APPLICANT: GRANT, HUGH

APPLICANT: MACDONALD, IAN D.

TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN

NUMBER OF SEQUENCES: 80

CORRESPONDENCE ADDRESS:

ADDRESS: NIXON & VANDERHAYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VA

COUNTRY: USA

ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/751,767A

FILING DATE: 08-NOV-1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: SADOFF, B.J.

REGISTRATION NUMBER: 36,663

REFERENCE/DOCKET NUMBER: 117-221

TELECOMMUNICATION INFORMATION:

TELEPHONE: 7038164091

TELEFAX: 7038164100

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1399 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 43..1026

US-08-751-767A-3

Alignment Scores:

Pred. No.: 5,88e-161

Score: 1501.50

Percent Similarity: 92.02%

Best Local Similarity: 85.28%

Query Match: 53.55%

DB: 2

Gaps: 1

US-09-917-265-62 (1-533) x US-08-751-767A-3 (1-1399)

QY 4 GlnGlnLeuValIleSerTrpPheSerLeuValLeuLeuAlaSerProLeuMetAlaIle 23
 Db 52 CACAGAGTGGTCACTCTTCTGCTTTTCCCTGGTTTCTGGCATCTCCCTCGTGCCATA 111
 QY 24 TrpGluLeuGluIlyAspValTyrValValGluLeuAspTrpPheIleProAspAlaProGly 43
 Db 112 TGGGAAGTGAAGAAAGATGTTTATGTCGTAGAAATGGATGGTATCCGATGCCCTGGA 171
 QY 44 GluMetValValLeuThrCysHisThrProGluGluAspIleThrTrpThrSerAla 63
 Db 172 GAATGATGGTCTGCTCACCCTGACACCCCTGAAGAACATGGTATCACCCTGGACCTTGAC 231
 QY 64 GlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPheGly 83
 Db 232 CAGAGCAGTGAAGCTTAAAGCTCTGGCAAAACCCTGACCATCCAAAGTCAAGACTTTGGA 291
 QY 84 AspAlaGlyGlnTyrThrCysHisLysGlyLysValLeuSerAspSerLeuLeu 103
 Db 292 GATGCTGGCCAGTACACTCTGCACAAAGAGCGAGGTTTCAAGCATTCCTGCTCTGCTG 351

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OY 11eh1slslysgluaspolyllertpserthrapsileuleylsgluinlysgluser 123
Db 332 CTTCCAAAAGAGAGATGGAATTGGTCCACTGATATTTTAAAGACCAGAAAGACC 411
OY 124 LysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrp 143
Db 412 AAAAATAGACCTTTCTTAAGATGCGAGGCCAAGATTAATTCGACGTTTCACCTGCG 471
OY 144 TrrPleuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgLysPheSer 163
Db 472 TGGCTGACGACATCATGATGATTTGACATTGCTCAAAAGACGACGAGGCTCTTCT 531
OY 164 AspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgValAsp 183
Db 532 GACCCCAAGGGGTGACGTCGCGAGCTGCTACACTCTCGCAGAGAGAGTCAAGAGGAGC 591
OY 184 AsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProSerAla 203
Db 592 AACAGAGAGTAT---GAGTACTGACGTGCGAGTCCAGAGAGACAGTCCCTGCGACCTGCT 648
OY 204 GluGluSerLeuProIleGluValValAlaAspAlaIleHisLysLeuLysTyrGluAsn 223
Db 649 GAGGAGAGCTGCTCCATTGAGGTGATGATGCGGATGCGTCAACAAGCTCAAGTATGAAAC 708
OY 224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeuGln 243
Db 709 TACACCAGCAGCTTCTTCATCAGGACATCATCAACCTGACCCCAAGAGACTTGCGAG 768
OY 244 LeuLysProLeuLysAsnSerArgHisValGluValSerTrrPgluTyrProAspThrTrp 263
Db 769 CTGAAGCCATTAAAGAAATCTCGGAGGTGCGAGGTGAGAGTACCTGACACCTG 828
OY 264 SerThrProHisSerTyrPheSerLeuThrPheCysIleGluAlaGlnGlyAsnAsn 283
Db 829 AGTACCCACATTCCTACTTCTCCTGACATTCCTGCTTCAAGCTCCAGGCGCAAGACAG 888
OY 284 ArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValAlaCysHisLys 303
Db 889 AAGAGAAAGAAAGATAGACTCTTCACGAGCAAGACCTGACCGCTCATCTGCGCCAAA 948
OY 304 AspAlaLysIleArgValAlaAlaArgAspArgTyrTyrSerSerSerTrpSerAspTrp 323
Db 949 AATGCCAGCATTAAGCTCGGCGCCAGACCGCTACTATAGCTCATCTTGAGAGCAATG 1008
OY 324 AlaSerValSerCysSer 329
Db 1009 GCATCTGCTGCTGCGAGT 1026

RESULT 15
US-08-265-087-1
; Sequence 1, Application US/08265087
; Patent No. 5571515
; GENERAL INFORMATION:
; APPLICANT: Scott, Phillip
; APPLICANT: Trinchieri, Giorgio
; TITLE OF INVENTION: Compositions and Methods for use of
; TITLE OF INVENTION: IL-12 as an Adjuvant
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Center, PO Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/265,087
; FILING DATE:
```

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; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/229,282
; FILING DATE: 18-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST51AUSA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9206
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2362 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 33..1016
; US-08-265-087-1

Alignment Scores:
Pred. No.: 1,43e-160 Length: 2362
Score: 1501.50 Matches: 278
Percent Similarity: 92.02% Conservative: 22
Best Local Similarity: 85.28% Mismatches: 25
Query Match: 53.55% Gaps: 1

US-09-917-265-62 (1-533) x US-08-265-087-1 (1-2362)
OY 4 GlnGluLeuValIleSerThrPheSerLeuValLeuLeuAlaSerProLeuMetAlaIle 23
Db 42 CAGCAGTTGGTCATCTCTTGGTTTCCCTGCTTTTTCGCACTCCCTCGTGGCCAAA 101
OY 24 TrrPgluLeuGluLysAspValTyrValValGluLeuAspTrrPheIleProAspAlaProGly 43
Db 102 TGGAACTCAGAGAAAGATGTTATGCTGAGAAATGGATGGATGCCGATCCCTGGA 161
OY 44 GluMetValValLeuThrCysHisThrProGluGluAspIleThrTrpSerAla 63
Db 162 GAAATGGTGGTCTCCTACCTGTGACACCCCTGAAGAGATGATACCTGACCTTGGAC 221
OY 64 GlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGluValLysGluPheGly 83
Db 222 CAGAGCAGTACGCTTACGCTCTGCAAAACCTGACCATCCAAAGTCAAAAGATTGGA 281
OY 84 AspAlaGlyGlnTyrThrCysHisLysGlyLysValLeuSerArgSerLeuLeu 103
Db 282 GATGCTGGCCAGTACACCTGTCAAAAGAGGCGAGGCTTCAAGCATTCGCTCGCTG 341
OY 104 IleHisLysLysGluAspGlyLleTrrPheSerThrAspIleLeuLysGluGlnLysGluSer 123
Db 342 CTTCCAAAAGAGAGATGGAATTGGTCCACTGATATTTTAAAGACCAGAAAGACC 401
OY 124 LysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrp 143
Db 402 AAAAATAGACCTTTCTTAAGATGCGAGGCCAAGATTAATTCGACGTTTCACCTGCG 461
OY 144 TrrPleuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgLysPheSer 163
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Db 522 GACCCCAAGGGGTGACGTCGCGAGCTGCTACACTCTCGCAGAGAGAGTCAAGAGGAGC 581
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Job time : 90.1634 secs

GenCore version 5.1.6
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Run on: July 16, 2003, 19:59:04 ; Search time 364.136 seconds
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Searched: 1439767 seqs, 1031500376 residues

Total number of hits satisfying chosen parameters: 2879534

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No | Score | Query Match | Length | DB ID | Description |
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| C | 4 | 2693 | 96.0 | 1533 | 10 | US-09-917-265-68 | Sequence 68, Appl |
| C | 5 | 2643 | 94.3 | 1599 | 10 | US-09-917-265-38 | Sequence 38, Appl |
| C | 6 | 2643 | 94.3 | 1599 | 10 | US-09-917-265-40 | Sequence 40, Appl |
| C | 7 | 2546 | 90.8 | 1533 | 10 | US-09-917-265-43 | Sequence 43, Appl |
| C | 8 | 2546 | 90.8 | 1533 | 10 | US-09-917-265-45 | Sequence 45, Appl |
| C | 9 | 2392 | 85.3 | 8608 | 10 | US-09-828-825-7 | Sequence 7, Appl |
| C | 10 | 2392 | 85.3 | 8629 | 10 | US-09-828-825-15 | Sequence 15, Appl |
| C | 11 | 2389.5 | 85.2 | 8623 | 10 | US-09-828-825-5 | Sequence 5, Appl |
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| C | 13 | 2387 | 85.1 | 8638 | 10 | US-09-828-825-9 | Sequence 9, Appl |
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| C | 21 | 1657 | 59.1 | 987 | 10 | US-09-917-265-29 | Sequence 29, Appl |
| C | 22 | 1657 | 59.1 | 987 | 10 | US-09-917-265-31 | Sequence 31, Appl |
| C | 23 | 1653 | 59.0 | 921 | 10 | US-09-917-265-52 | Sequence 52, Appl |
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| C | 25 | 1653 | 59.0 | 985 | 10 | US-09-917-265-55 | Sequence 55, Appl |
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| C | 27 | 1651 | 58.9 | 2193 | 15 | US-10-079-616-5 | Sequence 5, Appl |
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| C | 29 | 1554 | 55.4 | 921 | 15 | US-10-079-616-7 | Sequence 7, Appl |
| C | 30 | 1546 | 55.1 | 921 | 10 | US-09-917-265-26 | Sequence 26, Appl |
| C | 31 | 1546 | 55.1 | 921 | 10 | US-09-917-265-28 | Sequence 28, Appl |
| C | 32 | 1503.5 | 53.6 | 1870 | 15 | US-10-172-811-4 | Sequence 4, Appl |
| C | 33 | 1502.5 | 53.6 | 987 | 11 | US-09-828-025-24 | Sequence 24, Appl |
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| C | 36 | 1501.5 | 53.5 | 987 | 11 | US-09-754-014-3 | Sequence 3, Appl |
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| C | 38 | 1501.5 | 53.5 | 987 | 11 | US-09-836-866-2 | Sequence 2, Appl |
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| C | 40 | 1141.5 | 40.7 | 1840 | 15 | US-10-172-399-3 | Sequence 3, Appl |
| C | 41 | 970 | 34.6 | 666 | 10 | US-09-917-265-46 | Sequence 46, Appl |
| C | 42 | 970 | 34.6 | 666 | 10 | US-09-917-265-48 | Sequence 48, Appl |
| C | 43 | 970 | 34.6 | 1455 | 10 | US-09-917-265-104 | Sequence 104, App |
| C | 44 | 970 | 34.6 | 1455 | 10 | US-09-917-265-106 | Sequence 106, App |
| C | 45 | 969 | 34.6 | 591 | 10 | US-09-917-265-49 | Sequence 49, Appl |

ALIGNMENTS

RESULT 1
US-09-917-265-61
Sequence 61, Application US/09917265
Patent No. US20020052030A1
GENERAL INFORMATION:
APPLICANT: Wonderlign, Ramani S.
APPLICANT: Borouh, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/09/917, 265
PRIOR FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223, 016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 109
SOFTWARE: PatentIn version 3.1
SEQ ID NO 61
LENGTH: 1599
TYPE: DNA
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1599)
OTHER INFORMATION:
US-09-917-265-61

Alignment Scores:

Pred. No.: 1,41e-317 Length: 1599
 Score: 2804.00 Matches: 533
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

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 QY 21 MetAlaIleThrPheLeuGlnLeuLysAspValTyrValValGluLeuAspThrPheProAsp 40
 DB 61 ATGCGCATATGGCACTGGAGAAAGATGTTATGTTGTAGAGTTGGACTGGACCTGAT 120
 QY 41 AlaProGlyLysMetValValLeuThrCysHisThrProGluLysAspIleThrTrp 60
 DB 121 GCCCCGAGAAATGGTGTCTCCCTGACCTGACATACCCCTGAAAGACATGACATCTGG 180
 QY 61 ThrSerAlaGlnSerSerGluValIleGlySerGlyLysThrLeuThrIleGlnValLys 80
 DB 181 ACCTCAGCGCAGACAGCTGAAGTCTAGTTCGTGTAACCTGTGACCATCCAGTCAAA 240
 QY 81 GluPheGlyAspAlaGlyGlnTyrThrCysHisLysGlyGlyLysValLeuSerArgSer 100
 DB 241 GAATTTGGAGATCTGGCCAGTATACCTGCCATAAAGAGAGCAAGTTCTGAGCCCTCA 300
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 QY 261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGly 280
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 QY 501 AspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAla 520
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RESULT 2

US-09-917-265-63/C
 ; Sequence 63, Application US/09917265
 ; Patent No. US20020052030A1

GENERAL INFORMATION:

; APPLICANT: Wonderling, Ramani S.
 ; APPLICANT: Boroughs, Karen L.
 ; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
 ; FILE REFERENCE: IM-5
 ; CURRENT APPLICATION NUMBER: US/09/917,265
 ; CURRENT FILING DATE: 2001-07-27
 ; PRIOR APPLICATION NUMBER: 60/223,016
 ; PRIOR FILING DATE: 2000-08-04
 ; NUMBER OF SEQ ID NOS: 109
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 63

LENGTH: 1599

TYPE: DNA

ORGANISM: Canis familiaris

US-09-917-265-63

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Pred. No.: 1,41e-317 Length: 1599
 Score: 2804.00 Matches: 533
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
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QY      181 ArgAlaAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluLysSerAlaCys 200
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QY      281 LysAsnAsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValAl 300
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QY      301 CysHisLysAspAlaLysIleArgValIcIlnAlaArgAspArgTyrTyrSerSerTrp 320
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QY      321 SerAspTrpAlaSerValSerCysSerGlyGlyLysGlyLysSerArgAsnLeuPro 340
Db      639 AGCGACTGGCATCTGTCTATGACAGTGGTGGCGGTGGCGGATCTAGAAACTTGGCCA 580
QY      341 ThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArg 360

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QY      441 IleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsnAlaLysLeuLeu 460
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QY      461 MetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 480
Db      219 ATGATGCCCAAGAGGACAGATCTTCTGGATCAAAAACATGCTGACAGTATGATGAGCTG 160
QY      481 LeuGlnAlaLeuAsnPhaAsnSerValThrValProGlnLysSerSerLeuGluLeuPro 500
Db      159 TTACAGGCCCTGAATTTTACAGAGTGTGACTGTGCCACAGAAATCCTCCCTGAAAGCGG 100
QY      501 AspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAla 520
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QY      521 ValThrIleAsnArgMetMetSerTyrLeuAsnSerSer 533
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RESULT 3

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US-09-917-265-66
; Sequence 66, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Karen L.
; APPLICANT: Borroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1533)
; OTHER INFORMATION:
US-09-917-265-66

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Alignment Scores:

| Pred. No.: | 8.55e-305 | Length: 1533 |
|------------------------|-----------|-----------------|
| Score: | 2693.00 | Matches: 511 |
| Percent Similarity: | 100.00% | Conservative: 0 |
| Best Local Similarity: | 100.00% | Mismatches: 0 |
| Query Match: | 96.04% | Indels: 0 |
| DB: | 10 | Gaps: 0 |

US-09-917-265-62 (1-533) x US-09-917-265-66 (1-1533)

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QY 23 ILETRPGLULEUGLULYSASPVALTYRVALGLULEUASPTRPHISPROASAPALAPRO 42
    |||
    1 ATATGGGAACACTGAGAAAGATGTTATGTTAGTAGAGTTGAGTGGCAACCTGATGCCCC 60
QY 43 GLYGLUMETVALVALLLEUTHRCYSHISTHPRGUGLUNASPSPILETHTRPTPHRSER 62
    |||
    61 GGAGAAATGGTGTCTCCACCTCCATACCCCTGAAGAAATGACATCACTTGAGACTCA 120
QY 63 ALGLISERSERGLUVALLEUGLYSERGLYSTRHLEUTHRIEGLINVALYSGLUPLHE 82
    |||
    121 GCCCAGACGACGTGAAGCTCCTAGTTCGGTAAACCTGACCATCCAGCAAGCAAGATTT 180
Db 121 GCCCAGACGACGTGAAGCTCCTAGTTCGGTAAACCTGACCATCCAGCAAGCAAGATTT 180
QY 83 GLYASPLAGLYGLINTYRTHRCSHLSYSGLYGLYLYSVALLEUSERARGSERLEU 102
    |||
    181 GGAGATGCTGGCAGTACCTACCTCCATTAAGAGAGCAAGGTCTGAGACCCCTCACTCCTG 240
QY 103 LEULIEHISLYSGLYUASPGLYILETRPSETRTHASPLILEUUSGLUGLUNLYSGLU 122
    |||
    241 TTGATTTCAAAAAAGAAAGATGAAATTTGGTCCACTGATATCTTAAAGGAACGAAAGAA 300
QY 123 SERLYSASNLYSILEPHELEULYSYSGLYALALYSANLYSERGLYATGPHETHRCS 142
    |||
    301 TCCAAAAATAGATCTTTCGAAATGAGAGCAAAAGATATTTCTGAGCTTTACACTGC 360
QY 143 TRPTTRPLEUTHRALILESERTHASPLEULYSPHESERVALYSSERSEARAGLYPHE 162
    |||
    361 TGTGTGGCTGACGGCAATCACTACTGATTTGAAATTCAGTGTCAAAAGATACAGAGGCTTC 420
QY 163 SERASPROGLINGLYVALTHRCYSGLYVALVALLTHREUSERLAGLUAAGVALARGVAL 182
    |||
    421 TCTGACCCCAAGGGGGGAGACATGGGAGAGTGCCTTCACAGAGAGAGGAGGTCAGAGTG 480
QY 183 ASPASNARGSPTRYLYSTRYLYSTRYTHRVALGLUCYSGLINGLYSERALACYSPROSER 202
    |||
    481 GACAACAGGAGATTATAGAGATACACAGTGGAGTGTAGAGAGGCAATGCTGCCCTCT 540
Db 203 ALGLUGLUSERLEUPROILLEGLUVALVALLASPLALLEHISLYSLEULYTRYGLU 222
    |||
    541 GCGGAGAGAGGCTTACCACATCGAGAGTGTGTGATCTCTATTCAACAGCTCAAGTATGAA 600
QY 223 ASNTYTRHSESERPHEPHEILEARGASPLILELLEYSPROASPPROPOTPHASLEU 242
    |||
    601 AACACACCCAGCAGCTTCTTCACTACAGACATCACTCAACACAGACCCACCAACACCTG 660
QY 243 GLNLEULYSPROLEULYSASNSEARFHHISVALGLUVALSERTRPGIUTYRPROASPTH 262
    |||
    661 CAGCTGAAGCCATTGAAATAATTCGCGACGTGAGAGTCAAGCTGGGAATCCCGACACCC 720
Db 263 TRPSETRHTRHISSETRYRPHESERLEUTHRPHECYSILEGLINAGLYLYSASN 282
    |||
    721 TGGAGCACCCCAATTCCTACTCTCTCCCTGACATTTTGACATACGCGCCAGGGCAAGAAC 780
QY 283 ASNARGGLULYSLYSASPARGLEUCYSVALASPLYSTRHSEARALALYVALCYSHIS 302
    |||
    781 AATAGAGAAAAGAAAGATAGACTTCGCTGACAGACACTCAGCCAAAGGCTGTGTCCAC 840
Db 303 LYSASPLALALYSILEARGVALGLINALAARGASPARGYTRYRSESRSETRTPSERASP 322
    |||
    841 AAGGATGCCAAGATCCGCTGCAAGCCGAGACCGGCTACTAGTATAGTTCATCTTGAGAGC 900
QY 323 TRPALASERVALSERCYSSESGLYGLYGLYGLYLYSERARGANLEUPROTHPRO 342
    |||
    901 TGGGCACTGTGTATCACTGATGTGGCGGGTGGCGGCAATCTGAACAACTGCCAACCCCT 960
QY 343 THRPROSERPROGLYMETPHEGLINCYSEUASNHISSESGINTHRLLEUATARGALVAL 362
    |||
    961 ACTTCATACCCCGGATATGTTCCATATGTTGACACCACTCCCAACACTTGTGAGAGCCGCTC 1020
QY 363 SERASNTHRLLEUGLUNLYSALAARGINTHRLLEUGLULEUTHRYSERCYSTRHSEGLU 382
    |||
    1021 AGCAACACGCTTCAGAAAGGCGAGCAACAACCTAGAAATATATTCCTGACCTCCGAGAGAG 1080
Db 383 ILEASPHISGLUASPILETHRLYASPSLYSTRHSETRHVALGLUALACYLSEUPROLEU 402

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Db 1081 ATTGATCATGAACATATTCACAAAGATTAACACAGACAGTGGAGGCTGCTTACACATG 1140
QY 403 GLULEUTHRMELASNLUSERCYSLEUALASERARGLUIILESEULEITHRANGLY 422
    |||
    1141 GAATTAACCATGATAGACTTCCCTGCTTCAGAGACATCTTTGATTAACATGAGG 1200
QY 423 SERCYSLEUALASERGLYLYSALASERPHMETHRVALLEUCYSLEUSERILETYR 442
    |||
    1201 AGTTGGCTGGCCCTTGGAAGGCGCTTTATAGACGGCTGCTGCTTAGACAGCATCTAT 1260
QY 443 GLUASPLEULYSMETLYRGLINMETGLUPHELYSALAMELASNALYLSLEUWETAP 462
    |||
    1261 GAGGACTTGAAGATGTACAGATGGAATTCAGAGCCATGACGCAAGCAAGCTTTAAAGAT 1320
QY 463 PROLYSARGGLINLEPHELEUASPGINASMETLEUTHRALILEASPLILEUUGLIN 482
    |||
    1321 CCCAAGAGCAGATCTTTCTGATTCAAACATCTCAGCTATGATGATGAGCTTACAG 1380
Db 1381 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCCTTGAAAGCGCGATTTT 1440
QY 483 ALALEUASNPHESANSERVALTHRALPROGLINLYSERSEULEUGLUPROASPH 502
    |||
    503 TYRLYSTRHLYSTRILEYLSLEUCYSILELEULHISALAPHEARGLILEARGALVALTHR 522
Db 1441 TATTAACCTAAATCAAGCTCTGCTCATCTTCACTTTCAGATGCTTGAATGCTGGAGTAC 1500
QY 523 ILEASNARGMETSETRYRLEUASNSESR 533
    |||
    1501 ATCAATAGATGATGTCTACTGTAAGTCTGTC 1533

RESULT 4
US-09-917-265-68/c
; Sequence 68, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Canis familiaris
; US-09-917-265-68

Alignment Scores:
Pred. No.: 8,55e-305 Length: 1533
Score: 2693.00 Matches: 511
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 96.04% Indels: 0
DB: 10 Gaps: 0

US-09-917-265-62 (1-533) x US-09-917-265-68 (1-1533)
QY 23 ILETRPGLULEUGLULYSASPVALTYRVALGLULEUASPTRPHISPROASAPALAPRO 42
    |||
    1533 ATATGGGAACACTGAGAAAGATGTTATGTTAGTAGAGTTGAGTGGCAACCTGATGCCCC 1474
Db 43 GLYGLUMETVALVALLLEUTHRCYSHISTHPRGUGLUNASPSPILETHTRPTPHRSER 62
    |||
    1473 GGAGAAATGGTGTCTCCACCTCCATACCCCTGAAGAAATGACATCACTTGAGACTCA 1414
QY 63 ALGLISERSERGLUVALLEUGLYSERGLYSTRHLEUTHRIEGLINVALYSGLUPLHE 82
    |||
    1413 GCCCAGACGACGTGAAGCTCCTAGTTCGGTAAACCTGACCATCCAGCAAGCAAGATTT 1354

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OY      83  GLVAspAlaGlyGlnTrpThrcysHisLysGlyGlyLysValLeuSerArgSerLeuLeu 102
      |||||||
Db      1353 GGAATCTCTGGCCAGTATTACCTGCCATAAAGAGGCAAGGTTCTGAGCCCTCTCCTCTG 1294

OY      103  LeuLeuHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGlu 122
      |||||||
Db      1293 TTGGATTACAAAAGAAAGAAAGATGGAAATTGGTCCACTGATATCTTAAGAAACAGAAAGAA 1234

OY      123  SerLysAsnLysIlePheLeuLysGlyAlaLysAsnTrpSerGlyArgPheTrpCys 142
      |||||||
Db      1233 TCCAAAATAAGATCTTTGAAATCGAGCCAAAGAAATATCTGACGCTTGCATATGC 1174

OY      143  TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 162
      |||||||
Db      1173 TGGTGGCTGACGGCAATCACTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 1114

OY      163  SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgVal 182
      |||||||
Db      1113 TCTGACCCCGCAGGGCTGACATGTGAGAGAGTGCACCTTTCAGCAGAGAGGGCTCAGAGTG 1054

OY      183  AspAsnArgAspTrpLysLysTrpThrValGluCysGlnGlySerAlaCysProSer 202
      |||||||
Db      1053 GACACACAGGATTTATAAGAGTACACAGTGGAGTGTGAGGAGCGCATGCTGCCCTCT 994

OY      203  AlaGlnGlnSerLeuProIleGlnValValAlaValAspAlaIleHisLysLeuLysTrpGlu 222
      |||||||
Db      993 GCGGAGAGAGCCCTACCCATCGAGTGTGGTGGATCTATTCACAAAGCTCAAGTATAGAA 934

OY      223  AsnTrpThrSerSerPhePheIleArgAspIleIleLysProAspProPheThrAsnLeu 242
      |||||||
Db      933 AACTACACCGCAGAGCTTCTTCATCAGAGACATCATCAACCGACCGCCACCAACCTG 874

OY      243  GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTrpProAspThr 262
      |||||||
Db      873 CACCTGAAGCATTGAAATAATTCGCGACCTGAGCTGCAGCTGGAATACCCGACACCC 814

OY      263  TrpSerThrProHisSerTrpPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 282
      |||||||
Db      813 TGGAGCACCCACACTTCTCTACTTCTCCCTGACATTTTGCATACAGGCCCGCAGGGAAGAAC 754

OY      283  AsnArgGlnLysLysAspArgLeuCysValAspLysThrSerAlaLysValAlaCysHis 302
      |||||||
Db      753 AATAGAGAAAGAAAGATAGACTGTGCTGGCAAGACCTCAGCCAAAGTGTGTGCCAC 694

OY      303  LysAspAlaLysIleArgValGlnAlaArgAspArgTrpTrpSerSerSerTrpSerAsp 322
      |||||||
Db      693 AAGGATGCCAAGATCCCGTGCAGAGCCGAGACCGCTACTATGCTTCACTCGGAGCGCAC 634

OY      323  TrpAlaSerValSerCysSerGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 342
      |||||||
Db      633 TGGGCATCTGTGTATCTCAGTGGTGGGGTGGCGGCGGATCTAGAAACTTGGCCAAACCT 574

OY      343  ThrProSerProGlnMetPheGlnCysLeuAsnHisSerGlnThrLeuAlaArgAlaVal 362
      |||||||
Db      573 ACTTCATCCCGCGGTATGTTCCAAATGTTTGAACCACTGCCAAACCTTGTTGAGAGCGTCC 514

OY      363  SerAsnThrLeuGlnLysAlaArgGlnThrLeuGlnLeuTrpSerCysThrSerGluGln 382
      |||||||
Db      513 AGCAACAGCCTTCGAAAGGCCAGCAAACTCTAGAAATATATCTCTCCACTTCGAGAGAG 454

OY      383  IleAspHisGlnAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 402
      |||||||
Db      453 ATTTCATATGAAATATACAAAGATAAACACAGCAGCTGGAGGCGCTGTTACCATG 394

OY      403  GluLeuThrMetAsnGlnSerCysLeuAlaSerArgGluLysSerLeuIleThrAsnGly 422
      |||||||
Db      393 GAATTAACCATGAAATGAGAGTGGCTGCTGCCAGAGAGATCTTTCATTAACTAACGGG 334

OY      423  SerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeuCysLeuSerSerIleTrp 442
      |||||||
Db      333 AGTTGCTGGCTCTCGAAAGGCCCTTTTATGAGCGGCTGTGCTTACGAGCATGTAT 274
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OY      443  GluAspLeuLysMetTrpGlnMetGlnPheLysAlaMetAsnAlaLysLeuMetAsp 462
      |||||||
Db      273 GAGACATTTGAAGATGTACACAGATGGAAATTCAGGCCCATGAAGCGAAGCTTTAATGAT 214

OY      463  ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGlnLeuGln 482
      |||||||
Db      213 CCCAAGAGCGCAGATCTTTCTGGATCAAAACATGCTGCAGCTATGATGAGCTGTACAG 154

OY      483  AlaLeuAsnPheAsnSerValThrValProGlnLysSerSerLeuGlnGluProAspPhe 502
      |||||||
Db      153 GCCCTGAATTTCAACAGCTGTGACGTGTCCACAGAAATCTCCCTTGAAGACCGGATTTT 94

OY      503  TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 522
      |||||||
Db      93 TATTAACCTAAATCAAGCTGTGCATATCTTTCATATGCTTTGACAAATTCGTGGGTGACC 34

OY      523  IleAsnArgMetMetSerTrpLeuAsnSerSer 533
      |||||||
Db      33 ATCAATAGAAATGATGCTCTACTTGAACCTTCC 1

RESULT 5
US-09-917-265-38
: Sequence 38, Application US/09917265
: Patent No.: US20020052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
: FILE REFERENCE: IM-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: CURRENT FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: PRIOR FILING DATE: 2000-08-04
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 38
: LENGTH: 1599
: TYPE: DNA
: ORGANISM: Felis catus
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(1599)
: OTHER INFORMATION:
US-09-917-265-38

Alignment Scores:
Pred. No.: 6,51e-299 Length: 1599
Score: 2643.00 Matches: 501
Percent Similarity: 96.44% Conservative: 13
Best Local Similarity: 94.00% Mismatches: 19
Query Match: 94.26% Indels: 0
Dbs: 10 Gaps: 0

US-09-917-265-62 (1-533) x US-09-917-265-38 (1-1599)
OY      1  MethisProGlnGlnLeuValIleSerTrpPheSerLeuValLeuLeuAlaSerProLeu 20
      |||||||
Db      1  ATGCATCCTCAGCAGTGTGATGATGCGCTTTCCTCCGCTTGTGGCTGACCTCCCTC 60

OY      21  MetAlaIleTrpGlnLeuGlnLysAspValTrpValValGlnLeuAspTrpHisProAsp 40
      |||||||
Db      61 ATGGCATATGGGAAGTGGAGAAACGTTATATGTTAGAGTTGGAGCTGCACCCGAT 120

OY      41  AlaProGlyGluMetValValLeuThrCysHisThrProGlnGlnAspAspIleThrTrp 60
      |||||||
Db      121 GCCCGCGAGAAAGGCTGTCTCACCCTGCATATCTCTGTAAGAAATGACATGACCTCG 180

OY      61  ThrSerAlaGlnSerSerGluValLeuGlnLysSerGlyLysThrLeuThrIleGlnValLys 80
      |||||||
Db      181 ACCTGTGACCGACAGCAGTGAAGTCCTAAGCTGTGTAACCTGTGACCATGCAAGTCAA 240

OY      81  GluPheGlnAspAlaGlyGlnTrpThrcysHisLysGlyGlyLysValLeuSerArgSer 100
      |||||||
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| | | | | | | |
|---|---|--|------|-----|--|------|
| D | b | | 241 | GAA | TTCGAGATGCCTGGCCAGCATACCTCCTCATAAAGAGGCGAGGTCTGACCATTCG | 300 |
| O | y | | 101 | Leu | LeuLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGln | 120 |
| D | b | | 301 | TTC | CCTCGAATACAAAAAGGAAGATGGAATTGGTCCACTGATATCTTAAGGGAACAG | 360 |
| O | y | | 121 | Lys | GluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyIarPhe | 140 |
| D | b | | 361 | AAG | AATCCAAAATAATGATCTTTCTAAATGTGAGGCCAAAAGAATATCTGGACGTTTC | 420 |
| O | y | | 141 | Thr | CysTPRPLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArg | 160 |
| D | b | | 421 | ACG | TGCTGTGGCTACGGCAATACGTACCATTGGAATTCACCTGCTAAAAGCAGCGA | 480 |
| O | y | | 161 | Gly | PheSerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgVal | 180 |
| D | b | | 481 | GGC | TCTCTGACCCCCAGAGGTGACTTGTAGAGCAGCACACTCTCAGCAGAGAAGTTC | 540 |
| O | y | | 181 | Arg | ValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys | 200 |
| D | b | | 541 | AG | AGGAGCAACAGAGGATTATAGAACAGACAGAGGTGTCAAGAGCGCAGTCCGTC | 600 |
| O | y | | 201 | Pro | SerAlaGluGluSerLeuProIleGluValValAspAlaIleHisLysLeuLys | 220 |
| D | b | | 601 | CCG | GTGCGGAGAGAGCCCTACCATTAAGTCTGGTGGAGCGCTATTACAAGCTCAAG | 660 |
| O | y | | 221 | Tyr | GluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProThr | 240 |
| D | b | | 661 | TAC | GAANAACCTACACAGCAGCTTCTTCATCAGGCGACATCAACACCGCACCCCAAG | 720 |
| O | y | | 241 | Asn | LeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro | 260 |
| D | b | | 721 | AAC | CTGCACACGTGAACCACTTAAAAATTCCTGGCATGTGGAAAGTAGCTGGGAATACCT | 780 |
| O | y | | 261 | Asp | ThrTPSPSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnIly | 280 |
| D | b | | 781 | GAC | ACCTGACACCCCACATTCCTCCTACTTCCTTAACATTTGGCGTACAGTCCAGGCG | 840 |
| O | y | | 281 | Lys | AsnAsnArgGluLysLysAspArgLeuCysValAspLysTrpSerAlaLysValAl | 300 |
| D | b | | 841 | AAG | AACAACAAGAAAAAAGAACAGACACTCTCCGTCGACAGACCTCAGCCAAGTGTGTG | 900 |
| O | y | | 301 | Cys | HisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp | 320 |
| D | b | | 901 | TGC | CAACAAGATGCCAAMATCCGGCTGCMAACCCAGAGACCCCTACTAAGCTCATCCGG | 960 |
| O | y | | 321 | Ser | AspTRPALaservalSerCysSerGlyGlyGlyGlyGlySerArgAsnLeuPro | 340 |
| D | b | | 961 | AGC | AACGTGGCATCCGTCTCTCGCAGTGTGTGGCGTGGCGCGGATCTAGAAACTTGCCA | 1020 |
| O | y | | 341 | Thr | ProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArg | 360 |
| D | b | | 1021 | ACC | CTACTCATCCGCCGGGATGTTCCAGTGCCTCAACCACTCCCAAACCTCGTGCGA | 1080 |
| O | y | | 361 | Ala | ValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGlnLeuTyrSerCysThrSer | 380 |
| D | b | | 1081 | GCC | AATCACCAACACGCTTCAGAAAGCCAGCAAACTCAGAAATTTACTCTCGCACTTCC | 1140 |
| O | y | | 381 | Glu | GluIleAspHisGluAspIleThrLysAspLysTrpSerTrpValGluAlaCysLeu | 400 |
| D | b | | 1141 | GAC | AGATGTGATCATCAGATATATCACAAAATATAAACACACACAGTGGAGCGCTGCTTA | 1200 |
| O | y | | 401 | Pro | LeuGlnLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThr | 420 |
| D | b | | 1201 | CC | ACTGGAAATTAACCATGAATGAGAGTGGCTTGCTTCCAAAGAGATCTCTGATAACT | 1260 |
| O | y | | 421 | Asn | GlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeuCysLeuSerSer | 440 |
| D | b | | 1261 | AAT | GAGGATTCCTCGGCTCCAGAAAGACCTCTTTATAGACAGACCTGTGCTTAGCAGT | 1320 |
| O | y | | 441 | Ile | TyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsnAlaLysLeuLeu | 460 |
| D | b | | 1321 | ATC | TATGAGGACTTGAAGATGTACCAAGTGGAGTTCAAGGCGCATGAATGCAAACTGTTA | 1380 |

| | | | |
|--|------|--|------|
| OY | 461 | MetaspProLysArGgInIllePheLeuAspInsmLeuTrAlIleAspGluLeu | 480 |
| Db | 1381 | ATGATCTCTAAAAAGCAGATCTTTCTGGATCTAAACATGCTGCACAGCTATTGATGACCTG | 1440 |
| OY | 481 | LeuGlnAlaLeuAsnPheAsnSerValThrValProInLysSerSerLeuGluPro | 500 |
| Db | 1441 | TTACAGGCGCTGATGATGTCACAGTGTGACTGTGCCACAGAACTCTCTCTTGGAAGAACCG | 1500 |
| OY | 501 | AspPheTyrThrLysIleLeuLysCysIleLeuLeuHisAlaPheArgIleArgAla | 520 |
| Db | 1501 | GATTTTATATAAACTAAATCAACCTCGCATCTTTCTTCATCGCTTTTCAGAAATTCGTGCA | 1560 |
| OY | 521 | ValThrIleAsnArgMetSerTyrLeuAsnSerSer | 533 |
| Db | 1561 | GTGACCATCATATAGATATGAGCTACTCTGATCTCTCC | 1599 |
| RESULT 6 | | | |
| US-09-917-265-40/c | | | |
| ; Sequence 40, Application US/09917265 | | | |
| ; Patent No. US20020052030A1 | | | |
| ; GENERAL INFORMATION: | | | |
| ; APPLICANT: Wonderling, Ramani S. | | | |
| ; APPLICANT: Boroughs, Karen L. | | | |
| ; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH | | | |
| ; FILE REFERENCE: IM-5 | | | |
| ; CURRENT APPLICATION NUMBER: US/09/917, 265 | | | |
| ; PRIOR FILING DATE: 2001-07-27 | | | |
| ; PRIOR APPLICATION NUMBER: 60/223, 016 | | | |
| ; PRIOR FILING DATE: 2000-08-04 | | | |
| ; NUMBER OF SEQ. ID NOS: 109 | | | |
| ; SOFTWARE: PatentIn version 3.1 | | | |
| ; SEQ. ID NO. 40 | | | |
| ; LENGTH: 1599 | | | |
| ; TYPE: DNA | | | |
| ; ORGANISM: Felis catus | | | |
| US-09-917-265-40 | | | |
| Alignment Scores: | | | |
| Pred. No.: 6,51e-299 Length: 1599 | | | |
| Score: 2643.00 Matches: 501 | | | |
| Percent Similarity: 96.44% Conservative: 13 | | | |
| Best Local Similarity: 94.00% Mismatches: 19 | | | |
| Query Match: 94.26% Indels: 0 | | | |
| DB: 10 Gaps: 0 | | | |
| US-09-917-265-62 (1-533) x US-09-917-265-40 (1-1599) | | | |
| OY | 1 | MetHisProGInGluLeuValIleSerTyrPheSerLeuValLeuLeuAlaSerProLeu | 20 |
| Db | 1599 | ATGCATCCTCAGCAGTGTGTCATCGCTCGGCTTCCCTGGTTTGGCGCACCTCCCTC | 1540 |
| OY | 21 | MetAlaIleTrrpGluLeuGluLysAspValTyrValAlaGluLeuAspTrrpHisProAsp | 40 |
| Db | 1539 | ATGGCCATATGGGAACGAGAAAAACGTTATGTTTAAAGTTGGAGCTGGACACCTGAT | 1480 |
| OY | 41 | AlaProGlyGluMetValIleLeuThrCysHisThrProGluGluAspAspIleThrTrrp | 60 |
| Db | 1479 | GCCCCCGAGAAATGGTGGTCTCTCACCCTGCATATCTCTGAAGAAGATGACATCACCCTG | 1420 |
| OY | 61 | ThrSerAlaGlnSerSerGluValLeuGlySerCylsTyrThrLeuThrIleGlnValLys | 80 |
| Db | 1419 | ACCTCTGACCGACGACGTAAGTCCCTFAGGCTCTGTGTAACACTCGACACATCCAAATCAAA | 1360 |
| OY | 81 | GluPheGlyAspAlaGlyGlnTyrThrCysHisLysGlyGlyLysValIleLeuSerArgSer | 100 |
| Db | 1359 | GAAATTTTCAGATGCTGGCCAGTATACCTGTGCATAAAGACGCGAGTTCGTGACCATATCG | 1300 |
| OY | 101 | LeuLeuLeuLeuIleHisLysLysGluAspGlyIleTrrpSerThrAspIleLeuLysGluGln | 120 |
| Db | 1299 | TTCTCTCTGATACCAAAAAGAGATGGATTTGGTCCACTGATATCTTAAAGGAACAG | 1240 |
| OY | 121 | LysGluSerLysAsnLysIlePheLeuLysCysGlnAlaLysAsnTyrSerGlyArgPhe | 140 |

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Db      1239 AAGAAATCCAAAAATAAGATCTTTCTAAATGTGAGGCAAGAAATTATTGTGACGTTTC 1180
Qy      141  ThcYstrpTrpleuThrAlaIleSerThrspleuLysPheSerValLysSerArg 160
Db      1179 ACCGCTGGTGGCTGGACGGCAATCAGTACCGATTGTGAATTCACGTCTCAAGAAAGCAGCA 1120
Qy      161  GlyPheSerAspProGlnGlyValThrcysGlyAlaValThrLeuSerAlaGluArgVal 180
Db      1119 GGCCTCCTGTACCCCCCAAGAGGTACTTGTGGACGAGGACACTCTCGCAGAGAGGTC 1060
Qy      181  ArgValAspAsnArgAspTyrLysLysTyrThrValGluGlyGlnGluLysSerAlaCys 200
Db      1059 AGAGTGGACAACAGAGATTATTAAGAGTACACAGCTGAGGTGTCCAGAGCGCAGTGGCTGC 1000
Qy      201  ProSerLagluGluSerLeuProLleGluValValValAspAlaIleHisLysLeuLys 220
Db      999  CCGGCTCCGAGGAGACCTTACCATTTGACGTGCTGCGACGCTATTCCACAACTCAG 940
Qy      221  TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProThr 240
Db      939  TACGAAACTACACACAGAGCTTCTTCATCGAGGACATCATCAACCGACGCCACCCAG 880
Qy      241  AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTyrGluTyrPro 260
Db      879  AACCTGCACACTGAAGCCATTAAAAAATTCTCGCATGTGCAAGTGTGGAATACCT 820
Qy      261  AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGly 280
Db      819  GACACCTGGAGACACCCACATCTCTACTCTCTCTTAACTTTGGCCAGACAGTCCAGG 760
Qy      281  LysAsnAsnArgGluLysLysAspArgLeuGlyValAspLysTrpSerAlaLysValVal 300
Db      759  AAGACACACAGAGAAAAAGAACAGACTCTCCCTGGACAGACACTCAGCCAAAGTCTG 700
Qy      301  CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTrpSerSerTrp 320
Db      699  TGGCACAAGATGCCAGATCCCGGTCAACCCAGACACCCCTACTATAGCTCATCTGG 640
Qy      321  SerAspTrpAlaSerValSerCysSerGlyGlyGlyGlyGlySerArgAsnLeuPro 340
Db      639  AGCACTGGGCTATCCGTCTCTGCAAGTGGCGGTGGCGGAGTCTAGAAACTTGCCA 580
Qy      341  ThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArg 360
Db      579  ACCGCTACTCCATCCCGGGGATGTTCAGTGCCTCAACCACTCCCAAACTCTCTGCGA 520
Qy      361  AlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGlnLeuTyrSerCysThrSer 380
Db      519  GCCATCAGCAACACGCTTCAAGAAAGCCAGACAACTCTAGAAATTTACTCTCGCACTCC 460
Qy      381  GluGlnIleAspHisGluAspIleThrLysAspLysTrpSerThrValGluAlaCysLeu 400
Db      459  GAAGAGATTGATCATGATGATATTCACAAAGATTAACACAGACAGTGGAGCGCTGCTTA 400
Qy      401  ProLeuGlnLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThr 420
Db      399  CCACTGGAATTAAACCATGAGATGAGAGTTGCCCTGGCTTCCAGAGAGATCTCTGATTA 340
Qy      421  AsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeuCysLeuSerSer 440
Db      339  AATGGAGTTGCTCGGCTCCAGAAAGACCTCTTTTATGACGACCTGTGCTTAGAGAGT 280
Qy      441  IleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsnAlaLysLeuLeu 460
Db      279  ATCTATGAGGACTTGAAGATGTACCCAGTGTGAGTTCAGGCGCAATGCAAAACCTGTTA 220
Qy      461  MetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGlnLeu 480
Db      219  ATGATGCTTAAAGGCGAGATCTTCTGTGATCAAAACATGCTGACAGCTATTGATGACTG 160
Qy      481  LeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSerLeuGluPro 500

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Db      159  TTACAGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCTGGAAGAACCG 100
Qy      501  AspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAla 520
Db      99  GATTTTATAAACTAAATCAATCACTGCTGCTACTTCTTCATGCTTTCAGAAATTCGTCA 40
Qy      521  ValThrIleAsnArgMetSerTyrLeuAsnSerSer 533
Db      39  GTGACCATCATATAGATGATGAGCTATCTGATGATGCTTCC 1

RESULT 7
US-09-917-265-43
: Sequence 43, Application US/09917265
: Patent No. US20020052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: APPLICANT: Boroughs, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
: FILE REFERENCE: IM-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: PRIOR FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 43
: LENGTH: 1533
: TYPE: DNA
: ORGANISM: Felis catus
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(1533)
: OTHER INFORMATION:
US-09-917-265-43

Alignment Scores:
Pred. No.: 1,37e-287 Length: 1533
Score: 2546.00 Matches: 482
Percent Similarity: 96.67% Conservative: 12
Best Local Similarity: 94.32% Mismatches: 17
Query Match: 90.80% Indels: 0
Gaps: 0
DB: 10

US-09-917-265-62 (1-533) x US-09-917-265-43 (1-1533)
Qy      23  IleTrpGluLeuGluLysAspValTyrValAlaLeuAspTrpHisProAspAlaPro 42
Db      1  ATATGGAACTCGAGAAAAACGTTTATGTTGTAGAGTTGCACTGGACCCCTGATGCCCC 60
Qy      43  GlyIleuValValIleuThrCysHisThrProGluGluAspArgIleThrTrpThrSer 62
Db      61  GGAGAAATGGTGGCTCTCCTGCAATCTCTGAAGAAAGTGAATCACTGACCTGACCTCT 120
Qy      63  AlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
Db      121  GACCAAGAGAGTGAAGTCCAGCTCTGTAAACTCTGACCAATCCAAAGTCAAGAAATTT 180
Qy      83  GlyAspAlaGlyGlnTyrThrCysHisLysGlyGlyLysValLeuSerArgSerLeuLeu 102
Db      181  GCAATGCTGCGCAGTATACCTGCAATAAAGAGGAGGAGGTTTCGAGCCATTCTGCTCTC 240
Qy      103  LeuIleHisLysLysGluAspGlyTleTrpSerThrAspIleLeuLysGluGlnLysGlu 122
Db      241  CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
Qy      123  SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
Db      301  TCCAAAAATTAAGATCTTCTTAATAATGAGAGCAAAAGATTAATCTGAGCGTTTCACCTGC 360
Qy      143  TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 162
Db      361  TGTGTCTGACGGCAATCACTACGATTTGAATTCACGTCTCAAAACACAGAGGCTCC 420

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QY 163 SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgVal 182
DB 421 TCTGACCCCAAGAGGTGACTTGTGGAGCAGCCACTCTCAGCAGAAAGGTCAAGTGG 480
QY 183 AspAsnArgAspTyrIleLysIleValGluCysGlnGluGlySerAlaCysProSer 202
DB 481 GACAAACAGGAGATTATTAAGAGATACACAGTGGAGTCCAGAGAGGCGTCCGCCGCT 540
QY 203 AlaGluGluSerLeuProIleGluValAlaValAlaSerAlaIleHisIleLysIleValGlu 222
DB 541 GCCGAGGAGACGCTACCCATTGACAGTGGTGGAGCCATTTCACAAAGCTCAAGTACGAA 600
QY 223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProthrasLeu 242
DB 601 AACTACACGACGAGCTTCTTCATCAGGACATCATCAAAACCGGACCCACCAAGAACCTGG 660
QY 243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTyrProLysProAspThr 262
DB 661 CAACGTGAACCATTAATAAAATCTCGCATGTGGAGTGAAGTGAAGTGAAGTGAAGTGAAGT 720
QY 263 TrpSerThrProHisSerTyrPheSerLeuThrPheCysAlaIleGlnIleGlnLysAsn 282
DB 721 TGGAGACACCCCACTTCTTACTTCTTCTTAACTTTGGCGTACAGGTCCAGGCGCAAGAAC 780
QY 283 AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValValCysHis 302
DB 781 AACAGAGAAAGAAAGACAGACTCTCCGGAGCAAGACCTCAGCCAAAGGCGTGGCCAC 840
QY 303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTyrProAsp 322
DB 841 AAGGATGCCAAGATCCGCTGCAAGCAGACAGCCGCTACTTAAAGTCAATCCGAGACAC 900
QY 323 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 342
DB 901 TGGCGATCCGCTGCTCCAGTGGTGGCGGGGGGAGCTTGAAGAACTTGGCAACCCCT 960
QY 343 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaVal 362
DB 961 ACTCCATCCCGGGGGAGTGTCCAGTCCCAACCACTCCCAAAACCTGGCGCAGCAGCATC 1020
QY 363 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyrSerCysThrSerGluGlu 382
DB 1021 AGCAACAGCCTTCAGAGGCGCAGACAACTCTAGAAATTTTACTCTCCGACCTTCGAGAG 1080
QY 383 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 402
DB 1081 ATTGATCATGAAGATATCAACAAAGATTAACACAGACAGTGGAGGCGCTGTACACATG 1140
QY 403 GlnLeuThrMetAsnGluSerCysLeuAlaSerArgGluLeuSerLeuIleThrAsnGly 422
DB 1141 GAATTTAACCATGATAGAGTTGCTGGCTCCAGAGAGATCTCTGTGATTAATGGG 1200
QY 423 SerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeuCysLeuSerSerIleTyr 442
DB 1201 AGTTGGCTGGCTCCGAAAGAACCTCTTTATACACACCTGTGGCTTACAGATATCTAT 1260
QY 443 GlnAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 462
DB 1261 GAGGACTGTGAAGTATGACAGGTGTGAGTTCAGAGCCATGAAATCAAAAGCTGTTAATGAT 1320
QY 463 ProLysArgGlnIlePheLeuAsnGlnAsnMetLeuThrAlaIleAspGluLeuGln 482
DB 1321 CCTAAAGAGCAGATCTTTCTGGATCAAAACATGCTACAGCTATGATGAGCTGTATACAG 1380
QY 483 AlaLeuAsnPheAsnSerValThrValProGlnLysSerSerLeuGluLysProAspPhe 502
DB 1381 GCCCTAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCTGGAAGAACCGGATTTT 1440
QY 503 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 522
DB 1441 TATTAACATCAAAATCAAGCTGTGCATCTTCTTCATGAGTTCGAGATTCGTGAGTGAAC 1500
QY 523 IleAsnArgMetSerTyrLeuAsnSerSer 533

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DB 1501 ATCAATAGATGATGAGTATCTGAATGCTTCC 1533
RESULT 8
US-09-917-265-45/c
; Sequence 45, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917, 265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223, 016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265-45
Alignment Scores:
Pred. No.: 1,37e-287 Length: 1533
Score: 2546.00 Matches: 482
Percent Similarity: 96.67% Conservative: 12
Best Local Similarity: 94.32% Mismatches: 17
Query Match: 90.80% Indels: 0
Gaps: 0
DB:
US-09-917-265-62 (1-533) x US-09-917-265-45 (1-1533)
QY 23 IletPrGlnLeuGlnLysAspValTyrValAlaGluLeuAspTrpHisProAspAlaPro 42
DB 1533 ATATGGGAACCTGAGAGAAACCTTATGTGTGAGATTGAGCTGGACCCCTGATGGCCCC 1474
QY 43 GlyLMetValValLeuThrCysHisThrProGluGluAspAspIleThrTrpThrSer 62
DB 1473 GGAAGAAATGGTGCTCTCACTGCAATFACTCTGGAAGAGATGACATCACTGAGACTCT 1414
QY 63 AlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
DB 1413 GACCAAGAGAGAGAACTCTAGGCTGTGTAATAACTCAGCATCCAACTCAAGAAATTT 1354
QY 83 GlyAspAlaGlyGlnTyrThrCysHisLysGlyLysValLeuSerArgSerLeuLeu 102
DB 1353 GCAGATGCTGGCCAGATATACCTGTCTATAAGAGAGCGAGGCTTGTGACCATTCGTTCTC 1294
QY 103 LeuIleHisLysGluAspGlyIleTyrSerThrAspIleLeuLysGluGlnLysGlu 122
DB 1293 CTGATACACAAAGAGAAATGGAATTTGGTCCACATGATCTTAAGGGAACAGAAAGAA 1234
QY 123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
DB 1233 TCCAAAAATPAAGATCTTTTAAATGTGAGCCAAATAATTAATTCGAGCTTCACTGC 1174
QY 143 TrpTrpLeuThrAlaIleSerThrAspLysLysPheSerValLysSerSerArgLysPhe 162
DB 1173 TGGTGGCTAGCGCAATCACTGATCCGATTTGAAATTTACTGTCAAAAGACGAGAGGCTCC 1114
QY 163 SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgVal 182
DB 1113 TCTGACCCCAAGAGGTGACTTGTGGAGCAGCCACTCTCAGCAGAAAGGTCAAGTGG 1054
QY 183 AspAsnArgAspTyrIleLysIleValGluCysGlnGluGlySerAlaCysProSer 202
DB 1053 GACAAACAGGAGATTATTAAGAGATACACAGTGGAGTCCAGAGAGGCGAGTCCGCCGCT 994
QY 203 AlaGluGluSerLeuProIleGluValAlaValAlaSerAlaIleHisIleLysIleValGlu 222
DB 993 GCCGAGGAGAGCCTTACCCATTGAAGTGGTGGAGCGCTATTACAAAGCTCAAGTACGAA 934

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Qy 1223 AsnYrThrSerSerPhePheIleArgAspIleIleLeuYsProAspProThrAsnLeu 242
Db 933 AACACACACGACGACCTTCTTCATCAGGACATCATCAACCGGACCCACCAACACTG 874
Qy 243 GluLeuYsProLeuYsAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
Db 873 CAACCTGAAGCCATTAATAAATTTCTCGCATGTGGAAGTGAAGCTGGGAATACCCGACACC 814
Qy 263 TrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLeuAsn 282
Db 813 TGGAGCACCCACACATTCCTACTCTCTTAAACATTTGGCGGACAGGTCAGGGAACAAC 754
Qy 283 AsnArgGluYsLysValSAspArgLeuCysValAspLysThrSerAlaLysValCysHis 302
Db 753 AACGAGAAAAAAGAAAGACAGACTCCCTCGACAAAGACCTCAGCAAGTGTGTGCCAC 694
Qy 303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTrpSerSerTrpSerAsp 322
Db 693 AAGGATGCCAAGATCCCGCTCCAGCCAGACCGCTACTATACCTCATCTCGAGCAAC 634
Qy 323 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 342
Db 633 TGGGACATCCGTCCTCAGTGTGGCGGTGGCGGATCTTAAACACTTGCACACCCCT 574
Qy 343 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuArgAlaVal 362
Db 573 ACTGCATCCCGGGGATGTCCTCAAGTGCCTCACCACCTCCCAACCCCTGCGAGCCATC 514
Qy 363 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyrSerCysThrSerCylu 382
Db 513 AGCAACACGCTTCAGAGGCGACAGCAAACTAGAAATTTACTCTCTGACACTTCGGAAGAG 454
Qy 383 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 402
Db 453 ATTGATATGAGATATACACAAAGATPAAACACAGACAGTGAAGGCTGCTTACCATG 394
Qy 403 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluLeuSerLeuIleThrAsnGly 422
Db 393 GAATTAAACCATGATGAGAGTGGCTGCTGCTCCAGAGAGATCTCTGCATACCTAATGG 334
Qy 423 SerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeuCysLeuSerSerIleTyr 442
Db 333 AGTTGCCCTGGCTCACAAGAACCTCTTTTATGACGACCCGTCCCTTAGCAGATCTAT 274
Qy 443 GluAspLeuYsMetTyrGlnMetGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 462
Db 273 GAGGACTTGAAGATGTACCAAGGTGAGTTCAGGCCATGATGCAAAAGCTGTTAATGAT 214
Qy 463 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuGln 482
Db 213 CCTAAAGCGCATCTTCTGATCAAAACATGCTGACAGCTATTGATGAGACTGTACAG 154
Qy 483 AlaLeuAsnPheAsnSerValThrValProGlnYsSerSerLeuGlnGluProAspPhe 502
Db 153 GCCCTGAATGTCAACACTGTGACTGTGCCAGAGAATCTCTTGGAAAGACCCGATTTT 94
Qy 503 TyrTrpThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 522
Db 93 TATTAACCTAAATCAAGCTCTGCATACCTCTTCATGCTTTCAAGATTGCGAGTGACC 34
Qy 523 IleAsnArgMetSerTyrLeuAsnSerSer 533
Db 33 ATCAATAGAAATGATGACTATCTGAATGCTTCC 1

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RESULT 9

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: Sequence 7, Application US/09828825
: Patent No. US20020018767A1
: GENERAL INFORMATION:
: APPLICANT: Lee, Seewoo
: APPLICANT: Kim, Han-soo
: TITLE OF INVENTION: Anti-cancer Cellular Vaccine

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: FILE REFERENCE: 84906-102
: CURRENT APPLICATION NUMBER: US/09/828, 825
: CURRENT FILING DATE: 2001-04-10
: PRIOR APPLICATION NUMBER: KR00-43498
: PRIOR FILING DATE: 2000-07-27
: NUMBER OF SEQ ID NOS: 16
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 7
: LENGTH: 8608
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: plasmid
: NAME/KEY: misc.feature
: LOCATION: (1)..(750)
: OTHER INFORMATION: CMV enhancer and promoter
: NAME/KEY: misc.feature
: LOCATION: (890)..(1002)
: OTHER INFORMATION: Intervening sequence
: NAME/KEY: promoter
: LOCATION: (1067)..(1085)
: OTHER INFORMATION: 77 RNA polymerase promoter
: NAME/KEY: misc.feature
: LOCATION: (1090)..(1984)
: OTHER INFORMATION: Human B7.1 (1090-1956 is coding sequence)
: NAME/KEY: RBS
: LOCATION: (2013)..(2593)
: OTHER INFORMATION: IRES sequence
: NAME/KEY: misc.feature
: LOCATION: (2627)..(4263)
: OTHER INFORMATION: Human IL12.2 sequence (2460-4253 is coding
: OTHER INFORMATION: sequence, 13 amino acid flexible linker at
: OTHER INFORMATION: 3606-3676)
: NAME/KEY: CDS
: LOCATION: (2640)..(4253)
: OTHER INFORMATION: IL12.2 coding sequence (13 amino acid linker)
: NAME/KEY: promoter
: LOCATION: (4362)..(4383)
: OTHER INFORMATION: T3 RNA Polymerase promoter
: NAME/KEY: polyA_signal
: LOCATION: (4393)..(4614)
: OTHER INFORMATION: SV40 fragment containing polyadenylation signal
: NAME/KEY: rep_origin
: LOCATION: (4709)..(5164)
: OTHER INFORMATION: fl origin of replication
: NAME/KEY: misc.feature
: LOCATION: (5228)..(6595)
: OTHER INFORMATION: Neo r expression cassette
: NAME/KEY: misc.feature
: LOCATION: (7006)..(7866)
: OTHER INFORMATION: Ampicillin resistance
: US-09-828-825-7

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Alignment Scores:

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Pred. No.: 2,27e-268 Length: 8608
Score: 2392.00 Matches: 456
Percent Similarity: 90.47% Conservative: 28
Best Local Similarity: 85.23% Mismatches: 45
Query Match: 85.31% Indels: 6
DB: 10 Gaps: 3

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US-09-917-265-62 (1-533) x US-09-828-825-7 (1-8608)

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Qy 4 GlnGluLeuValIleSerTrpPheSerLeuValLeuLeuAlaSerProLeuMetAlaIle 23
Db 2649 CAGCAGTTGGTCATCTCTGTTTCCCTGATTTTCTTGGCATGTCCCTGTGCGCATTA 2708
Qy 24 TrpGluLeuGluLysAspValTyrValValGluLeuAspTrpHisProAspAlaProGly 43
Db 2709 TGGGACATGAGAAAGATGTTATCTGCTACAAATTGATGATGCGGATGCCCTTGA 2768
Qy 44 GluMetValIleLeuThrCysHisThrProGluLysAspIleThrTrpThrSerAla 63

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Db 2769 GAAATGGTGGTCTCACCCTGTGACACCCCTGAAGAAGATGATACCTCGACCTTGAC 2828
QY 64 GlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPheGly 83
Db 2829 CAGAGCAGTGGAGTCTTAGGCTCTGGCAAAACCTTACCATCCAAATGCAAGAGTTTGA 2888
QY 84 AspaIaGlyGlnThrCysHisLysGlyLysValLeuSerArgSerLeuLeu 103
Db 2889 GATGCGCCGACAGTACCTGTCCAAAGAGGCGAGGTCTTAAGCATTCGCTCGCTG 2948
QY 104 IleHisLysLysGluSpGlyIleTrpSerThrAspIleLeuLysGluGlnLysGluSer 123
Db 2949 CTTCACAAAAGAAAGATGGAATTTGGTCCACTGATTTTAAAGACCAAGAAAGACCC 3008
QY 124 LysAsnLysIlePheLeuLysCysGluAlaLysAsnTrpSerGlyArgPheThrCysTrp 143
Db 3009 AAAAATAAGACCTTTCTAGATTCGAGGCCAAGATATTATTCGAGCTTTCACCTCTG 3068
QY 144 TrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgLysPheSer 163
Db 3069 TGGCTGACGACATCAGTACTGATTGACATTCAGTGTCAAAAGCAGAGGCTCTTCT 3128
QY 164 AspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValAlaArgValAsp 183
Db 3129 GACCCCAAGGGGTGAGGTGGAGGCTGCTACACTCTCTGACAGAGAGTCAAGAGGGGAC 3188
QY 184 AsnArgAspTrpLysLysTrpThrValGluCysGlnGluLysSerLysLysProSerAla 203
Db 3189 AACAGAGAGTAT---GAGTACTCAGTGGAGTGGCAGAGAGAGAGAGTCCCTGCCAGCTGC 3245
QY 204 GluGluSerLeuProIleGluValValAlaAspAlaIleHisLysLeuLysTrpGluAsn 223
Db 3246 GAGGAGAGTGTGCCCTTGGAGTCATGAGTGAGTGCCTTCAAGCTCAAGTGTGAAGAAC 3305
QY 224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProProThrThrAsnLeuGln 243
Db 3306 TACACCAAGCAGCTTCTTATCATCAGAGCATCATCAAACTGACCCCAACCAACTTGCAG 3365
QY 244 LeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTrpProAspThrTrp 263
Db 3366 CTGAGCCCATTAAGAATTCTCGGAGTGAGTGCAGTGGAGTAGTACCTCGACACTGG 3425
QY 264 SerThrProHisSerLysTrpPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsnAsn 283
Db 3426 AGTACTCCAACTTCCACTTCTCCGACATTCGTGGTTCAGGTCACAGGCAAGACCAAC 3485
QY 284 ArgGluLysLysAspTrpLeuLysValAspLysThrSerAlaLysValLysHisLys 303
Db 3486 AGAGAAAGAGAGATAGAGTCTTACCGACAGACCACTCAGCCGATCATCTCCGCAAA 3545
QY 304 AspaIaLysIleArgValGlnAlaArgAspArgTrpTrpSerSerSerTrpSerAspTrp 323
Db 3546 AATGCCAGCATTAGCGGGGCCAGGACCGCTACTATAGTCAATCTTGAGCAGATGG 3605
QY 324 AlaSerValSerLysSerGlyGly-----GlyGlyLysLysSer-----ArgAsn 338
Db 3606 GCATCTGTGCGCCAGTGTGGCGGTGGAAGCGGTGGCGGTGAAGCCCATGAGAGAAC 3665
QY 339 LeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeu 358
Db 3666 CTCGCCGTGGCCACTCCAGACCAAGCATTTCCCATGCTTACACCACTCCCAAAACCTG 3725
QY 359 LeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTrpSerCys 378
Db 3726 CTGAGGGCGCTCAGCAACATGCTCCAGAGGCGCAGCAAACTCTAGAAATTTTACCTTGC 3785
QY 379 ThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAla 398
Db 3786 ACTTTCGAAGAGATTGATCATGGAAGATATCACAAAAGATAAACCAAGCAGAGGAGGCC 3845
QY 399 CysLeuProLeuGluLeuThrMetAsnGluSerCysLeuLysLysArgGluIleSerLeu 418
Db 3846 TGTTTACCATGGAATTAAACCAAGATGAGAGTTGCTTAAATTCCAGAGAGACTCTTTTC 3905

QY 419 IleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeuCysLeu 438
Db 3906 ATAACATAATGGAGTGTGCTGGCTCCAGAAAGACCTTTTATGATGGCCCTGAGCCTT 3965
QY 439 SerSerIleTrpGluAspLeuLysMetLysTrpGlnMetGluPheLysAlaMetAsnLys 458
Db 3966 AGTAGATATTATGAACACTTGAAGATGTCCAGGTCGAGTTCATAAGCCTGATGATCAAG 4025
QY 459 LeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAsp 478
Db 4026 CTTCGTATGATCCTTAGAGGCGAGATCTTCTTAGATCAAAACATGCTGGCAATTGTAT 4085
QY 479 GluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSerLeuGlu 498
Db 4086 GAGCTGATGACAGCCCTGATTTCAACAGTGAAGACTGTCCACAAAATCCTCCCTGAA 4145
QY 499 GluProAspPheTrpLysThrLysIleLysLysCysIleLeuLeuHisAlaPheArgLys 518
Db 4146 GAACCGGATTTTATATAAACTAAATCAAGCTGTGCATCTTCTCATGCTTTCAAGAAAT 4205
QY 519 ArgAlaValThrIleAsnArgMetMetSerTrpLeuAsnSerSer 533
Db 4206 CGGCGATGACTATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4250

RESULT 10
US-09-828-825-15
Sequence 15, Application US/09828825
Patent No. US20020018767A1
GENERAL INFORMATION:
APPLICANT: Lee, Seewoo
APPLICANT: Kim, Han-soo
TITLE OF INVENTION: Anti-cancer Cellular Vaccine
FILE REFERENCE: 84906-102
CURRENT APPLICATION NUMBER: US/09/828,825
CURRENT FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: KR00-43498
PRIOR FILING DATE: 2000-07-27
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 8629
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: plasmid
NAME/KEY: misc.feature
LOCATION: (1)-(750)
OTHER INFORMATION: CMV enhancer and promoter
NAME/KEY: promoter
LOCATION: (1067)-(1085)
OTHER INFORMATION: T7 RNA polymerase promoter
NAME/KEY: misc.feature
LOCATION: (1090)-(2726)
OTHER INFORMATION: Human IL12.2 (coding sequence is 1103-2716, 10 amino acid linker at 2087-2116)
NAME/KEY: CDS
LOCATION: (1103)-(2716)
OTHER INFORMATION: Human IL12.2 (10 amino acid linker)
NAME/KEY: RBS
LOCATION: (2752)-(3332)
OTHER INFORMATION: IRES sequence
NAME/KEY: misc.feature
LOCATION: (3369)-(4263)
OTHER INFORMATION: Human B7.1 sequence
NAME/KEY: promoter
LOCATION: (4383)-(4404)
OTHER INFORMATION: T3 RNA Polymerase promoter
NAME/KEY: polyA_signal
LOCATION: (4414)-(4635)
OTHER INFORMATION: SV40 fragment containing polyadenylation signal
NAME/KEY: rep_origin
LOCATION: (4730)-(5185)

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; OTHER INFORMATION: fl origin of replication
; NAME/KEY: misc_feature
; LOCATION: (5249)..(6616)
; OTHER INFORMATION: Neo r expression cassette
; NAME/KEY: misc_feature
; LOCATION: (7027)..(7887)
; OTHER INFORMATION: Ampicillin resistance gene
US-09-828-825-15

Alignment Scores:
Pred. No.: 2,28e-268 Length: 8629
Score: 2392.00 Matches: 456
Percent Similarity: 90.47% Conservative: 28
Best Local Similarity: 85.23% Mismatches: 45
Query Match: 85.31% Indels: 6
DB: 10 Gaps: 3

US-09-917-265-62 (1-533) x US-09-828-825-15 (1-8629)

QY 4 GlnGlnLeuValIleSerTrpPheSerLeuValLeuAlaSerProLeuMetAlaIle 23
DB 1112 CAGCAGTGGTCATCTCTGGTTTCCCTGGTTTTCGGCATCTCCCTCGTGGCATA 1171
QY 24 TrpGluLeuGluYsAspValTyrValValGluLeuAspTrpPheSerProAlaProGly 43
DB 1172 TGGGCACTGAAGAAAGATGTTATGTCCTAGAAATGATGTTATGTCGATGCCATGCCCTGGA 1231
QY 44 GluMetValIleLeuThrCysHisSerProGluGluAspAspIleThrTrpPheSerAla 63
DB 1232 GAATGTGGTCTCCTACCTGTACACCCCTGAAGAGATGATGATCCTGGACCTTGGAC 1291
QY 64 GlnSerSerGluValLeuGlySerGlyLeuThrLeuThrIleGlnValIleGlySerPheGly 83
DB 1292 CAGAGCACTGAGGCTTACGCTCGGCAAAACCTGCAGCATCCAGTCAAGACGTTTGA 1351
QY 84 AspAlaGlyGlnTyrThrCysHisGlyGlyLeuValLeuSerArgSerLeuLeu 103
DB 1352 GATGCTGGCCAGTACACCTGTACACAAAGAGCGAGTTCAGCATTCGCTCGCTG 1411
QY 104 IleHisGlyGlyGluAspGlyIleThrSerThrAspIleLeuGlyGlnGlnLeuSer 123
DB 1412 CTTGACAAAGAGAGATGAGATTTGGTCCACTGATATTATTAAGACGACCAAAACCC 1471
QY 124 LysAsnLysIlePheLeuLysCysGluValLysAsnTyrSerGlyArgPheThrCysTrp 143
DB 1472 AAAAATAAGACCTTCTTAAGATGCGAGGCCAAAGATTATTTCTGACGTTTACCTCGCTG 1531
QY 144 TrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPheSer 163
DB 1532 TGGCTGACGACAACTACGATGATTGACATTTCAGTTCAAAGACGACGAGGCTCTTCT 1591
QY 164 AspProGlnIleValIleThrCysGlyAlaValIleThrLeuSerAlaGluArgValAlaAsp 183
DB 1592 GACCCCAAGGGGAGCGTGGAGCGTGTACACTCTCTGAGAGAGAGTGAAGAGGGGAC 1651
QY 184 AsnArgAspTyrLysTyrThrValGluCysGlnGlnGlySerAlaCysProSerAla 203
DB 1652 AACCAAGAGAT--GAGTACTCAAGTGAAGGCCAGGAGACAGTGCCTGCCACACTGCT 1708
QY 204 GluGluSerLeuProIleGluValValAlaAlaIleHisLysLeuLysTyrGluAsn 223
DB 1709 GAGGAGAGTGTGCCATTGAGAGTCAATGATGATGCCCTTCAAGCTCAAGTATGAAGAAC 1768
QY 224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProPheThrAsnLeuGln 243
DB 1769 TACACCGACGACCTTCTTATAGGAGCATCATCAAACTGACCCACCAACAACTTTGAG 1828
QY 244 LeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThrTrp 263
DB 1829 CTGAAGCCATTAAAGAAATCTCGCGAGGTGAGAGTCACTGGAGTACCTGACACACCTGG 1888
QY 264 SerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsnAsn 283
DB 1888 SerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsnAsn 283
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DB 1889 ACTACTCCACATTCCTACTTCCCTGCATTCCTGCATTCGCTGACGTCAGGCAAGACAAG 1948
QY 284 ArgGluLysAspArgLeuGluValAspLysTrpSerAlaIleValValCysHisLys 303
DB 1949 AGAGAAAGAAAGATAGAGTCTTCCACGACCAAGACCTGACCGCATCTGCGCGCAA 2008
QY 304 AspAlaLysIleArgValGlnAlaArgAspArgTyrTrpSerSerSerTrpSerAspTrp 323
DB 2009 AATGCCAGCATTAAGCTGCGGGGCCAGGACCGCTCTATAGTCAATCTTTGAGACCAATGG 2068
QY 324 AlaSerValSerCysSerGlyIle-----GlyGlyGlyGlySer-----ArgAsn 338
DB 2069 GCATCTGAGCCCTGCATGAGTGGTGGGAGAACCGTGGCGGCGGAACCCATGAGAAAC 2128
QY 339 LeuProThrProThrProSerProGluMetPheGlnCysLeuAsnHisSerGlnThrLeu 358
DB 2129 CTCGCCGTGGCCACGACAGCCAGAGATGTTCCATGCTCTTCACTCCACCAAACTGTG 2188
QY 359 LeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuThrSerCys 378
DB 2189 CTGAGGCGCCGTGACAGACATGCTCCAGAAAGCGACAGACAACTGTGAATTTTACCCCTGC 2248
QY 379 ThrSerGluGluIleAspHisGlnAspIleThrLysAspLysThrSerThrValGluAla 398
DB 2249 ACTTCTGAAGATTCATCATGAAATATCATCAAAAGATTAACCAAGCAGACAGTGGAGGCC 2308
QY 399 CysLeuProLeuGluLeuThrMetLysGlnSerCysLeuAlaSerArgGluIleSerLeu 418
DB 2309 TGTTTACATTTGAATTAACCAAGATAGAGATGCTCAATTCACAGAGACCTCTTTC 2368
QY 419 IleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeuCysLeu 438
DB 2369 ATAATTAATGGAGATGGCTGCTGGCCCTCCAGAAAGACCTTTTATATATGCGCTGCTT 2428
QY 439 SerSerIleTyrGluAspLeuLysMetLysGlnMetGluPheLysAlaMetAsnAlaLys 458
DB 2429 AGTAGTATTATTAAGACCTTAAGATGATACCAAGGAGGTTCACAGACCATGATGCAAG 2488
QY 459 LeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAsp 478
DB 2489 CTTCTGATGAGATCCTTAAGAGCGAGATCTTCTAGTCAAAACATGCTGCGATTAATGAT 2548
QY 479 GluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSerLeuGln 498
DB 2549 GAGCGATGACAGCGCCCTGAATTTTCAACAGTGAAGATGTGGCCACAAATTCCTCCTTAA 2608
QY 499 GluProAspPheTyrLysThrLysIleLysLeuGlyIleLeuLeuHisAlaPheArgIle 518
DB 2609 GAACCGGATTTTATTAATAAATAAATCAAGCTCTGCATAGTCTTCATGCTTTCAGAAAT 2668
QY 519 ArgAlaValThrIleAsnArgMetLysSerTyrLeuAsnSerSer 533
DB 2669 CGGCGAGTCACTATTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2713

RESULT 11
US-09-828-825-5
; Sequence 5, Application us/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Han-soo
; APPLICANT: Kim, Seewoo
; TITLE OF INVENTION: Anti-cancer Cellular Vaccine
; FILE REFERENCE: 84906-102
; CURRENT APPLICATION NUMBER: US/09/828, 825
; CURRENT FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: KR00-43498
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 8623
; TYPE: DNA
; ORGANISM: Artificial Sequence
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Db 2069 GCATCTGTGCGCCCTGACGTGTGGGGGTGGAACCGGTGGAGCGGTGGAACGGGTGGGGGTGGA 2138
QY 336 Ser-----ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsn 353
Db 2129 AGCCCATGGAGAAACCTCCCGTGGCCACTCCACAGACCAGAAATGTTCCCATGGCTTCCAC 2188
QY 354 HisSerGlnThrLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeu 373
Db 2189 CACTCCCAAAACCTGCTGGAGGGCCGTGACAAACATGCTGCAGAAAGCCAGCAAAACCTCTA 2248
QY 374 GluLeuThrSerCysThrSerGluGluLeuPheGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 393
Db 2249 GAATTTTACCTTCCACTTCTGGAAGAGATTGATCATGATGATCATGACAAAGATPAAACC 2308
QY 394 SerThrValGluAlaCysLeuProLeuGluLeuThrLeuAsnGlnSerCysLeuAlaSer 413
Db 2309 AGCAGAGTGGAGGCGCTGTTTACATGGAATTAACCAAGATGAGAGTGGCTTAATTC 2368
QY 414 ArgGluLeuSerLeuLeuThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMet 433
Db 2369 AGAAGAGCCTCTTCAATACAAATGAGAGTGGCTGCGCTCCAGAAAGACCTCTTTATG 2428
QY 434 ThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLys 453
Db 2429 ATGGCCCTGTGCTTCTAGTATTTATGAGACTTGAAGATGATGACAGGTGGAGTTCAAG 2488
QY 454 AlaMetAsnAlaLysLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMet 473
Db 2489 ACCATGATGCAGAACTTCTGATGATCTTAAAGAGCAGATCTTTCAGATCAAAACATG 2548
QY 474 LeuThrAlaIleAspGluLeuGlnAlaLeuAsnPheAsnSerValThrValProGln 493
Db 2549 CTGGCACTTATGTATGAGCTGATGATCGAGCCCTGAATTTCAACATGAGACTGTCACAA 2608
QY 494 LysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeu 513
Db 2609 AAATCCCTCCCTTGAAGAACCGGATTTTATTAATAATCAAGCTCTGCTATCTTCTT 2668
QY 514 HisAlaPheArgIleArgAlaValThrIleAsnArgMetSerTyrLeuAsnSerSer 533
Db 2669 CAGCTTTCAGAAATTCGGGAGTGCATGATGATGATGATGATGATGATGATGATGATGATG 2728

RESULT 13
US-09-828-825-9
? Sequence 9, Application US/09828825
? Patent No. US2002018767A1
? GENERAL INFORMATION:
? APPLICANT: Lee, Seewoo
? APPLICANT: Kim, Han-soo
? TITLE OF INVENTION: Anti-cancer Cellular Vaccine
? FILE REFERENCE: 84906-102
? CURRENT APPLICATION NUMBER: US/09/828, 825
? CURRENT FILING DATE: 2001-04-10
? PRIOR APPLICATION NUMBER: KR00-43498
? PRIOR FILING DATE: 2000-07-27
? NUMBER OF SEQ ID NOS: 16
? SOFTWARE: Patent Ver. 2.1
? SEQ ID NO 9
? LENGTH: 8638
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: plasmid
? NAME/KEY: misc_feature
? LOCATION: (1)..(750)
? OTHER INFORMATION: CMV enhancer and promoter
? NAME/KEY: misc_feature
? LOCATION: (890)..(1002)
? OTHER INFORMATION: Intervening sequence
? NAME/KEY: promoter
? LOCATION: (1067)..(1085)
? OTHER INFORMATION: T7 RNA polymerase promoter
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? NAME/KEY: misc_feature
? LOCATION: (1090)..(1984)
? OTHER INFORMATION: Human B7.1 (1090-1954 is coding sequence)
? NAME/KEY: RBS
? LOCATION: (2013)..(2593)
? OTHER INFORMATION: IRES sequence
? NAME/KEY: misc_feature
? LOCATION: (2627)..(4293)
? OTHER INFORMATION: Human IL12.4 (coding sequence is 2640-4283, 33
? OTHER INFORMATION: amino acid linker at 3606-3706)
? NAME/KEY: CDS
? LOCATION: (2640)..(4283)
? OTHER INFORMATION: IL12.4 coding sequence (33 amino acid linker)
? NAME/KEY: promoter
? LOCATION: (4392)..(4413)
? OTHER INFORMATION: T3 RNA Polymerase promoter
? NAME/KEY: polyA_signal
? LOCATION: (4423)..(4644)
? OTHER INFORMATION: SV40 fragment containing polyadenylation signal
? NAME/KEY: rep_origin
? LOCATION: (4739)..(5194)
? OTHER INFORMATION: fl origin of replication
? NAME/KEY: misc_feature
? LOCATION: (5258)..(6625)
? OTHER INFORMATION: Neo r expression cassette
? NAME/KEY: misc_feature
? LOCATION: (7036)..(7896)
? OTHER INFORMATION: Ampicillin resistance
US-09-828-825-9

Alignment Scores:
Pred. No.: 8,78e-268 Length: 8638
Score: 2387.00 Matches: 456
Percent Similarity: 88.81% Conservative: 28
Best local Similarity: 83.67% Mismatches: 45
Query Match: 85.13% Indels: 16
DB: 10 Gaps: 3

US-09-917-265-62 (1-533) x US-09-828-825-9 (1-8638)
QY 4 GlnGlnLeuValIleSerTrpPheSerLeuValLeuLeuAlaSerProLeuMetAlaIle 23
Db 2649 CAGCAGTTGGTCACTCTTGTGTTTCCCTGCTTTTCTGCACTCCCTCGTGGCCATA 2708
QY 24 TrpGluLeuGluLysAspValTyrValAlaGluLeuAspTrpHisProAspAlaProGly 43
Db 2709 TGGGAATGAGAAAGATGTTTATGTCGTGAATGTGATGATGATGATGATGATGATGATG 2768
QY 44 GluMetValValLeuThrCysHisThrProGluGluAspIleThrTrpHisAla 63
Db 2769 GAAATGGTGGTCTCACTGCTGACACCCCTGAAGAAAGATGATGATGATGATGATGATG 2828
QY 64 GlnSerSerGluValLeuGlnSerGlyLysThrLeuThrIleGlnValLysGluPheGly 83
Db 2829 CAGAGCAGTAGGCTTTAGGCTTGGCAAAACCTGACCATCCAAAGTCAAAAGAGTTTGA 2888
QY 84 AspAlaGlyGlnTyrThrCysHisLysGlyLysValLeuSerArgSerLeuLeuLeu 103
Db 2889 GATGCTGGCCAGTACACTGTCACAAAGAGCGAGGCTTCAAGCATTCGCTCGCTGCTG 2948
QY 104 IleHisLysLysGlnLysPglYIleTrpSerThrAspIleLeuLysGluGlnGlnSer 123
Db 2949 CTTTCACAAAAGAGAAATGGAATTTGCTCCACATGATATTTTAAAGAGCAGAAAGAACCC 3008
QY 124 LysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrp 143
Db 3009 AAAAATTAAGACCTTTTAAAGATGCGAGCCCAAGATTTATTTGGAGCTTTCACCTCTGG 3068
QY 144 TrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgLysPheSer 163
Db 3069 TGGCTGACGACATCATGTAATGATTTGACATTCAGTGCACAAAGCAGAGGCTCTTCT 3128
QY 164 AspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValAsp 183
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| | | | |
|----|------|---|------|
| Dd | 3129 | GACCCCGCAGGGGCTGACCTGGCGAGCTCTACACTTCTGCAGAGAGCTAGAGGGCAC | 3188 |
| Oy | 184 | AsnArgAspTyrTlysTyrThrValGluCysGlnGlySerAlaCysProSerAla | 203 |
| Dd | 3189 | AACAAGAGCAAT---GACTACTCAGTGGAGTGGCAGGAGCAGCAGTGGCTGGCCAGAGTCT | 3245 |
| Oy | 204 | GluGluSerLeuProIleGluValValAlaIleHisTlysLeuTyrGluAsn | 223 |
| Dd | 3246 | GAGGAGATCGCCCATTTGAGTGGATGGATCCCGTTCACAACTCAACTAGTAAGAAAC | 3305 |
| Oy | 224 | TyrThrSerSerPhePheIleArgAspIleLeuLysProAspProProThrAsnLeuGln | 243 |
| Dd | 3306 | TACACCAAGACCTTCTTCATCAGGAGACTATCAAACTGCACCAACCAACACTTGCAG | 3365 |
| Oy | 244 | LeuLysProLeuTlysAsnSerArgHisValGluValSerTyrGluTyrProAspThrTyr | 263 |
| Dd | 3366 | CTGAAGCATTAAGAATTCCTGGCAGGTGAGGTGACACTGGAGTACCCTGCACCTCGG | 3425 |
| Oy | 264 | SerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsnAsn | 283 |
| Dd | 3426 | AGTACTCCACATTCCTACTTCTCCCTGCATCTTCGCTTCAGTCCAGGCCAAGCAAGCAAG | 3485 |
| Oy | 284 | ArgGluLysLysAspArgLeuCysValAlaLysThrSerAlaLysValValCysHisLys | 303 |
| Dd | 3486 | AGAGAAAAAGAAATAGAGTCTTCACCCAGCAAGCTCAGCCAGCGATCTGGCCGCAAA | 3545 |
| Oy | 304 | AspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTyrSerAspTyr | 323 |
| Dd | 3546 | AATGCCAAGCATTAACGTCGGGGCCAGCAGCCGCTACTATAGCTATCTTGGAGCGCAATGG | 3605 |
| Oy | 324 | AlaSerValSerCysSerCylGly----- | 331 |
| Dd | 3606 | GCATCTGTGCTCGCTCAGTGGTGGCGTGGAAGCGTGCGGTGGAAGCGGTGGCGGTGA | 3665 |
| Oy | 332 | ---GlyGlyGlyGlySer-----ArgAsnLeuProThrProThrProSerProGlyMet | 348 |
| Dd | 3666 | AGCGGTGGCGGTGGAAGCCCATGGAGAAACCTCCCGGCCACTCCAGACCCAGCAATG | 3725 |
| Oy | 349 | PheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaValSerAsnThrLeuGlnLys | 368 |
| Dd | 3726 | TTCCCATGGCTTCAACCACTGCCAAACCTGCTGAGGGCGCTGACAGCAATGCTCAGACAG | 3785 |
| Oy | 369 | AlaArgGlnThrLeuGluLeuTyrSerCysThrSerGluLysLeuAspHisGluAspIle | 388 |
| Dd | 3786 | GCCAGACAAACTAGATAATTTACCTCTTGCACTCTGGAAGATTTGATCATGAAGATATC | 3845 |
| Oy | 389 | ThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGlu | 408 |
| Dd | 3846 | ACAAATAATMAAACCAACCACTGAGTGGAGCCCTGTTCACATTGGAATTAAACCAAGATGAG | 3905 |
| Oy | 409 | SerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGly | 428 |
| Dd | 3906 | AGTTGGCTAAATTCCAGAGAGACCTCTTCTTAATGAAATGGACGCTTGGCTCCGACGA | 3965 |
| Oy | 429 | LysAlaSerPheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyr | 448 |
| Dd | 3966 | AAGACCTCTTTTATGATGAGCCCTGTGCTTGTAGTATTTTATGAAACTTGAACATGTAC | 4025 |
| Oy | 449 | GlnMetGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePhe | 468 |
| Dd | 4026 | CAGCTGCAAGTTCAAGACCATGAAATGCAAAAGCTTGTGATGCATCTTAAGACAGCAATCTTT | 4085 |
| Oy | 469 | LeuAspGlnAsnMetLeuThrAlaIleAspGluLeuGlnAlaLeuAsnPheAsnSer | 488 |
| Dd | 4086 | CTGATATMAAACATGCTGGCAGATTATGATGAGTGTGATGACGCCCTGAATTTTAAACAGT | 4145 |
| Oy | 489 | ValThrValProGlnLysSerSerLeuGlnGluProAspPheTyrTlysThrLysIleLys | 508 |
| Dd | 4146 | GAGACTGTGGCCAAAAAATCTCCCTTGAAGAACCGGATTTTATTAACATAAATATCAG | 4205 |
| Oy | 509 | LeuCysIleLeuLeuHisAlaIlePheArgIleArgAlaValThrIleAsnArgMetMetSer | 528 |

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Db          4206  CTCGCGACTCTTCTTCACGCTTTAGAGATTGGCGACGAGTACTATTGATAGAGTATGACG 4205
Oy          529   TyrLeuAsnSerSer 533
                |||||
Db          4266  TATCTGATGCTCTCC 4280

RESULT 14
US-09-828-825-11
: Sequence 11, Application US/09828825
: Patent No. US20020018767A1
: GENERAL INFORMATION:
: APPLICANT: Lee, Seewoo
: APPLICANT: Kim, Han-soo
: TITLE OF INVENTION: Anti-cancer Cellular Vaccine
: FILE REFERENCE: 84906-102
: CURRENT APPLICATION NUMBER: US/09/828-825
: CURRENT FILING DATE: 2001-04-10
: PRIOR APPLICATION NUMBER: KR00-43498
: PRIOR FILING DATE: 2000-07-27
: NUMBER OF SEQ ID NOS: 16
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 11
: LENGTH: 8659
: TYPE: DNA
: ORGANISM: Artificial Sequence
FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)..(750)
: OTHER INFORMATION: CMV enhancer and promoter
: NAME/KEY: promoter
: LOCATION: (1067)..(1085)
: OTHER INFORMATION: T7 RNA polymerase promoter
: NAME/KEY: misc_feature
: LOCATION: (1090)..(2756)
: OTHER INFORMATION: Human IL12.4 (coding sequence 1103-2746, 19 amino
: OTHER INFORMATION: acid linker at 2087-2146)
: NAME/KEY: CDS
: LOCATION: (1103)..(2746)
: OTHER INFORMATION: Human IL12.4 (19 amino acid linker)
: NAME/KEY: RBS
: LOCATION: (2782)..(3362)
: OTHER INFORMATION: IRES sequence
: NAME/KEY: misc_feature
: LOCATION: (3399)..(4293)
: OTHER INFORMATION: Human B7.1 sequence
: NAME/KEY: promoter
: LOCATION: (4413)..(4434)
: OTHER INFORMATION: T3 RNA polymerase promoter
: NAME/KEY: polyA_signal
: LOCATION: (4444)..(4665)
: OTHER INFORMATION: SV40 fragment containing polyadenylation signal
: NAME/KEY: rep_origin
: LOCATION: (4760)..(5215)
: OTHER INFORMATION: fl origin of replication
: NAME/KEY: misc_feature
: LOCATION: (5279)..(6646)
: OTHER INFORMATION: Neo r expression cassette
: NAME/KEY: misc_feature
: LOCATION: (7057)..(7917)
: OTHER INFORMATION: Ampicillin resistance gene
: OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-828-825-11

Alignment Scores:
Pred. No.:      8,82e-268      Length:      8659
Score:          2387.00        Matches:      456
Percent Similarity: 88.81%      Conservative: 28
Best Local Similarity: 83.67%      Mismatches:  45
Query Match:    85.13%         Indels:      16
Db:             10             Gaps:        3

US-09-917-265-62 (1-533) x US-09-828-825-11 (1-8659)

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QY      4 GlnGlnLeuValIleSerTrpPheSerLeuValLeuLeuAlaSerProLeuMetAlaIle 23
      1112 CAGCAATGGTGCATCTGGTTTCCCGTGGTTTCTGGCAATCTCCCTCGGGCCATTA 1171
QY      24 TrpGluLeuGluLysAspValIleValGluLeuAspTrpHisProAspAlaProGly 43
      1172 TGGGAACCTGAGAAATGTTATGTCAGAAATGGATGGATGATGCGATGCCCTGGA 1231
QY      44 GluMetValValLeuThrCysHisTrpProGluGluAspIleThrTrpTrpSerAla 63
      1232 GAAATGGTGGTCTCCACCTGCTGACACCCCTGAAAGAAATGATGATCACCCTGGACCTTGAC 1291
QY      64 GlnSerSerGluValLeuGlySerGlyLysTrpLeuThrIleGlnValLysGluPheGly 83
      1292 CAGAGCAGTAGAGTCTTACGCTCTGCAAAACCCCTGACCATCCCAAGCTTCAAGAGTTGGA 1351
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QY      104 IleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGlnSer 123
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QY      164 AspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgValAsp 183
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QY      184 AsnArgAspTyrLysLysTyrThrValGluCysGlnGluLysSerLacysProSerAla 203
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QY      204 GluGlnSerLeuProIleGluValValAlaAspAlaIleHisLysLeuLysTyrGluAsn 223
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QY      224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeuGln 243
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      1829 CTGAACCCATTTAAAGATTTCTCGGAGGTGGAGGTGAGTCAAGTCAACCTGACACCTGCG 1888
QY      264 SerThrProHisSerTrpPheSerLeuThrPheCysIleGlnIleGlnGlyLysAsnAsn 283
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QY      284 ArgGluLysLysAspArgLeuLysValAspLysThrSerAlaLysValLysCysHisLys 303
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QY      324 AlaSerValSerCysSerGlyLys----- 331
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QY      332 ---GlyGlyLysLys-----ArgAsnLeuProThrProThrProSerProGlyMet 348
      2129 AGCGGTGGCGGTGGAAGCCCATGAGAAACCTCCCGTGGCCACTCAGAGCCAGGAATG 2188
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Db

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RESULT 15
 US-09-828-825-1
 : Sequence 1, Application US/09828825
 : Patent No. US20020018767A1
 : GENERAL INFORMATION:
 : APPLICANT: Lee, Seewoo
 : APPLICANT: Kim, Han-soo
 : TITLE OF INVENTION: Anti-cancer Cellular Vaccine
 : FILE REFERENCE: 84906-102
 : CURRENT APPLICATION NUMBER: US/09/828,825
 : PRIOR FILING DATE: 2001-04-10
 : PRIOR APPLICATION NUMBER: KR00-43498
 : NUMBER OF SEQ ID NOS: 16
 : SOFTWARE: PatentIn Ver. 2.1
 : SEQ ID NO 1
 : LENGTH: 8578
 : TYPE: DNA
 : ORGANISM: Artificial Sequence
 : FEATURE:
 : NAME/KEY: enhancer
 : LOCATION: (1)..(659)
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 : NAME/KEY: promoter
 : LOCATION: (669)..(750)
 : OTHER INFORMATION: CMV IE
 : NAME/KEY: promoter
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 : OTHER INFORMATION: T7 RNA Promoter
 : NAME/KEY: mRNA
 : LOCATION: (1090)..(1984)
 : OTHER INFORMATION: Human B7.1 (1090-1956 is coding sequence)
 : NAME/KEY: RBS
 : LOCATION: (2013)..(2593)

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OTHER INFORMATION: T3 RNA polymerase promoter
NAME/KEY: polyA signal
LOCATION: (4362)..(4583)
OTHER INFORMATION: SV40 fragment containing polyadenylation signal)
NAME/KEY: rep_origin
LOCATION: (4678)..(5133)
OTHER INFORMATION: fl origin of replication
NAME/KEY: misc feature
LOCATION: (5197)..(6564)
OTHER INFORMATION: Neo r expression cassette
NAME/KEY: misc feature
LOCATION: (6975)..(7835)
OTHER INFORMATION: Ampicillin resistance
OTHER INFORMATION: Description of Artificial Sequence: Plasmid
NAME/KEY: CDS
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OTHER INFORMATION: 3624
US-09-828-825-1
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Alignment Scores:
Pred. No.: 2.15e-264 Length: 8578
Score: 2358.00 Matches: 449
Percent Similarity: 90.00% Conservative: 28
Best Local Similarity: 84.72% Mismatches: 47
Query Match: 84.09% Indels: 6
DB: 10 Gaps: 2
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US-09-917-265-62 (1-533) x US-09-828-825-1 (1-8578)

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Db 2769 GAATAGTGTGCTCCACCTGTGACACCCCTGAAGAAAGATGATACCTGGACCTTGAC 2828
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QY 84 AspAlaGlnYlnTrpThrCysHisLysGlnYValLeuSerArgSerLeuLeu 103
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QY 104 IleHisLysLysGlnAspGlnYIleTrpSerThrAspIleLeuLysGlnGlnLysGlnSer 123
Db 2949 CTTCACAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAAGAAAGAACCC 3008
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Db 3069 TGGCTGAGCAACAATCACTAGATTGACATTTCAGTGTCAAAAGACAGAGGCTCTTCT 3128
QY 164 AspProGlnGlnValThrCysGlnAlaValThrLeuSerAlaGlnArgValArgValAsp 183
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QY 364 AsnThrLeuGlnLysAlaArgGlnThrLeuGlnLeuTyrSerCysTrpSerGlnIle 383
Db 3711 AACATGCTCCGAAGGCGAGCAACAACCTAGAAATTTTAACTTGCATCTGGAAGAGATT 3770
QY 384 AspHisGlnAspIleThrLysAspLysThrSerThrValGlnAlaCysLeuProLeuGln 403
Db 3771 GATCATGAGATATCACAAAAGATAAACCGCACAGTGGAGGCTGTTATACCAATTGGAA 3830
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Db 3831 TTAACCAAGATGAGAGTGTCTTAATTTCCAGAGACACTTTCATTAACATAATGGAGCT 3890
QY 424 CysLeuAlaSerGlnLysAlaSerPheMetThrValLeuCysLeuSerSerIleTyrGln 443
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QY 444 AspLeuLysMetTyrGlnMetGlnPheLysAlaMetLysAlaLysLeuLeuMetAspPro 463
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QY 464 LysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGlnLeuLeuAla 483
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QY 484 LeuAsnPheAsnSerValThrValProGlnLysSerSerLeuGlnProAspPheTyr 503
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QY 504 LysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIle 523
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QY 524 AsnArgMetSerTyrLeuAsnSerSer 533
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Search completed: July 17, 2003, 09:56:54
Job time : 399.136 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: July 16, 2003, 15:58:34 ; Search time 4568.08 Seconds
(Without alignments)
3255.531 Million cell updates/sec

Title: US-09-917-265-67
Perfect score: 2693
Sequence: 1 IMELEKDVYVVELDHPDAP.....HAFRIRAVTINRMMSYINSS 511

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+P2n_model -DEV=xlh
-O=/cga2_1/USFIO.spool/US09917265/rnatc_15072003_092106_1601/app_query.fasta_1.3114
-DB=GenBdb1 -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blsum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-UFFMT=pio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=us09917265 @CGN_1_11328 @rnatc_15072003_092106_1601 -NCPU=6 -ICPU=3
-NO_MMAPP -LARGEOUTPRY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -Delop=6 -Delext=7

Database : GenBdb1 : *
1: gb_ba : *
2: gb_hgt : *
3: gb_in : *
4: gb_om : *
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6: gb_pat : *
7: gb_ph : *
8: gb_pl : *
9: gb_pr : *
10: gb_ro : *
11: gb_sts : *
12: gb_sy : *
13: gb_un : *
14: gb_vl : *
15: em_ba : *
16: em_fun : *
17: em_hum : *
18: em_in : *
19: em_mu : *
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21: em_or : *
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29: em_vl : *
30: em_htg_hum : *
31: em_htg_inv : *
32: em_htg_other : *
33: em_htg_mus : *
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35: em_htg_rnd : *
36: em_htg_mam : *
37: em_htg_vrt : *
38: em_sy : *
39: em_htgo_hum : *
40: em_htgo_mus : *
41: em_htgo_other : *

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 2360 | 87.6 | 1626 | 12 AF401989 | AF401989 Synthetic |
| 2 | 2309.5 | 85.8 | 1560 | 6 AR091395 | AR091395 Sequence |
| 3 | 2309.5 | 85.8 | 1623 | 6 AR091394 | AR091394 Sequence |
| 4 | 2309.5 | 85.8 | 6139 | 6 AR091393 | AR091393 Sequence |
| 5 | 1653 | 61.4 | 990 | 6 AR151071 | AR151071 Sequence |
| 6 | 1653 | 61.4 | 990 | 6 E15017 | E15017 Canine mRNA |
| 7 | 1652 | 61.3 | 1015 | 4 CFU49100 | U49100 Canis fam1 |
| 8 | 1640 | 60.9 | 990 | 6 AR151061 | AR151061 Sequence |
| 9 | 1613 | 59.9 | 1669 | 12 AF411293 | AF411293 Synthetic |
| 10 | 1555 | 57.7 | 4522 | 6 AX076209 | AX076209 Sequence |
| 11 | 1555 | 57.7 | 4522 | 6 AX076476 | AX076476 Sequence |
| 12 | 1554 | 57.7 | 990 | 6 AX076200 | AX076200 Sequence |
| 13 | 1554 | 57.7 | 990 | 6 AX076482 | AX076482 Sequence |
| 14 | 1552 | 57.6 | 990 | 4 FCU83184 | U83184 Felis catus |
| 15 | 1546 | 57.4 | 1006 | 4 FCIL12P40 | Y07762 F. catus mRN |
| 16 | 1484 | 55.1 | 990 | 6 AX154603 | AX154603 Sequence |
| 17 | 1471 | 54.6 | 1058 | 4 ECIL12P40 | Y11129 Equus caball |
| 18 | 1451 | 53.9 | 984 | 6 AX154600 | AX154600 Sequence |
| 19 | 1431 | 53.1 | 1389 | 6 AX084106 | AX084106 Sequence |
| 20 | 1429 | 53.1 | 984 | 6 AX154599 | AX154599 Sequence |
| 21 | 1427 | 53.0 | 993 | 4 CEU57752 | U57752 Cervus elap |
| 22 | 1421 | 52.8 | 984 | 6 AX154598 | AX154598 Sequence |
| 23 | 1420.5 | 52.7 | 1870 | 6 A92079 | A92079 Sequence |
| 24 | 1419.5 | 52.7 | 2318 | 9 HUMNKSFP40 | M65290 Human natur |
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| 28 | 1418.5 | 52.7 | 987 | 6 BD007076 | BD007076 Gene expr |
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| 33 | 1418.5 | 52.7 | 1018 | 6 AR052857 | AR052857 Sequence |
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| 35 | 1418.5 | 52.7 | 1399 | 6 HUMCLMP40 | M65272 Human cytot |
| 36 | 1418.5 | 52.7 | 2362 | 6 AR082684 | AR082684 Sequence |
| 37 | 1418.5 | 52.7 | 2362 | 6 ARI12960 | ARI12960 Sequence |
| 38 | 1418.5 | 52.7 | 2362 | 6 128325 | 128325 Sequence |
| 39 | 1418.5 | 52.7 | 2362 | 6 189770 | 189770 Sequence |
| 40 | 1411 | 52.4 | 1012 | 4 BU11815 | U11815 Bos taurus |
| 41 | 1411 | 52.4 | 1019 | 6 E35794 | E35794 Process for |
| 42 | 1407 | 52.2 | 984 | 4 AF004024 | AF004024 Ovis arie |
| 43 | 1407 | 52.2 | 984 | 4 AF0209435 | AF0209435 Ovis arie |
| 44 | 1407 | 52.2 | 1012 | 4 AF007576 | AF007576 Capra hir |
| 45 | 1406.5 | 52.2 | 1080 | 9 MMU19841 | U19841 Macaca mula |

RESULT 1

ALIGNMENTS

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DEFINITION      AF401989
ACCESSION      AF401989
VERSION      AF401989.1      GI:18656516
KEYWORDS
SOURCE      synthetic construct.
ORGANISM      synthetic construct.
ARTHRS      1 (bases 1 to 1626)
TITLE      McMonagle, E.L.J., Taylor, S., van Zullekom, H., Sanders, L.,
      Scholtes, N., Keanie, L.J., Hopkins, C.A., Logan, N.A., Bain, D.,
      Argye, D.J., Onions, D.E., Schijns, V.E., and Nicolson, L.
      Production of biologically active equine interleukin 12 through
      expression of p35, p40 and single chain IL-12 in mammalian and
      baculovirus expression systems
JOURNAL      Equine Vet. J. 33 (7), 693-698 (2001)
MEDLINE      21626920
PUBMED      11770992
REFERENCE      2 (bases 1 to 1626)
AUTHORS      McMonagle, E.L.J., Taylor, S., Keanie, L.J., Hopkins, C.A., Logan, N.A.,
      Argye, D.J., Onions, D.E. and Nicolson, L.
      Direct Submission
      Submitted (24-JUL-2001) Veterinary Pathology, Glasgow Veterinary
      School, Bearsden Rd, Glasgow G61 1QH, UK
FEATURES
source      1. 1626
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      misc_feature      /note="interleukin-12 p35 sequence"
      primer_bind      complement(1612..1626)
      BASE COUNT      429 a      425 c      427 g      345 t
      ORIGIN
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Pred. No.:      2.57e-209      Length:      1626
Score:      2360.00      Matches:      445
Percent Similarity:      91.33%      Conservative:      29
Best Local Similarity:      85.74%      Mismatches:      37
Query Match:      87.63%      Indels:      8
DB:      12      Gaps:      1
US-09-917-265-67 (1-511) x AF401989 (1-1626)
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Db      67      ATATGGGAACGTGGAAGATGCTATCTGTAGAAATGTGATGATCCCTGATGCCCT 126

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Qy      21      GlyIuMeIvalValLeuThrcysHisThrProGluGluaspPileThrTrpThrsr 40
      |||||.....:|||||
Db      127      GGAGAAATGCTGCTCCTCAGCTGCAATACCCCTGAAGAAAGACGATCGGACCTCG 186
Qy      41      AlaGlnSerSerGluValLeuGlySerGlyLysTrpLeuThrIleGluValIysGluPhe 60
      |||||.....:|||||
Db      187      GCCAGACGAATGAGGCTTGGCTGGCAAAACCTTGACCATCAAGTCAAGAGCTTT 246
Qy      61      GlyaspAlaGlyGlnThrThrcysHisLysGlyGlyValLeuSerArgSerLeuLeu 80
      |||||.....:|||||
Db      247      GGAGATGCTGCGCTGGTACACCTGTCACAAAGSAGSGAGGTCTGAGCATTCACCTG 306
Qy      81      LeuIleHisLysLysGluaspGlyIleTrpSerThrAspIleLeuLysGluGlnGlu 100
      |||||.....:|||||
Db      307      CTGCTTCACAAAGAGAGATGGAAATTGGTCCACTGACATTTTAAAGACCAGAAAGA 366
Qy      101      SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTrpSerGlyArgPheThrcys 120
      |||||.....:|||||
Db      367      TCCAAAAATTAACCTTTCTTAAATGTGAGGCAAGAAATATTCCGGACGTTCCATTC 426
Qy      121      TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerArgGlyPhe 140
      |||||.....:|||||
Db      427      TGGTGCTGACAGCAATCAGTACTGATTGAATTCAGTGCAAAAGCAGCAGAGTTCC 486
Qy      141      SerAspProGlnGlyValThrcysGlyAlaValThrLeuSerAlaGluArgValArgVal 160
      |||||.....:|||||
Db      487      TCTGACCCCGGAGGGGTGACGTGTGGACGACGACACTCCGCAAGAGAGGCTGACG 546
Qy      161      AspAsnArgAspTrpLysLysTrpThrValGluCysGlnGluGlySerAlaCysProSer 180
      |||||.....:|||||
Db      547      CACGACAGGAGATATAGAAAGTACACGATGAGATGTCACAGAGGCGAGTCCGCGCGGC 606
Qy      181      AlaGluGluSerLeuProIleGluValValAspAlaIleHisLysLeuLysTrpGlu 200
      |||||.....:|||||
Db      607      GCCGAGAGAGCGCTGCCCTTCAGATCGGTGATGCTGTACAAAGCTCAAGATATGAA 666
Qy      201      AsnTrpThrSerSerPheThrIleArgAspIleIleLysProAspProThrAsnLeu 220
      |||||.....:|||||
Db      667      AACTACACGAGCGGCTTCTTATCAGGACATATCAACCAAGACCGCCCAAGACCTG 726
Qy      221      GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTrpProAspThr 240
      |||||.....:|||||
Db      727      CAGCTAAGCCATTAAGAAATTCGCGAGGTGAGAGTACGCTGGAGTACCCCGAGAC 786
Qy      241      TrpSerThrProHisSerTrpPheSerLeuThrPheCysIleGlnAlaGlnGlyAsn 260
      |||||.....:|||||
Db      787      TGGAGCACCCACATTCCTACTTCCTCCAGACATTCCTATTCAGGTCACAGGCAAGAC 846
Qy      261      AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValCysHis 280
      |||||.....:|||||
Db      847      AAGAAAGAAAGAAAGACAGACTCTTCATGATGAGACTTCACGCCACAGTCATGCCCAC 906
Qy      281      LysAspAlaLysIleArgValGlnAlaArgAspArgTrpLysSerSerTrpSerAsp 300
      |||||.....:|||||
Db      907      AAGATGGCCAGATCGCTGTCACAGCCAGGAGACCGCTACTACAGCTCATCTGGAGCAGAA 966
Qy      301      TrpAlaSerValSerCysSerGlyGly.....-GlyGlyGly 312
      |||||.....:|||||
Db      967      TGGGCATCCGTATCCCTGACAGTGTGGCTGGCGTGGCGGTGGATCCGGTGGCGGC 1026
Qy      313      GlySerArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHis 332
      |||||.....:|||||
Db      1027      GGATCTAGGAACTCCGCCACAGCCACACCAAGCCGAGATGTTCAGATGCTCAACACAC 1086
Qy      333      SerGlnThrLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGlu 352
      |||||.....:|||||
Db      1087      TCCCAAAACCTGCTGAGGACCGTCACCAACACGCTTCAGAAAGCCAGCAAAACCTAGAA 1146
Qy      353      LeuTrpSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysTrpSer 372
      |||||.....:|||||
Db      1147      TTCCTACTCTGCACTTCTGAAGAGATCATGAGAGATATCACAAAAGACAGACGAC 1206
Qy      373      ThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArg 392

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||||| ||||||||||||||||||| |||||||||||||||||||
Db 1207 ACCGTGGCGGCTGCTCCCTGGAACCTGCCCCGAACGAGAGTGGCTGCTCCAGA 1266
QY 393 GluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyIlySAlaSerPheMetThr 412
Db 1267 GAGATCTCTTCAATACATAATGGAGATGGCTGACCCCGAAAGGCGCTTCTATATG 1326
QY 413 ValLeuCysLeuSerSerIleTyrGluAspLeuYsMetTyrGlnMetGluPheIlyAla 432
Db 1327 ACCGTGGCTTACACACATCTATAGAGACTTGAAGATGTACACAGGTGAGCTTCAAGGCC 1386
QY 433 MetAsnAlaIlyLeuLeuMetAspProIlyAsnArgGlnIlePheLeuAspGlnAsnMetLeu 452
Db 1387 ATGAATGCCAAGCTGTGATAGATCCTCAGACGAGATCTTTCGTGATGAGAACATGCTG 1446
QY 453 ThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnIlyS 472
Db 1447 ACAGCCATTGACAGATGATGACAGCCCTGAACTTCAACAGTGAGCTGTGCCAAG 1506
QY 473 SerSerLeuGluGluProAspPheTyrIlySerThrIlySLeuCysIleLeuLeuHis 492
Db 1507 CCTCCCTTGAAGAGCTGGATTTTATAAACTAAAGTCAAGCTTCATCCTTCTTCAT 1566
QY 493 AlaPheArgIleArgAlaValThrIleAsnArgMetSerTyrIleAsnSerSer 511
Db 1567 GCCTTCAGATCCGCGCAGTGCACATCAACAGATGATGGGCTATCTGAATGCTTCC 1623

RESULT 2
AR091395 AR091395 1560 bp DNA linear PAT 07-SEP-2000
LOCUS Sequence 11 from patent US 5994104.
DEFINITION AR091395
ACCESSION AR091395
VERSION AR091395.1 GI:10018150
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1560)
AUTHORS Andersen,R.James., Prentice,H.Grant, and Macdonald,I.Duncan.
TITLE Interleukin-12 fusion protein
JOURNAL Patent: US 5994104-A 11-30-NOV-1999;
FEATURES
source Location/Qualifiers
1..1560
/organism="unknown"

BASE COUNT 443 a 375 c 393 g 349 t
ORIGIN
Alignment Scores:
Pred. No.: 1.18e-204 Length: 1560
Score: 2309.50 Matches: 438
Percent Similarity: 89.60% Conserves: 27
Best Local Similarity: 84.39% Mismatches: 45
Query Match: 85.76% Indels: 9
Gaps: 2

US-09-917-265-67 (1-511) x AR091395 (1-1560)

QY 1 IletPrluLeuGluIlySAspValTyrValGluLeuAspTrrPrlSProAspAlaPro 20
Db 4 ATATGGAACTGAAGAAAGATGTTATGCTGATAATTTGATTCGGAGTCCCT 63
QY 21 G1G1UmeValValLeuThrCysHisThrProGluGluAspAspIleThrTrrPheSer 40
Db 64 GCGAATATGGTGGCTCCACCTGTGACACCCCTGAAACAGATGATACACTGACCTTG 123
QY 41 AlGlnSerSerGluValLeuGlySerGlyIlySThrLeuThrIleGlnValIlySgluPhe 60
Db 124 GACACGACAGCTGAGGCTTAGGCTGTGCAAAACCTGACCAATCCAAAGTCAAGAGTTT 183
QY 61 G1YAspRAlaGluInTrrThrCysHisIlySgluIlySValLeuSerArgSerLeuLeu 80
Db 184 GGAATGTGCGCCAGTACACCTGTGCAAAAGAGGAGGTTCTTAACCATTCGCTCTG 243

QY 81 LeuIleHisIlySgluAspGlyIleTrrSerThrAspIleLeuIlySgluIlySglu 100
Db 244 CTGCTTCACAAAAAGAAAGATGATTTGGTCCACTGATATTTTAAAGACAGACAAGAA 303
QY 101 SerIlySAsnIlyIlePheLeuIlySgluAlaIlySAsnTyrSerGlyIlyArgPheThrCys 120
Db 304 CCCAAAAATAGACCTTCTTCAAGATGCGAGCCAAAGATTTATTCGACGTTCCACTGCG 363
QY 121 TrrPrlLeuThrAlaIleSerThrAspLeuIlyStheserValIlySerSerArgGlyPhe 140
Db 364 TGGTGGCTGAGCAATTCAGTACATTTGATTCAGTTGCAAAAGCCAGAGAGCTCT 423
QY 141 SerAspProGlnIlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgVal 160
Db 424 TCTGACCCCAAGGGGTGACCTGGCGAGCTCTCACTCTTCCAGACAGAGTGAAGCG 483
QY 161 AspAsnArgAspTrrIlySgluIlySgluIlySgluIlySgluIlySgluIlySglu 180
Db 484 GACAACAAGAGTAT---GAGTACTCAGTGGAGTGGCCAGAGACAGTGGCTGCCAGCT 540
QY 181 AlaGluGluSerLeuProIleGluValValAlaIleHisIlySgluIlySglu 200
Db 541 GCTGAGAGAGCTGCCCCATTGAGTATGATGATGATGATGATGATGATGATGATGATG 600
QY 201 AsnTrrThrSerSerPhePheIleArgAspIleIleIlySProAspProPrrThrAsnLeu 220
Db 601 AACTACACACAGCTCTTCTATCAGGACATTCATCAACCTGACCCCAAGACCTTG 660
QY 221 GlnLeuIlySProLeuIlySAsnSerArgHisValGluValSerTrrPgluTrrProAspThr 240
Db 661 CAGCTGAAGCCATTAAAGAAATTCGCGAGGTGAGGTCAGCTGGAGTACCTGCACACC 720
QY 241 TrrSerThrProHisSerTrrPheSerLeuThrPheCysIleGlnAlaGlnGlyIlySAsn 260
Db 721 TGGATCTCCACATTCCT 780
QY 261 AsnArgGluIlySAspArgLeuCysValAspIlySThrSerAlaIlySValIlyCysHis 280
Db 781 AAGAGAGAAAGAAAGATAGAGTCTTCAGCGACAAAGACTAGCCAGCGTATCTGCCGC 840
QY 281 IlySAspAlaIlySgluIlySgluIlySgluIlySgluIlySgluIlySgluIlySglu 300
Db 841 AAAAATGCCAGCATTTACCTGCGCGCCAGAGACCGCTACTATTCATCTATCTTGAAGCGAA 900
QY 301 TrrPAlaSerValSerCysSerGlyIly-----GlyGlyGly 312
Db 901 TGGGCATCTGTGCCCTCAGTGGTGGCGGTGCAAGCGGCGGCGGAGCGGCGTGC 960
QY 313 GlySerArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHis 332
Db 961 GGCAGCAGAAACCTCCCTGCGCAGCTCCAGACCCAGAGAAATGTTCCCATGCTTACCCAC 1020
QY 333 SerGlnThrLeuLeuArgAlaValSerAsnThrLeuGlnIlySAlaIlySgluIlySglu 352
Db 1021 TCCCAAAAACCTGCTGAGCGCGCTGACGAAACATGCTCCAGAAAGCGCAGCAAACTGTGAA 1080
QY 353 LeuTrrSerCysTrrSerGluGluIleAspHisGluAspIleThrIlySAspIlySglu 372
Db 1081 TTTTACCTCTGCTTCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATG 1140
QY 373 ThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGlnIlySAspIlySglu 392
Db 1141 ACAGTGGAGGCTTTTACCTTGAATTTAACCAGAAATGAGATTTGCTTAATTTCCAGA 1200
QY 393 GluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyIlySAlaSerPheMetThr 412
Db 1201 GAGACCTCTTCAATAACTAATAGGAGTTCCTGCGCTCCGAAAGAGACCTCTTATATGATG 1260
QY 413 ValLeuCysLeuSerSerIleTyrGluAspLeuYsMetTyrGlnMetGluPheIlyAla 432
Db 1261 GCGCTGTGCTTATGATGATTTATGAAGACTTGAAGATGTACAGGTGAAGTCAAGAGCC 1320
QY 433 MetAsnAlaIlySLeuLeuMetAspProIlyAsnArgGlnIlePheLeuAspGlnAsnMetLeu 452

|||||
Db 1321 ATGAATGCAAGGCTTGTGATGATCCAGAGGAGAGTCTTCTAGATCAAAACATGCTG 1380
QY 453 ThrAlaIleAspGluLeuGlnAlaIleAsnPhaSerValThrValProGlnLys 472
Db 1381 GCAGTTATTGATGAGCGATGAGCGCCCTGAATTCACAGCTGAGACTGTGCCACAAAA 1440
QY 473 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuGlnLys 492
Db 1441 TCCTCCCTTGAAACCGGATTTTATTAATAAATCAAGCTGCACTCTTCAT 1500
QY 493 AlaPheArgIleArgAlaValThrIleAsnArgMetSerTyrLeuAsnSerSer 511
Db 1501 GCCTTCAGATTGGGCGAGTGAATTCAGAGAGTGAAGCATATCGAATGCTCC 1557
RESULT 3
AR091394 AR091394 1623 bp DNA linear PAT 07-SEP-2000
LOCUS Sequence 9 from patent US 5994104.
ACCESSION AR091394
VERSION AR091394.1 GI:10018149
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1623)
AUTHORS Anderson, R. James., Prentice, H. Grant. and MacDonald, I. Duncan.
TITLE Interleukin-12 fusion protein
JOURNAL Patent: US 5994104-A 9 30-NOV-1999;
FEATURES Location/Qualifiers
source 1..1623
BASE COUNT 449 a 393 c 408 g 373 t
ORIGIN
Alignment Scores:
Pred. No.: 1 24e-204 Length: 1623
Score: 2309.50 Matches: 438
Percent Similarity: 89.60% Conservative: 27
Best Local Similarity: 84.39% Mismatches: 45
Query Match: 85.76% Indels: 9
DB: Gaps: 2
US-09-917-265-67 (1-511) x AR091394 (1-1623)
QY 1 IleTPrGluLeuGluLysAspValTyrValValGluLeuAspTrpHisProAspAlaPro 20
Db 67 ATATGGGAAGTGAAGAAAGATGTTATGTCGTGAATTGGATGGATATCCGATGCCCT 126
QY 21 GlyGluMetValValLeuThrCysHisThrProGluGluAspAspIleThrTrpHisSer 40
Db 127 GGAGAAATGGTGGTCTCACTGTGACACCCCTGAAGAAAGATGTATCACTGTGACCTTG 186
QY 41 AlaGlnSerSerGlnValLeuGlnLysSerGlyLysThrLeuThrIleGlnValLysGluPhe 60
Db 187 GACCAAGACAGTACAGTCTTGAAGCTGTGCAAAACCTGACATCCAAAGTCAAAAGAGTTT 246
QY 61 GlyAspAlaGlyGlnTyrThrCysHisLysGlyGlyLysValLeuSerArgSerLeuLeu 80
Db 247 GGAGATGTGGCCAGTACACCTGTCAAAAGAGGAGGAGGTCTTAAGCCATTCGCTCCG 306
QY 81 LeuIleHisLysLysGlnAspGlyIleTPrSerThrAspIleLeuLysGluGlnLysGlu 100
Db 307 CTGCTTCACAAAAAGAGATGGAATTTGTCTCCACGATATTTAAAGGCCGAAAGAA 366
QY 101 SerLysAsnLysIlePheLeuLysCysGlnAlaLysAsnTyrSerGlyArgPheThrCys 120
Db 367 CCCAAAATTAAGACCTTTCTAAGATCGAGGCCAAGAAATTAATTCGAGCTTCACTGC 426
QY 121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
Db 427 TGGTGGCTGACGACATCACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGCTCT 486

QY 141 SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgVal 160
Db 487 TCTGACCCCCAAGGGGTGACGTGGGAGGTGCTACCTCTGCAAGAGAGTCAAGAGG 546
QY 161 AspAsnArgAspTyrLysTyrThrValGluCysGlnGluLysSerAlaCysProSer 180
Db 547 GACACACAGAGAT---GAGTACTGATGGAGTGGCCAGAGACAGTCCCTGCCAGCT 603
QY 181 AlaGluGluSerLeuProIleGluValAlaValAspAlaIleHisLysLeuLysTyrGlu 200
Db 604 GCTGAGAGAGTGTGCCCATTTGAGTCATGATGGATGCGGCTTCACAAGCTCAAGTATGAA 663
QY 201 AsnTyrThrSerSerPheHelleArgAspIleIleLysProAspProThrHisLeu 220
Db 664 AACTTACACAGCAGCTTCTTCAACAGGACATCATCAACCTGACCCACCAAGAACTTG 723
QY 221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
Db 724 CAGCTAAGCCATTAAAGAAATTCGCGCAGGTGGAGTCAAGTGGAGTCACTGACACC 783
QY 241 TrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnLysAsn 260
Db 784 TGGAGTACGCCACATTCCTACTCTCCCTGACATTCCTGGCTTCAGGTCACAGGCAAGAC 843
QY 261 AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValLysHis 280
Db 844 AAGAGGAAAGAAAGAAATGAGACTTCAAGGACAAACCTCAGCCGCTCATCTGCCCC 903
QY 281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsp 300
Db 904 AAAAATGCCACCATTAAGCTGGGCGCCAGGACCGCTCATTAAGCTCATTTGGAGCGAA 963
QY 301 TrpAlaSerValSerCysSerGlyLys-----GlyLysGly 312
Db 964 TGGCATCTGTGCGCTGACAGTGGTGGCGGTGAAGCGCGGTGCGGAAGCGAGGTGAC 1023
QY 313 GlySerArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHis 332
Db 1024 GGCAGGAGAAGCTCCCTCCCTGCGCACTCCAGACCCGAGATATTCCTCAACCC 1083
QY 333 SerGlnThrLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGln 352
Db 1084 TCCCAAAACCTGCTGAGGCGCCGTCACCAACATGCTCCAAAGCCAGCAAACTCAGAA 1143
QY 353 LeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSer 372
Db 1144 TTTTACCTTGCACTTCAAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1203
QY 373 ThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuLysSerArg 392
Db 1204 ACAGTGGAGGCGCTGTACCATTTGAATTAACCAAGAAATGAAGTGGCTTAATTCAGA 1263
QY 393 GluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThr 412
Db 1264 GAGACCTCTTTGATATGATGAGATTCGCTGCGCTCCAGAAAGACCTTTTATGAG 1323
QY 413 ValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAla 432
Db 1324 GCCCTGTGCTTATGATGATTTATGAAAGCTTGAAGATGTACAGGTGAGTCAAGACC 1383
QY 433 MetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeu 452
Db 1384 ATGAAGCAAAACCTTGTGATGATCTTAAGAGGAGAGATCTTCTGATCAAAAACATGCG 1443
QY 453 ThrAlaIleAspGluLeuGlnAlaIleAsnPhaSerValThrValProGlnLys 472
Db 1444 GCAGTTATTGATGAGTGTATGACAGCCCTGCAATTTCAACAGTGAAGACTGTGCCAAAAA 1503
QY 473 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 492
Db 1504 TCCTCCCTTGAAAGACCGGATTTTATAAATCAAAATCAAGCTGCACTACTCTCTCAT 1563
QY 493 AlaPheArgIleArgAlaValThrIleAsnArgMetSerTyrLeuAsnSerSer 511

Db 1564 GCTTTCAGAAATCGGCGACGTACTATTGACAGAGCTAGCAGACTATCTGAAATGCTTCC 1620
RESULT 4
LOCUS AR091393 6139 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 7 from patent US 5994104.
ACCESSION AR091393
VERSION AR091393.1 GI:10018148
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 6139)
AUTHORS Anderson,R.James., Prentice,H.Grant, and Macdonald,I.Duncan.
TITLE Interleukin-12 fusion protein
JOURNAL Patent: US 5994104-A 7 30-NOV-1999;
FEATURES
Location/Qualifiers
source 1..6139
BASE COUNT 1552 a 1538 c 1558 g 1491 t
ORIGIN
Alignment Scores:
Pred. No.: 8.19e-204 Length: 6139
Score: 2309.50 Matches: 438
Percent Similarity: 89..60% Conservative: 27
Best Local Similarity: 84..39% Mismatches: 45
Query Match: 85..76% Indels: 9
D: Gaps: 2
US-09-917-265-67 (1-511) x AR091393 (1-6139)
QY 1 IleGrrpIuencUlyuSAspValTyValGluLeuAspTrpHisProAspAlaPro 20
Db 3288 ATATGGAGACTGAAGAAGATGTTATGTCCTAGAAATGGATGGATCGGATGCCCT 3347
QY 21 G1yGluMeTyValLeuThrCyHisThrProGluGluAspArgIleThrTrpThrSer 40
Db 3348 GGAAGAAATGGTGGTCCCTCACCCTGACACCCCTGAAGAAGATGGATTCACCTGGACCTTG 3407
QY 41 AlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
Db 3408 GACCAGCAGCTGAGTCTTACCTCGCCAAACCCCTGACCACATCCAAAGTCAAGAGCTTT 3467
QY 61 GlyAspAlaGlyGlnTrpThrCyHisLysGlyLysValLeuSerArgSerLeuLeu 80
Db 3468 GGAAGATCGCGCCAGTACCTGTCCAAAGAGCGAGGCTTTAAGCCATTCCTCCTCG 3527
QY 81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGlu 100
Db 3528 CTGCTTCACAAAAGGAAGATGCAATTTGGTCCACTGATATTTAAAGGACCAAGAAAGAA 3587
QY 101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTySerGlyArgPheThrCys 120
Db 3588 CCCAAAATTAAGACCTTCTTAAGATGCGAGGCCAAAGATTAATCTGACGTTTCACCTG 3647
QY 121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
Db 3648 TGGGGCTGACGACAAATCAGTACGATTTGACATTCAGTGCACAAAGCAGCAGAGCCCT 3707
QY 141 SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgVal 160
Db 3708 TCTGACCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGACAGAGAGTACAGAGGG 3767
QY 161 AspAsnArgAspTrpLysLysTyThrValGluCysGlnGluLysSerAlaCysProSer 180
Db 3768 GACAAACAGAGATAT---GAGTACTCAGTGGAGTCCAGAGGAGCAGTGGCTGCCAGCT 3824
QY 181 AlaGluGluSerLeuProIleGluValValLysAlaIleHisLysLysLeuLysTyGlu 200
Db 3825 GCTGAGAGAGTGTGCCCATTTGAGTCATGTTGATGTCGCCGTTCAAGAGCTCAAGATGA 3884

QY 201 AsnTrpThrSerSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeu 220
Db 3885 AACTAACACACACACTTCTTATGAGGACATCATCAACCTGACCCCAAGAACTTG 3944
QY 221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyTrpAspThr 240
Db 3945 CAGCTGAAGCCATTAAAGAAATTCGCGAGGTGAGGACACTGGAGTACCTGCACACC 4004
QY 241 TrpSerThrProHisSerTrpPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 260
Db 4005 TGGAGTACTCCACATTCCTACTCTCTCCCTGACATTTCTGCTGAGTCCAGGCGCAAGAC 4064
QY 261 AsnArgGluLysLysAspArgLeuCysValAspLysTrpSerAlaLysValValCysHis 280
Db 4065 AAGAGAGAAAAGAAAGATAGAGTCTTCAGGACAAAGACCTGAGCAGGTATCTGGCCG 4124
QY 281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyTrpSerSerSerTrpSerAsp 300
Db 4125 AAAAATGCCACATTTACGCTGCGGGCCAGAGACGCTACTATTACCTCATCTTGGAGCGAA 4184
QY 301 TrpAlaSerValSerCysSerGlyGly-----GlyGlyGly 312
Db 4185 TGGGCATCTGTGCCCTGCAGTGTGGCGGTGGAACCGGCGGTGCCGGAAGCGGCGGTGC 4244
QY 313 GlySerArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHis 332
Db 4245 GGCAGCAGAAACCTCCCTGCGCAGCTCCACACCAGGAATGTTCCATGCTTCACCCAC 4304
QY 333 SerGlnThrLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGlu 352
Db 4305 TCCCAAAAACCTGTCAGAGCGCCGTGACGAACATGCTCCAGAGGCGCAGCAAACTGTGAA 4364
QY 353 LeuTrpSerCysTrpSerGluGlnIleAspHisGluAspIleThrLysAspLysThrSer 372
Db 4365 TTTTACCTTGTCACTTCTGAAGAATTCATCATGAATATCAACAAAGATTAACCAAGC 4424
QY 373 ThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGlnSerCysLeuAlaSerArg 392
Db 4425 ACAGTGAAGGCGCTTTTACCATTTGGAAATTAAACCAAGATAGAGATTGGCTTAATTCCGA 4484
QY 393 GlnIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThr 412
Db 4485 GAGACCTTTCATTAACTAATAGGAGTGGCTGCGCTCCAGAAAGACCTCTTTATGATG 4544
QY 413 ValLeuCysLeuSerSerIleTyrgLysAspLeuLysMetTyrgIleMetGluPheLysAla 432
Db 4545 GCCCTGTGCTTATGATGATTATTAAGAAGACTTGAAGATGTACCAAGTGGAGTGTCAAGC 4604
QY 433 MetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeu 452
Db 4605 ATGATGCGAAAGCTTTCATGATGATCTTAAGAGCGAGATCTTTTACATCAAAACATGCTG 4664
QY 453 ThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLys 472
Db 4665 GCAGTTATTGATGAGCTGATGACAGCCCTGAATTTCAACAAGTGAAGACTGCTCCCAAAA 4724
QY 473 SerSerLeuGluGluProAspPheTyrlsThrLysIleLysLysCysIleLeuLeuHis 492
Db 4725 TCCCTCCCTTGAAGAACCGGATTTTATTAACCTAAACCAAGCTCTGATACCTCTTCAT 4784
QY 493 AlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrlsLeuAsnSerSer 511
Db 4785 GCTTTCAGAAATTCGGGCGAGTACTATTGACAGAGTGAAGAGACTATCTGAATGCTTCC 4841
RESULT 5
LOCUS AR151071 990 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 11 from patent US 6231850.
ACCESSION AR151071
VERSION AR151071.1 GI:15117121
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
 1 (bases 1 to 990)
 AUTHORS Okano, F., Satoh, M. and Yamada, K.
 TITLE Canine interleukin 12
 JOURNAL Patent: US 6231850-A 11 15-MAY-2001;
 FEATURES Location/Qualifiers
 source 1..990
 BASE COUNT 279 a 244 c 249 g 218 t
 ORIGIN

Alignment Scores:
 Pred. No.: 5..2e-144 Length: 990
 Score: 1653.00 Matches: 307
 Percent Similarity: 100.00% Conservatave: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 61.38% Indels: 0
 DB: Gaps: 0

US-09-917-265-67 (1-511) x AR151071 (1-990)

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DB 67 ATATGGGAACCTGAGAAAGATGTTATGTTAGAGTGGAGCGACCCCTGATGCCCC 126
QY 21 GlyGlumetValValleuthrCysHsTrnProgluGluAspApIlleThrTrpTrser 40
DB 127 GGGAAGATGTTGCTCTCCACCTCCATCCCTCCGGAAGAGATGACATTCACCTGACCTCA 186
QY 41 AlaGlnSerSerGluValleuglYserGlyLysThrLeuThrIleGlnValLysGluPhe 60
DB 187 GCCCAGACGAGTGAAGATCCAGGTTCTGTAACCTCTGCACATCCAGTCAGCAAGCAAGATTT 246
QY 61 GlyAspAlaGlyIleThrThrCysHsLysGlyLysValleuSerArgSerLeuLeu 80
DB 247 GGAGATGCTGGCAGATACCTGCAATAAGGAGAGAGGTTCTGAGCCGCTCCTCTG 306
QY 81 LeuIleHsLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGln 100
DB 307 TTGATTCACAAAAGAGATGAGATTTGGTCCACATGATCTTAAGGAAAGCAAGAAAGAA 366
QY 101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTrpSerGlyArgPheThrCys 120
DB 367 TCCAAAATTAAGATCTTCTGAAATGAGGCAAGAAATATTCGACGTTTCAACATGC 426
QY 121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
DB 427 TGGTGGCTGACGGCAATCACTGATTTGAAATTCAGTCTCAAAAGTACAGAGCTTC 486
QY 141 SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgVal 160
DB 487 TCTGACCCCAAGGGGTGACATGTCGAGCAGTACACTTTCACAGAGAGGGTTCAGAGTG 546
QY 161 AspAsnArgAspTrpLysLysTrpThrValGluCysGlnLysSerAlaCysProSer 180
DB 547 GAAACACAGGATTAATTAAGATGACACAGTGTGAGGAGGAGGAGTCTCCCTCTCT 606
QY 181 AlaGluGlnSerLeuProIleGluValValAlaAspAlaIleHsLysLeuLysTrpGlu 200
DB 607 GCGGAGAGAGCTACCATCGAGTCTGTGTGATCTCTTTCACAAAGCTCAAGTATAGAA 666
QY 201 AsnTrpThrSerSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeu 220
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QY 221 GlnLeuLysProLeuLysAsnSerArgHsValGluValSerTrpGluTrpProAspThr 240
DB 727 CACCTGAAGCATTTGAAATTTCTCGGACAGTGTGAGTGTGAGGAAATGCCCGAGACCC 786
QY 241 TrpSerThrProHsSerTrpPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 260
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QY 261 AsnArgGluLysLysAspArgLeuCysValAspLysTrpSerAlaLysValAlcysHs 280
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QY 281 LysAspAlaLysIleArgValGlnAlaArgAspArgTrpYrsSerSerSerTrpSerAsp 300
DB 907 AAGGATGCCCAAGATCCGGCTGCACAGCCGAGACCGCTACTATAGTTCAATCTCGAGCAGC 966
QY 301 TrpAlaSerValSerCysSer 307
DB 967 TGGCATCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 987

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RESULT 6
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 LOCUS Canine mRNA for Interleukin 12 40kDa subunit, complete cds.
 DEFINITION
 ACCESSION E15017
 VERSION E15017.1 GI:5709700
 KEYWORDS JP 1998036397-A/1.
 SOURCE
 Canis sp.
 Canis sp.
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 1 (bases 1 to 990)
 Okano, F.
 CANINE INTERLEUKIN 12 AND ITS PRODUCTION
 Patent: JP 1998036397-A 1 10-FEB-1998;
 TORAY IND INC
 OS Canis sp. (dog)
 PN JP 1998036397-A/1
 PD 10-FEB-1998
 PE 08-NOV-1996 JP 1996296789
 PR 08-NOV-1995 JP 95P 289729, 23-MAY-1996 JP 96P 128104 PT
 OKANO FUMIYOSHI
 PC C07K14/54, C07H21/04, C12N5/10, C12N15/09, C12P21/02, (C12N5/10, PC
 C12R1:91)
 CC (C12P21/02, C12R1:91);
 CC strandedness: Double;
 CC topology: Linear;
 FH Key Location/Qualifiers
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 FT /organism='Canis sp.'
 FT /tissue-type='liver'
 FT 1..990
 FT CDS /product='interleukin 12 40kDa subunit'.
 FEATURES
 source 1..990
 BASE COUNT 279 a 244 c 249 g 218 t
 ORIGIN

Alignment Scores:
 Pred. No.: 5..2e-144 Length: 990
 Score: 1653.00 Matches: 307
 Percent Similarity: 100.00% Conservatave: 0
 Best Local Similarity: 100.00% Mismatches: 0
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US-09-917-265-67 (1-511) x E15017 (1-990)

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| Db | 187 | GCGCAGACAGTGAAGTCTTACGTTCTTGCTGTAAACCTCTGACCAATCCAAAGTCAAAAGATTT | 246 |
| Oy | 61 | GIyspAlaGIyGlnTyrThrCysHisLysGlyGlyLysValLeuSerArgSerLeuLeu | 80 |
| Db | 247 | GGACATGCTGGCCAGTATATACCTGCCATTAAGACGACGAAGCTTGAGCCCTCCTCCTG | 306 |
| Oy | 81 | LeuIleHisLysLysGlnAspGlyValTyrPheSerThrAspIleLeuLysGlnLysGln | 100 |
| Db | 307 | TTTGATTCCACAAAAAGAAAGATGCAATTGGTCCACTGATATCTTAAAGGAACACAAAGAA | 366 |
| Oy | 101 | SerLysAsnLysIlePheLeuLysCysGlnLalaLysAsnTyrSerGlyArgPheThrCys | 120 |
| Db | 367 | TCCAAAATAATGAATCTTTCTTGAAATGTGACGCAAAAGATTATTCCTGGACGTTTCACATGC | 426 |
| Oy | 121 | TTPHrPheLthrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe | 140 |
| Db | 427 | TGCTGGCTGACGGCAATCAGTACGATGATTGAAATTCACTGTCACAAAGTAGCAGAGCTTC | 486 |
| Oy | 141 | SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgVal | 160 |
| Db | 487 | TCTACACCCCAAGGGGTGACATGTCGACACACTGACACTTCCACAGAAAGCGTCAGAGTG | 546 |
| Oy | 161 | AspAsnArgAspTyrLysLysTyrThrValGlnLysGlnLysLysSerAlaCysProSer | 180 |
| Db | 547 | GACAAACAGGGGTTTATTAAGAACTACACAGTGAAGTCAAGGAGGCGAGTCCCTGCCCTCT | 606 |
| Oy | 181 | AlaGlnLysSerLeuPheProGlnGlyValValAlaAlaIleHisLysLeuLysTyrGln | 200 |
| Db | 607 | GCCGACGACAGACCTACCCATCGAGTCTCGTGGATGCTATTCCAAAGCTCAAGTATGAA | 666 |
| Oy | 201 | AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPheThrAsnLeu | 220 |
| Db | 667 | AACTAACACACACACTCTTCTCATCAGACATCATCAACACAGACCCACCAAACTCTG | 726 |
| Oy | 221 | GlnLeuLysProLeuLysAsnSerArgHisValGlnValSerTTPGlnTyrProAspThr | 240 |
| Db | 727 | CAGCTGAAGCCATTGAAAAATTCTCCGGCACCTGAGGTGACCTGGGAATTACCCGACACC | 786 |
| Oy | 241 | TTPSerThrProHisSerTyrPheSerLeuThrPheCysLleGlnAlaGlnGlyLysAsn | 260 |
| Db | 787 | TGGAGCACCCACATTTCTTCTTCTCTCTGACATTTTGCATACAGGCCACAGGCGCAAGAAC | 846 |
| Oy | 261 | AsnArgGlnLysLysAspArgLeuCysValAspLysThrSerAlaLysValLysHis | 280 |
| Db | 847 | AATGAGAGAAAGAAAGATAGACTCTCGCTGGACAAGACCTCAGCCAAAGCTCGTGCCAC | 906 |
| Oy | 281 | LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTyrSerAsp | 300 |
| Db | 907 | AAGGATGCCAAGATCCCGGTGCAAGCCGAGACCGCTACTATAGTTTCCTCTGAGAGCGAC | 966 |
| Oy | 301 | TTPAlaSerValSerCysSer | 307 |
| Db | 967 | TGGGCATCTGTCCTCTGCAGT | 987 |
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| LOCUS | CFU49100 | 1015 bp | mRNA linear MAM 13-MAR-1996 |
| DEFINITION | Canis familiaris interleukin-12 p40 subunit mRNA, complete cds. | | |
| ACCESSION | U49100 | | |
| VERSION | 049100.1 | GI:1223907 | |
| KEYWORDS | | | |
| SOURCE | | | |
| ORGANISM | Canis familiaris. Canis familiaris Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis. | | |
| REFERENCE | | | |
| AUTHORS | 1 (bases 1 to 1015) Belke-Louis, G.F. and Buettnier, M. | | |
| TITLE | Cloning and sequence analysis of the p35 and p40 subunits of canine interleukin-12 | | |
| JOURNAL | Unpublished | | |
| REFERENCE | 2 (bases 1 to 1015) | | |
| AUTHORS | Belke-Louis, G.F. | | |
| TITLE | Direct Submission | | |

| JOURNAL | Submitted (13-FEB-1996) Georg F. Belke-Louis, Institute of Med. Microbiology, Veterinärstr. 13, Muenchen, D-80539, Germany |
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| FEATURES | Location/Qualifiers |
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| | /organism="Canis familiaris" |
| | /db_xref="taxon:9615" |
| CDS | 1..990 |
| | /codon_start=1 |
| | /product="Interleukin-12 p40 subunit" |
| | /protein_id="AA92059.1" |
| | /db_xref="GI:1223908" |
| | /translation="MHPQQLVSWFSLVILASSLMTIMLEKDYVVEIDMHPDAGNVLTCHPTEEDDITWTSQSSSEVLGSGTTLTYKEPEDAQDYTHKGKYLRSLLIHKEDEGIWSTDLKEOKESKNKIFLKEAANYSGRFQWMLTALSTDLKSVKSSGSDPGVGCAGVATVLAERVRVNDNRDYLKYTYVECGSGSPSAEESLPIEVVDALHLYKENTSSFFRIDIIKPPDNPVLIQKTPLNKRHRHVEVMEYPTWETPSYSFLTPCQAOGKNRHKRRLICVDKPSAKVNLGKDKATIVQARDRIYSSWSMDMASVCS" |
| BASE COUNT | 285 a 251 c 254 g 225 t |
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| Pred. No.: | 6, 67e-144 |
| Score: | 1652.00 |
| Percent Similarity: | 100.00% |
| Best Local Similarity: | 99.67% |
| Query Match: | 61.34% |
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| US-09-917-265-67 (1-511) x CFU49100 (1-1015) | |
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| QY | 21 GYGLUMETVALLEUTHRCYSHISTHPRROGLUGLASPASPILEHTRPTTHRSER 40 |
| DB | 127 GGAGAAATGGTGCTCTCCACCTGCACCTATACCCTTGAAAGAAATGACATCACTTGAGACCTCA 186 |
| QY | 41 AAGINSERSEGLVALLEUGLYSERGLVYSTHLEUTHRLIEGINVALVSGIUPHE 60 |
| DB | 187 GCGCAGAGCAGTGAACCTCTAGGTTCTGGTAAACCTGACCTCCAAAGTCAAGTCAAGAAATTT 246 |
| QY | 61 GIYASPALAGLGLNTHRCYSHISLYSGIYLYVALLEUSERARGSERLEULEU 80 |
| DB | 247 GGAGATGCTGGCGCAGATACCTGCACTTAAGAGGACGAGGTCTGAGCCGCTCATCTCTG 306 |
| QY | 81 LEULIEHISLYSGIUSPGLIETTPSERTHASPILEULEULSGIUGIINLYGLU 100 |
| DB | 307 TTGATTTACAAAAAGAAAGATGGAATTTGGTCCACATGATATCTTAAAGGACAGAAAGAA 366 |
| QY | 101 SERLYSASPLYSILPEHEULYSCYSGIUALALYASPTYSERGIYARQPHETRCYS 120 |
| DB | 367 TCCAAAAATAAATCTTTCTGAAATGTGAGGCAAGAAATTAATTCGTGACGTTTCAACATGC 426 |
| QY | 121 TPTTPLEUTHALALESERTHRSAPLEULYSPHESERVALYSSERSEARGIYLPE 140 |
| DB | 427 TGGTGCGTACGGCAATCAGTACTGATTTGAAATTCAGTGCATAAAGTATGACAGGCTTC 486 |
| QY | 141 SERASPPROGLINGLYVALTHRCYSGIYALVALTHLEUSERALAGIULARYVAL 160 |
| DB | 487 TCTGACCCCCCAAGGGGTGACATGTGGAGCAGTGCACCTTTCAGCAGAGGGGTCAAGATG 546 |
| QY | 161 ASPASPARASPTLYSTLYSTYTRTHRVALLIGUCYSGIUGLYSERLACYSPROSER 180 |
| DB | 547 GACAAACAGGATTTATPAGAAATACACAGTGGAGTGCAGAGAACGCACTGCTGCCCTCT 606 |
| QY | 181 ALAIGLUGLISERLEUPROGLEUVALVALVALASPALAILHISLYSLEULYSTYRGLU 200 |
| DB | 607 GCGGAGAGAGAGCTTACCCATCGACAGTGGTGGTGGATTCGATTCACAAAGCTCAAGTATGAA 666 |
| QY | 201 ASNTYTRTHRSERPHETHELEARSPILIELLYSPROASPPROPTHASLEU 220 |
| DB | 667 AACTCACACAGAGCTTTCTTCAATCAGAGATCATCAACACAGACCCACACCAAACTCG 726 |

QY 221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTrpProAspThr 240
 DB 727 CAGCTAAGCCATTGAAAAATTTCTGGCAGCTGGAGTGCAGCTGGAGAAATACCCGACACC 786
 QY 241 TrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 260
 DB 787 TGGAGCACCACCATTCTCTCTCTCCGACATTTTGGCTACGAGCCGACGAGCAAGAAC 846
 QY 261 AsnArgGluLysLysAspArgLeuGlyValAspLysThrSerAlaLysValAlaGlyHis 280
 DB 847 AATAGCAAAAGAAATAGACTCTGCTGGACAAAGACTCAGCCAAAGTCTGTCTCCAC 906
 QY 281 LysAspAlaLysIleArgValGlnAlaAArgAspArgTyrTyrSerSerSerTrpSerAsp 300
 DB 907 AAGGATGCCAAGATCCGCGTGCAGAACGCCGAGACCGCTACTAGTTCATCTCTGAGCAGC 966
 QY 301 TrpAlaSerValSerCysSer 307
 DB 967 TGGGCATCTGTCTCTGACAGT 987

RESULT 8
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 LOCUS Sequence 1 from patent US 6231850.
 ACCESSION ARI51061
 VERSION ARI51061.1 GI:15117111
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 990)
 AUTHORS Okano, F., Satoh, M. and Yamada, K.
 TITLE Canine interleukin 12
 JOURNAL Patent: US 6231850-A 1 15-MAY-2001;
 FEATURES
 source location/Qualifiers
 1..990
 BASE COUNT 278 a 243 c 251 g 218 t
 ORIGIN

Alignment Scores:
 Pred. No.: 8 36e-143 length: 990
 Score: 1640.00 matches: 304
 Percent Similarity: 99.67% Conservative: 2
 Best Local Similarity: 99.02% Mismatches: 1
 Query Match: 60.90% Indels: 0
 DB: Gaps: 0

US-09-917-265-67 (1-511) x ARI51061 (1-990)

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 QY 41 AlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
 DB 187 GCCCAGAGCAGTGAAGCTCCTAGTCTGTGTAACCTCTGACCATCCAAAGTCAAGATTT 246
 DB 247 GGAGATGCTGGCAGTATACCTGCATTAAGAGGCAAGGTCTGAGCCGCTCAGCTCTG 306
 QY 61 GlyAspAlaGlyGlnTyrThrCysHisLysGlyGlyLysValLeuSerArgSerLeuLeu 80
 DB 247 GGAGATGCTGGCAGTATACCTGCATTAAGAGGCAAGGTCTGAGCCGCTCAGCTCTG 306
 QY 81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGlu 100
 DB 307 TTGATTCACAAAAAAGATGAATTTGCTCCACTGATATCTTAAAGGAACAGAAAGAA 366
 QY 101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120

DB 367 TCCAAAAATAGACTTTCTGAAATGTCAGCAAGAAATATTCTGACGTTTCACATGC 426
 QY 121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerArgGlyPhe 140
 DB 427 TGTGTGCTGACGCGAATGATGCTACTGATTGAAATTCAGTGTCAAAAGTGCAGAGGCTTC 486
 QY 141 SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValAla 160
 DB 487 TCTGACCCCAAGGCGTGCATGTCGACGAGCAGACACTTTCAGCAGAGAGGCTCAGAGTG 546
 QY 161 AspAsnArgAspTyrLysLysTyrThrValGluGlyGlnGlySerAlaCysProSer 180
 DB 547 GACACAGGAGATTATAGAAATGACAGTGCAGTGCAGAGAGGCAAGTCTGCTCTCT 606
 QY 181 AlaGluGluSerLeuProIleGluValValAspAlaIleHisLysLeuLysTyrGlu 200
 DB 607 GCCGAGAGAGGCTTACCATCGAGTGGTGGTGGATGCTATTACAAAGCTCAAGTATGAA 666
 QY 201 AsnTyrThrSerSerPheIleArgAspIleIleLysProAspProThrAsnLeu 220
 DB 667 AACTACACGACAGCTTCTTCATCAGACATCATCAAAACAGACCCACCAAAACCTG 726
 QY 221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTrpProAspThr 240
 DB 727 CAGCTAAGCCATTGAAAAATTTCTGGCAGCTGGAGTGCAGCTGGAGAAATACCCGACACC 786
 QY 241 TrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 260
 DB 787 TGGAGCACCACCATTCTCTCTCTCCGACATTTTGGCTACGAGCCGACGAGCAAGAAC 846
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 DB 847 AATAGCAAAAGAAATAGACTCTGCTGGACAAAGACTCAGCCAAAGTCTGTGCTCCAC 906
 QY 281 LysAspAlaLysIleArgValGlnAlaAArgAspArgTyrTyrSerSerSerTrpSerAsp 300
 DB 907 AAGGATGCCAAGATCCGCGTGCAGAACGCCGAGACCGCTACTAGTTCATCTCTGAGCAGC 966
 QY 301 TrpAlaSerValSerCysSer 307
 DB 967 TGGGCATCTGTCTCTGACAGT 987

RESULT 9
 AF411293 1669 bp mRNA linear SYN 10-SEP-2001
 LOCUS Synthetic construct bioactive single-chain murine interleukin 12
 DEFINITION mRNA, complete cds.
 ACCESSION AF411293
 VERSION AF411293.1 GI:15529754
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE 1 (bases 1 to 1669)
 AUTHORS Jiang, C., Magee, D.M. and Cox, R.A.
 TITLE Construction of a single-chain interleukin-12-expressing retroviral vector and its application in cytokine gene therapy against experimental coccidioidomycosis
 JOURNAL Infect. Immun. 67 (6), 2996-3001 (1999)
 MEDLINE 99270963
 PUBMED 10338510
 REFERENCE 2 (bases 1 to 1669)
 AUTHORS Jiang, C., Magee, D.M. and Cox, R.A.
 TITLE Co-administration of interleukin 12 expression vector with antigen 2 CDNA enhances induction of protective immunity against *Coccidioides immitis*
 JOURNAL Infect. Immun. 67 (11), 5848-5853 (1999)
 MEDLINE 20002565
 PUBMED 10531239
 REFERENCE 3 (bases 1 to 1669)
 AUTHORS Jiang, C., Magee, D.M. and Cox, R.A.
 TITLE Direct Submission
 JOURNAL Submitted (17-AUG-2001) Microbiology, University of Health Science

Center at San Antonio, 15355 Lambda Drive, San Antonio, TX
78245-3027, USA

FEATURES

Location/Qualifiers
1..1669

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17..1648
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CDS

BASE COUNT

459 a 429 c 434 g 347 t

ORIGIN

Alignment Scores:

Pred. No.: 5.61e-140 Length: 1669
Score: 1613.00 Matches: 319
Percent Similarity: 72.64% Conservative: 66
Best Local Similarity: 60.19% Mismatches: 117
Query Match: 59.90% Indels: 28
DB: 12 Gaps: 6

US-09-917-265-67 (1-511) x AF411293 (1-1669)

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QY 21 GLYLUMELVALVLEUThrCysHisThrProGluGluuAspAspIleThrTrpThrSer 40
Db 143 GGAGAACAGTGAACCTGACCTGTGACACGCCCTGAGAGAGATGATACCTGGAGCTCA 202
QY 41 AlaInserSerGluValLEUgluSerGlyLysThrLeuThrIleGlnValLysGluPhe 60
Db 203 GACCAAGACATGGAGATATAGGCTGTGAAAGACCCGACCATCATCTGTAAGAGATT 262
QY 61 GLYASPAAGIYNTYrThCysHisLysGlyLysValLysSerArgSerLeuLeu 80
Db 263 CTGATGCTGCGCCAGTACCTGCCACAAAGAGCGGAGCTGTGAGCACTCATCTTG 322
QY 81 LeuIleHisLysLysGluuAspGlyIleTrpSerThrAspIleLeuLysGluLysGlu 100
Db 323 CTGCTCCACAAAGAGAAATGATGTGTGCTCCACTGAAATTTTA-----AAAAT 373
QY 101 SerLysnLysIlePheLeuLysCysGluValLysanLysanLysSerGlyArgPheThCys 120
Db 374 TTCAAAACAAAGACTTTCTGTAAGTGAAGCACCAAAATTACTCGGAGCGTTGACGTGC 433
QY 121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
Db 434 TCATGGCTGCTGCCAAAGACATGACCTTGAAGTTCAACATCAAGAGAGTACAGCACTGCC 493
QY 141 SerAspProGlnGlyValIleThrCysGlyAlaValIleThrLeuSerAlaGluValArgVal 160
Db 494 CCCAGCTCTCGGAGACATGTGCAATGGCGTCTCTGTGTCAGAGAAAGTCAACACTG 553
QY 161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProSer 180
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 DEFINITION Sequence 1 from Patent WO0104155.
 ACCESSION AX076200
 VERSION AX076200.1 GI:12710825
 KEYWORDS
 SOURCE
 ORGANISM
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 synthetic construct.
 synthetic construct
 artificial sequences.
 REFERENCE
 AUTHORS Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittlig,B.
 TITLE Peptide Interleukin-12 as an Immune Stimulant
 JOURNAL Patent: WO 0104155-A 1 18-Jan-2001;

FEATURES
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 Score: 1554.00 Matches: 288
 Percent Similarity: 96.74% Conservative: 9
 Best Local Similarity: 93.81% Mismatches: 10
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 QY 21 G1yG1uMetVal1a1leUeUThrCysH1sThrProG1nG1yUaSpAsp1leThrTrpTrSer 40
 Db 127 GGAGAAATGGTGGTCTTACTGCATATCTCTGAAGAAGATGACATACCTGGAGCTCT 186
 QY 41 AlaG1nSerSerG1uVal1leUg1ySerG1yLysThrLeuThr1leG1nVal1ySg1uPhe 60
 Db 187 GACCAGACAGCATGAAGTCTAGCGTCTGTAAACTGTGACCATTCAGTCAAGTCAAGAATTT 246
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 QY 81 Leu1eH1s1yS1ySg1yUaSpG1y1LeTrrSerThrAsp1leUeUySg1Ug1n1ySg1U 100
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| Db | 847 | AACGAGAAAAAGAAAGACAGACTCTCCGTGGACAAAGACCTCAGCCAAAGCTGTGTCCAC | 906 |
| QY | 281 | LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsp | 300 |
| Db | 907 | AAGGATGCCAAAGATCCGCTGGCAAGCGACCGCTACTATAGCTCATCTCGAGACAAAC | 966 |
| QY | 301 | TrpAlaSerValSerCysSer | 307 |
| Db | 967 | TGGGCATCCGTCTCTGCACT | 987 |
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| AX076482 | | | |
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| DEFINITION | Sequence 8 from Patent WO0104280. | | linear |
| ACCESSION | AX076482 | | |
| VERSION | AX076482.1 | GI:12711034 | |
| KEYWORDS | | | |
| SOURCE | | | |
| ORGANISM | | | |
| REFERENCE | | | |
| AUTHORS | | | |
| TITLE | | | |
| JOURNAL | | | |
| FEATURES | | | |
| source | | | |
| BASE COUNT | 283 a | 249 c | 248 g |
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| Best Local Similarity: | 93.81% | Mismatches: | 10 |
| Query Match: | 57.71% | Indels: | 0 |
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| QY | 21 | GlyLueIleValIleLeuThrCysHisThrProGluGluAspIleThrTrpTrpSer | 40 |
| Db | 127 | GGAAATATGGTGGCTTACCTGCATACCTCTCGAAGAAGATGACATCAGCTGAGACTCT | 186 |
| QY | 41 | AlaGlnSerSerGluValIleLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe | 60 |
| Db | 187 | GACCAAGCGAGTGAAGTCTAGGCTCTGTGTAACCTGCATCCATCCAAAGCAATTT | 246 |
| QY | 61 | GlyAspAlaGlnGlnTyrThrCysHisLysGlyGlyLysValLeuSerArgSerLeuLeu | 80 |
| Db | 247 | GCAAGATCTGCGCAGTATACCTGTCAATAAGGAGGAGGAGTTCGAGCCATTCGTTCC | 306 |
| QY | 81 | LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGlu | 100 |
| Db | 307 | CTGATACACAAAAAGAAAGATGAATTTGGTCCATCATGATATCTTAAGGACAGAAAGAA | 366 |
| QY | 101 | SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys | 120 |
| Db | 367 | TCCAAAAATAGATCTTTCTAAATGTGAGGCGAAAGAAATTAATCTGAGCGTTTCACTGC | 426 |
| QY | 121 | TrpIlePheThrIleIleSerThrAspLeuLysPheSerValLysSerArgGlyPhe | 140 |
| Db | 427 | TGTTGGCTGACGGCAATCACTACCGATTTGAAATTCATGTCTCAAAAGCAGCAGAGCTCC | 488 |
| QY | 141 | SerAspProGlnGlyValIleThrCysGlyAlaValIleThrLeuSerAlaGlnArgValArg | 160 |
| Db | 487 | TCTGACCCCCCAAGGGGGTGGACTTGTGGAGCGCACACTCTCAGCAGAGAGGTCTGAGAG | 546 |
| QY | 161 | AspAsnArgAspTyrLysLysTyrThrValGlnCysGlnGlnGlySerIleLysProSer | 180 |
| Db | 547 | GACAAACAGGGATTTTAAAGAGTACACAGTGGAGTGTGAGAGGCGAGTCTGCGCCGCT | 606 |
| QY | 181 | AlaGlnLysSerLeuProIleGlnValValIleAlaLysAlaIleHisLysLeuLysTyrGlu | 200 |
| Db | 607 | GCCAGAGAGACCTACCATTTGAAGTGTGTGTGAGCAGTATTCACAAAGCTCAAGTACGAA | 666 |
| QY | 201 | AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeu | 220 |
| Db | 667 | AACATCACCGACAGCTTCTTCATCAGGAGCATCATCAACCGACCCCAAGAAACCTG | 726 |
| QY | 221 | GlnLeuLysProLeuLysAsnSerArgHisValGlnValSerTrpGlnLysTrpAspThr | 240 |
| Db | 727 | CAACTGAAGCCATTAAAAAATTCCTCGCATGTGGAAGTACGCGGGAATACCTTCACACC | 786 |
| QY | 241 | TrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnLysLysAsn | 260 |
| Db | 787 | TGGAGACACCCACATCT | 846 |
| QY | 261 | AsnArgLysLysAspArgLeuLysValAspLysThrSerAlaLysValCysHis | 280 |
| Db | 847 | AACAGAGAAAAAGAAAGACAGACTCTCCGTGGACAAAGCTCAGCCAAAGCTGTGTCCAC | 906 |
| QY | 281 | LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsp | 300 |
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| QY | 301 | TrpAlaSerValSerCysSer | 307 |
| Db | 967 | TGGGCATCCGTCTCTGCACT | 987 |
| RESULT 14 | | | |
| FCU83184 | | | |
| LOCUS | FCU83184 | 990 bp | mRNA |
| DEFINITION | Felis catus Interleukin-12 p40 subunit (IL-12) mRNA, complete cds. | | |
| ACCESSION | U83184 | | |
| VERSION | U83184.1 | GI:2735050 | |
| KEYWORDS | | | |
| SOURCE | | | |
| ORGANISM | | | |
| Felis catus. | | | |
| Felis catus | | | |
| Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis. | | | |
| REFERENCE | | | |
| AUTHORS | | | |
| TITLE | | | |
| JOURNAL | | | |
| MEDLINE | | | |
| PUBMED | | | |
| 9522125 | | | |
| 2 (bases 1 to 990) | | | |
| Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W., | | | |
| Pedersen,N.C. and Lutz,H. | | | |
| Nucleotide and predicted peptide sequence of feline interleukin-12 | | | |
| (IL-12) | | | |
| DNA Seq. 8 (1-2), 77-82 (1997) | | | |
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BASE COUNT      283 a      251 c      249 g      207 t
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Score:          1552.00      Matches:      288
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Query Match:    57.63%      Indels:      0
DB:             4      Gaps:      0

US-09-917-265-67 (1-511) x FCU83184 (1-990)

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QY      21  GYGLUWELVALLEUTHRCYSHISTHPRGUGLUASPAPIETHTRTPHISER 40
      127  GGAGAAATGCTGGTCCCTCACCTGTGACACCCCTGAACAGATGACATCAGCTGACCTCT 186
QY      41  AIGLINSERGLUVALLEUGLYSERGLYLYSTRLEUTHRIEGLIVALLYSLUHPHE 60
      187  GACCAAGACAGTGAAGCTTAGCTGTGTAACAACTGACCAATCAAGCAAGAAATT 246
QY      61  GLYASPALAGLYINTYRTHRCYSHISLYSGLYGLYLYSVALLEUSERARGSERLEUEN 80
      247  GCAGATCTGCTGCCAGTACTGTCATMAAGAGGCGAGGTTCTGACCATTCCTCTCCTC 306
QY      81  LEULIETHISLYSLYSGLUASPGIYLIETRPSERTHASPILIEULYSGLUGLULYSGLU 100
      307  CTGATACACAAAAGAGATGATGATTCCTCCATGATATCTTAAGGAGAAAGAAAGAA 366
QY      101  SERLYASNLYSILIEPELEULYSGYGLVALYASANTYRSEGLYARGPHETHCYS 120
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QY      121  TTRTPLEUTHRALALIESERTHASPULYSHESERVALLYSSERTSERARGLYPHE 140
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QY      301  TRPALASERVALSERCYSSER 307
      967  TGGCATCTGCTGCTGACACT 987
DB

RESULT 15
LOCUS   FCIL12P40      1006 bp      mRNA      Linear      MAM 13-MAY-1997
DEFINITION F.catus mRNA for interleukin-12 p40 chain.
ACCESSION Y07762
VERSION   Y07762.1 GI:2102664
KEYWORDS  interleukin-12 p40.
SOURCE    cat.
ORGANISM  Fells catus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Fells.
REFERENCE 1 (bases 1 to 1006)
AUTHORS   Schjins,V.E., Wierda,C.M., Vahlenkamp,T.W. and Horzinek,M.C.
TITLE     Molecular cloning of cat interleukin-12
JOURNAL   Immunogenetics 45 (6), 462-463 (1997)
MEDLINE   97246745
PUBMED    9089110
REFERENCE 2 (bases 1 to 1006)
AUTHORS   Schjins,V.E.C.J.
TITLE     Direct Submission
JOURNAL   Submitted (03-SEP-1996) V.E.C.J. Schjins, Virology Division,
           Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL
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ORIGIN

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Score:          1546.00      Matches:      287
Percent Similarity: 96.42%      Conservative: 9
Best Local Similarity: 93.49%      Mismatches: 11
Query Match:    57.41%      Indels:      0
DB:             4      Gaps:      0

US-09-917-265-67 (1-511) x FCIL12P40 (1-1006)

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OY 21 GlyMetValValLeuThrcYshThrProGluAspPheThrTrpThrSer 40
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DB 127 GGAGAAATGGTGTCTCTACCTGCACATCTCTGAGAGAGATGACATCACTGGACCTCT 186
    |||
OY 41 AlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
    |||
DB 187 GACCGAGCAGCAGTGAAGCTCTAGGCTCTGTGTAACCTGTGACCATCTCAAGTCAAGAAATTT 246
    |||
OY 61 GlyAspAlaGlyGlnTyrThrCysHisLysGlyLysValLeuSerArgSerLeu 80
    |||
DB 247 GCAGATGCTGGCCAGTATACCTGTATAAAGGAGCGAGGTTCTGAGCCATTCTGCTCC 306
    |||
OY 81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGlu 100
    |||
DB 307 CTGATACACAAAAAGAGATGGAATTGGTCTCCTGATATCTTAAGGAAACAGAAAGAA 366
    |||
OY 101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
    |||
DB 367 TCCAAAATTAAGATCTTCTTAATAATGTGAGCAAAAGAAATTAATCTGACGTTTCACCTGC 426
    |||
OY 121 TrpTrpLeuThrAlaIleSerThrAspLysPheSerValLysSerSerArgGlyPhe 140
    |||
DB 427 TGGTGGCTGACGGCATAGTACCATTTGAAATTCACGTCAAAAGCAGCAGAGGCTCC 486
    |||
OY 141 SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgVal 160
    |||
DB 487 TCTGACCCCAAGAGAGTGACTGTGTGAGAGCGACACACTCTCAGCAGAGAGAGTCAAGTGT 546
    |||
OY 161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGlySerAlaCysProSer 180
    |||
DB 547 GACAACAGGAGATTATAGAAAGTACACAGTGAAGTGTGAGAGGAGGAGTCCGCCGGCT 606
    |||
OY 181 AlaGluGlnSerLeuProIleGluValValAlaAspAlaIleHisLysLeuLysTyrGlu 200
    |||
DB 607 GCCGAGGAGAGCGCTTACCCATTGAAAGTGTGAGAGCTTATTCACAGACTCAAGTACGAA 666
    |||
OY 201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProThrAsnLeu 220
    |||
DB 667 AACTACACAGCAGCGTCTTCAATCAGGAGCATCATCAACCGAGCCCAAGAACCTG 726
    |||
OY 221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
    |||
DB 727 CAACGTAAGCCATTGAAAAATTCGCGCATGTGGAAGTGAAGGGAATACCCCTGCACCC 786
    |||
OY 241 TrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnLysLysAsn 260
    |||
DB 787 TGGAGACACCCCATTCCTACTTCTCTTAACATTGGCGTACAGGTCACAGGCAAGAAC 846
    |||
OY 261 AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValValCysHis 280
    |||
DB 847 AACAGAGAAAGAAAGACAGACTCTCGTGACAAAGACCTCAAGCTCGTGTGCCAC 906
    |||
OY 281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsp 300
    |||
DB 907 AAGGATGCCAAGATCCGCTGCAAGCCAGACAGCGCTACTATAGCTCATCTGAGACAAAC 966
    |||
OY 301 TrpAlaSerValSerCysSer 307
    |||
DB 967 TGGGCATCCGTCCTGCACT 987
    |||
```

Search completed: July 17, 2003, 06:41:11
Job time : 4585.08 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: July 16, 2003, 13:41:48 ; Search time 361.279 Seconds
(without alignments)
3185.273 Million cell updates/sec

Title: US-09-917-265-67
Perfect score: 2693
Sequence: 1 IWELEKDVYVELDHMPDAP.....HAFRIRAVTINRMSTYLNSS 511

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=xlh
-Q=/c9q2_1/USTO.spool/US09917265/r/unat_15072003_092106_1592/app.query.fasta.1.3114
-DB=N.Lceneseq.101002 -QEMT=fastlap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosun62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTEMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N.Geneseq.101002.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|--------------|---------------------|
| 1 | 2309.5 | 85.8 | 6139 | 21 AA240023 | Interleukin-12 fus |
| 2 | 2309 | 85.7 | 8608 | 24 AAD31548 | PIRES-hb7-1-IL12.2 |
| 3 | 2309 | 85.7 | 8629 | 24 AAD31552 | PIRES-IL12.2-hb7-1 |
| 4 | 2306.5 | 85.6 | 8623 | 24 AAD31547 | PIRES-hb7-1-IL12.3 |
| 5 | 2306.5 | 85.6 | 8644 | 24 AAD31551 | PIRES-IL12.3-hb7-1 |
| 6 | 2304 | 85.6 | 8638 | 24 AAD31549 | PIRES-hb7-1-IL12.4 |
| 7 | 2304 | 85.6 | 8659 | 24 AAD31550 | PIRES-IL12.4-hb7-1 |
| 8 | 2275 | 84.5 | 8578 | 24 AAD31545 | PIRES-hb7-1-IL12.1 |
| 9 | 2275 | 84.5 | 8578 | 24 AAD31546 | PIRES-hb7-1-IL12.0 |
| 10 | 1653 | 61.4 | 990 | 19 AAV13817 | Canine IL-12 p40 s |
| 11 | 1653 | 61.4 | 990 | 20 AAX35625 | Nucleic acid encod |
| 12 | 1653 | 61.4 | 990 | 20 AAX03162 | Nucleic acid encod |
| 13 | 1653 | 61.4 | 990 | 22 AAI64388 | Canine coding sequ |
| 14 | 1644 | 61.0 | 990 | 19 AAV13816 | Canine IL-12 p40 s |
| 15 | 1644 | 61.0 | 990 | 20 AAX35615 | Nucleic acid encod |
| 16 | 1644 | 61.0 | 990 | 20 AAX03152 | Nucleic acid encod |
| 17 | 1644 | 61.0 | 990 | 22 AAI64378 | Canine coding sequ |
| 18 | 1618.5 | 60.1 | 924 | 20 AAX18177 | Canine mature CLAF |
| 19 | 1618.5 | 60.1 | 2154 | 20 AAX18176 | Canine full length |
| 20 | 1555 | 57.7 | 4522 | 22 AAF26076 | Feline IL-12p40 en |
| 21 | 1555 | 57.7 | 4522 | 22 AAF26094 | plasmid pMOI-f1112 |
| 22 | 1554 | 57.7 | 921 | 19 AAV56626 | Feline FLARPp40 cDN |
| 23 | 1554 | 57.7 | 921 | 19 AAV56627 | Feline FLARPp40 cDN |
| 24 | 1554 | 57.7 | 990 | 22 AAF26082 | Feline IL-12p40 en |
| 25 | 1554 | 57.7 | 990 | 22 AAF26085 | Feline IL-12p40 en |
| 26 | 1554 | 57.7 | 2193 | 19 AAV56625 | Feline FLARPp40 cDN |
| 27 | 1484 | 55.1 | 990 | 22 AAD15209 | Modified human cyt |
| 28 | 1451 | 53.9 | 984 | 22 AAD15206 | Modified human cyt |
| 29 | 1431 | 53.1 | 1389 | 22 AAF76880 | Human p40-IL-2 cod |
| 30 | 1429 | 53.1 | 984 | 22 AAD15205 | Modified human cyt |
| 31 | 1421.5 | 52.8 | 5686 | 20 AAZ40415 | Plasmid pIN1143 co |
| 32 | 1421 | 52.7 | 984 | 22 AAV815204 | Modified human cyt |
| 33 | 1419.5 | 52.7 | 987 | 20 AAV813199 | Interleukin (IL)-1 |
| 34 | 1418.5 | 52.7 | 987 | 16 AAG97464 | Human Interleukin- |
| 35 | 1418.5 | 52.7 | 987 | 19 AAV07273 | Human Interleukin- |
| 36 | 1418.5 | 52.7 | 987 | 19 AAV07217 | DNA encoding human |
| 37 | 1418.5 | 52.7 | 987 | 20 AAZ40404 | Human Interleukin |
| 38 | 1418.5 | 52.7 | 987 | 20 AAZ40405 | Human Interleukin |
| 39 | 1418.5 | 52.7 | 987 | 20 AAZ40406 | Human Interleukin |
| 40 | 1418.5 | 52.7 | 987 | 22 AAD15210 | Human cytokine p40 |
| 41 | 1418.5 | 52.7 | 1007 | 22 AAD18585 | Human Interleukin- |
| 42 | 1418.5 | 52.7 | 1018 | 15 AAO67879 | EPV 42 kD promoter |
| 43 | 1418.5 | 52.7 | 1018 | 20 AAO67879 | EPV 42 kD/human I |
| 44 | 1418.5 | 52.7 | 1397 | 18 AAV00401 | 40 kDa subunit of |
| 45 | 1418.5 | 52.7 | 1397 | 18 AAT77849 | 40 kDa subunit of |

ALIGNMENTS

RESULT 1
AA240023
AA240023 standard; DNA; 6139 BP.
AC AA240023:
XX
XX
DT 14-FEB-2000 (first entry)
XX
XX DE Interleukin-12 fusion protein, Flex1-12, coding sequence.
XX
XX KW Interleukin-12; IL-12; fusion protein; IL-12 p35 subunit; B7 protein;
XX IL-12 p40 subunit; gene therapy; leukemia; Flex1-12; ss.
XX
XX OS Synthetic.
XX Homo sapiens.
XX
XX US5994104-A.
XX


```

Oy 453 ThrAlaIleasPgluleuLeuGlAlaIleuAsnPhaenSerValThrValProClnlys 472
    |||||
Db 4665 GCACTTATGATGAGCTGATCATGAGCCCTGCAATTTCAACAGTGAAGCTGTGCCACAAAA 4724
Oy 473 SerSerLeuGlucIuProAspPheTyrLysThrLysIleLysCysIleleuLeuHis 492
    |||||
Db 4725 TCTTCCTTGAAGAACCGCATTTTATTAACATAAATCAAGCTCTGCATCTCTTCAT 4784
Oy 493 AlaPheArGileArGAlaValThrIleAsnArgMetCetSerTyrLeuAsnSerSer 511
    |||||
Db 4785 GCTTCAGAAATTCGGCGAGTACTATTCACAGAGTACAGACTATCTGTAATGCTTCC 4841

RESULT 2
AAD31548
ID AAD31548 standard; DNA: 8608 BP.
AC AAD31548;
XX
XX 18-JUN-2002 (first entry)
XX
XX PIRRES-hb7-1-IL12.2 vector DNA.
XX
XX Expression system; interleukin-12; cancer therapy; cellular vaccine;
KW immunotherapeutic response; IL-12.2; chimeric; human; Simian virus 40;
KW SV40; cytomegalovirus; CMV; ds.
XX
XX Chimeric - Cytomegalovirus.
OS Chimeric - Bacteriophage T7.
OS Chimeric - Homo sapiens.
OS Chimeric - Bacteriophage T3.
OS Chimeric - Rhesus macaque polyoma virus.
OS Chimeric - Unidentified.
XX
XX Key
FH Location/Qualifiers
FT 1..750
FT enhancer
FT /tag= a
FT /note= "CMV enhancer; Also serves as a promoter"
FT misc_feature
FT 890..1002
FT /tag= b
FT /note= "Intervening sequence"
FT promoter
FT 1067..1085
FT /tag= c
FT /note= "T7 RNA polymerase promoter"
FT misc_feature
FT 1090..1984
FT /tag= d
FT /note= "Human B7-1 DNA"
FT misc_feature
FT 1090..1956
FT /tag= e
FT RBS
FT 2013..2593
FT /tag= f
FT /note= "IRES sequence"
FT misc_feature
FT 2627..4263
FT /tag= g
FT /note= "Human IL-12.2 DNA"
FT CDS
FT 2640..4253
FT /tag= h
FT /product= "Human IL-12.2 protein"
FT misc_feature
FT 3606..3676
FT /tag= i
FT promoter
FT 4362..4383
FT /tag= j
FT /note= "T3 RNA polymerase promoter"
FT polyA_signal
FT 4393..4614
FT /tag= k
FT /note= "SV40 fragment containing polyadenylation signal"
FT rep_origin
FT 4709..5164
FT /tag= l
FT /note= "f1 origin of replication"
FT misc_feature
FT 5228..6595
FT /tag= m

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FT /note= "Neo r expression cassette"
FT misc_feature
FT /tag= n
FT /note= "Ampicillin resistance"

US2002018767-A1.
XX
XX
XX
XX 14-FEB-2002.
XX
XX
XX 10-APR-2001; 2001US-0828825.
XX
XX
XX 27-JUL-2000; 2000KR-0043498.
XX
XX (LEES/) LEE S.
XX (KIMH/) KIM H.
XX
XX Lee S, Kim H;
XX
XX WPI; 2002-239247/29.
XX
XX P-PSDB: AAE19820.
XX
XX New expression system, useful as vaccine for treating cancer, comprises
XX DNA molecule encoding Interleukin-12 and costimulatory molecule,
XX operably linked to promoter that directs the expression of DNA molecule
XX
XX Example 1; Page 31-36; 76pp: English.
XX
XX The invention relates to an expression system which comprises a DNA
XX molecule encoding interleukin (IL)-12 and a costimulatory molecule,
XX operably linked to a promoter that directs the expression of the DNA
XX molecule. Expression vectors of the invention are useful for in vitro
XX generation of genetically modified human cancer cells for cancer
XX therapy. These cells share phenotypes of both antigen presenting cells
XX and cancer cells and are suitable as a cellular vaccine for certain
XX types of cancer. Expression vectors are useful for eliciting an anti
XX tumor immune response in a individual. They are useful for activating
XX T cells for immunotherapeutic responses against primary or metastatic
XX cancers. The present sequence is PIRRES-hb7-1-IL12.2 vector DNA.
XX This vector comprises cytomegalovirus (CMV) promoter and enhancer,
XX bacteriophage T7 RNA polymerase promoter, human B7-1 DNA, IRES sequence,
XX human IL-12.2 DNA, bacteriophage T3 RNA polymerase promoter,
XX Simian virus 40 (SV40) fragment containing polyadenylation signal, f1
XX origin of replication, Neo r expression cassette and ampicillin
XX resistance sequence.
XX
XX Sequence 8608 BP: 2180 A; 2126 C; 2138 G; 2164 T; 0 other.
XX
XX
XX
XX Alignment Scores:
XX Pred. No.: 8,69e-194 Length: 8608
XX Score: 2309.00 Matches: 439
XX Percent Similarity: 90.31% Conservative: 27
XX Best Local Similarity: 85.08% Mismatches: 44
XX Query Match: 85.74% Indels: 6
XX DB: 24 Gaps: 3
XX
XX US-09-917-265-67 (1-511) x AAD31548 (1-8608)
Oy 1 IleTpgIuLeuGlulysAspValYrValValGluleuAspTPrHisProAspAlaPro 20
    |||||
Db 2706 ATATGCGAACTGAAGAAAGATGTATTATGCGTAAGAAATGGATTGGATCCGATGCCCT 2765
Oy 21 GlyGluMeValValLeuThrCysHisThrProGluGluuAspAspIleThrTrrPhSer 40
    |||||
Db 2766 GGAGAAATGGTGTCTCTACCTGACACCCCTGAAGAAAGATGATACCTGGACCTTG 2825
Oy 41 AlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValysgluPhe 60
    |||||
Db 2826 GACACAGACAGAGAGCTCTTAGCTCTGCAAAACCCGTACCATCAATCAAGAGTTT 2885
Oy 61 GlyAspAlaGlyGlnTrrThrCysHisLysGlyGlyValLeuSerArgSerLeuLeu 80
    |||||
Db 2886 GCAGATGCTGGCCAGTACACCTGTCAACAAAGAGAGGAGGTTTAAAGCATTCGCTCG 2945

```

| | | | |
|----|------|---|------|
| QY | 81 | LeuIleHISLysLysGluAspGlyTLeuPheSerThrAspIleLeuLysGluGlnIleSglu | 100 |
| Db | 2946 | CTGCTTCCACAAAAAGAGATGCAATTTGGTCTCCACTGATATTTTAAAGGCCACAAAGAA | 3005 |
| QY | 101 | SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys | 120 |
| Db | 3006 | CCCAAAATTAAGACCTTTCTAAGATCGCAGGCCAAAGATTTATCTGGACGTTTCACTGCG | 3065 |
| QY | 121 | TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe | 140 |
| Db | 3066 | TGGTGGCTGACACATCAGTACGATTTGGATTCATTCATGTCCAAAGCAGAGAGGCTCT | 3125 |
| QY | 141 | SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgVal | 160 |
| Db | 3126 | TCTGACCCCCCAAGGGGTGACGTGGGAGACTCTACACTCTGTGCAGAGAGTCAAGAGG | 3185 |
| QY | 161 | AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProSer | 180 |
| Db | 3186 | GACAAACAAGGAGATT- -GACTACTACATGGAGTCCCGAGGAGCAGTGGCTGGCCAGCT | 3242 |
| QY | 181 | AlaGluGluSerLeuProIleGluValValAlaAlaIleHISLysLeuLysTyrGlu | 200 |
| Db | 3243 | GCTGAGGAGAGTCTGCCATTGAGTGCTAGTGTGGTGGCTTCCACAACTCAAGATGAA | 3302 |
| QY | 201 | AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProThrAsnLeu | 220 |
| Db | 3303 | AACTACACACACAGCTTCTTCATCAGGAGCATCATCAAACTGACCCCAACAACTTG | 3362 |
| QY | 221 | GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr | 240 |
| Db | 3363 | CAGCTGAAGCCATTAAAGATTTCTGGCAGGTGGAGGTCACTGGGATACCCTGACAC | 3422 |
| QY | 241 | TrpSerThrProHISSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn | 260 |
| Db | 3423 | TGGAGTACTCCACATCTCTACTTCTCCCTGACATCTGCTGTTCAAGTCCAGGCAAGAC | 3482 |
| QY | 261 | AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValAlaCysHis | 280 |
| Db | 3483 | AAGAGAGAAAGAAAGATAGAGTCTCCACGCACAAAGACCTGACCGCATCTGCGCG | 3542 |
| QY | 281 | LysAspAlaLysIleArgValGlnAlaIleArgAspArgTyrTyrSerSerSerTrpSerAsp | 300 |
| Db | 3543 | AAAATGCCACACATTAGCGTGGGGGCCAGGACCCGTCATCTAGCTACTTTGGAGCGAA | 3602 |
| QY | 301 | TrpAlaSerValSerCysSerGlyGly- - - - -glyIglyIglySer- - - - -Arg | 315 |
| Db | 3603 | TGGCGATCTGTGCCCTCGCAGTGGTGGCGGTGGAGACGGTGGCGGTGGAAGCCCATGAGGA | 3662 |
| QY | 316 | AsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHISerGlnThr | 335 |
| Db | 3663 | AACCTCCCCGTTGCCACTCCAGACCCCAAGATGTTCCATCCTTCAACACTCCCAAAAC | 3722 |
| QY | 336 | LeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGlnLeuTyrSer | 355 |
| Db | 3723 | CTGCTGAGGCGCGTCAGCACATGCTCCAGAAGGCCACAAACTGTGAATTTTACCCT | 3782 |
| QY | 356 | CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu | 375 |
| Db | 3783 | TGCACCTTCTGGAAGATGTGATCATCAATATTCACAAAAGATTAATAAACGACAGTGGAG | 3842 |
| QY | 376 | AlaCysLeuProLeuGlnLeuThrMetKsnLusSerCysLeuAlaSerArgGluIleSer | 395 |
| Db | 3843 | GCGCTTTTACCATTTGGAATTAACCAAGAAATGAGACTTGCCTTAATTTCCAGAGAACCTCT | 3902 |
| QY | 396 | LeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeuCys | 415 |
| Db | 3903 | TTTCATAACTAATGGCAGTTGGCTGGCCCTCCGAAAGACCTCTTTTATGATGCGCCTGTGC | 3962 |
| QY | 416 | LeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluIlePheLysAlaMetAsnAla | 435 |
| Db | 3963 | CTTACGACTATTTTGAAGACTGTGAAGATGTACAGAGGTGGAGTTTCACACCATGAATGCA | 4022 |

| | | | | | |
|----------|--|--|------|--|--|
| Oy | 436 | LysineLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIle | 455 | | |
| Db | 4023 | AAAGCTTGGATGGATCCCTAAGAGCGAGATCTTTTACGATCAAAACATGCTGGCAGTATT | 4082 | | |
| Oy | 456 | AspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSerIeu | 475 | | |
| Db | 4083 | GATGAGCTGCATGCAGGCCCTCAATTCCAAACAGTGCAGCTGCCACAAAATCCTCCCTT | 4142 | | |
| Oy | 476 | GIuGluProAspPheTyrLysThrLysIleLysLeuGlyIleLeuLeuHisAlaPheArg | 495 | | |
| Db | 4143 | GAGAGACCGGATTTTTATATAAACTAAATCAAGCTCTGCATACCTTTCATGCTTTCAGA | 4202 | | |
| Oy | 496 | IleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnSerSer | 511 | | |
| Db | 4203 | ATTGGCGAGTGACTATTGATAGATGATGATGAGCTATCGAATGCTTCC | 4250 | | |
| RESULT 3 | | | | | |
| AAD31552 | ID AAD31552 standard; DNA; 8629 BP. | | | | |
| XX | AAD31552; | | | | |
| XX | 18-JUN-2002 (first entry) | | | | |
| DE | PIRES-IL12.2-hb7-1 vector DNA. | | | | |
| XX | Expression system; interleukin-12; cancer therapy; cellular vaccine; | | | | |
| KW | immunotherapeutic response; IL-12.2; chimeric; human; Simian virus 40; | | | | |
| KW | SV40; Cytomegalovirus; CMV; ds. | | | | |
| XX | Chimeric - Cytomegalovirus. | | | | |
| OS | Chimeric - Bacteriophage T7. | | | | |
| OS | Chimeric - Homo sapiens. | | | | |
| OS | Chimeric - Bacteriophage T3. | | | | |
| OS | Chimeric - Rhesus macaque polyoma virus. | | | | |
| XX | Chimeric - Unidentified. | | | | |
| FT | Key | Location/Qualifiers | | | |
| FT | enhancer | 1..750 | | | |
| FT | /*tag= a | | | | |
| FT | /note= "CMV enhancer; Also serves as a promoter" | | | | |
| FT | promoter | 1067..1085 | | | |
| FT | /*tag= b | | | | |
| FT | /note= "T7 RNA polymerase promoter" | | | | |
| FT | 1090..2726 | | | | |
| FT | /*tag= c | | | | |
| FT | /note= "Human IL-12.2 DNA" | | | | |
| FT | 1103..2716 | | | | |
| FT | /*tag= d | | | | |
| FT | /product= "Human IL-12.2 protein" | | | | |
| FT | 2087..2116 | | | | |
| FT | /*tag= e | | | | |
| FT | /note= "Linker of human IL-12.2 sequence" | | | | |
| FT | 2752..3332 | | | | |
| FT | /*tag= f | | | | |
| FT | /note= "IRES sequence" | | | | |
| FT | 3369..4263 | | | | |
| FT | /*tag= g | | | | |
| FT | /note= "Human B7-1 DNA" | | | | |
| FT | 4383..4404 | | | | |
| FT | /*tag= h | | | | |
| FT | /note= "T3 RNA polymerase promoter" | | | | |
| FT | 4414..4635 | | | | |
| FT | /*tag= i | | | | |
| FT | /note= "SV40 fragment containing polyadenylation signal" | | | | |
| FT | 4730..5185 | | | | |
| FT | /*tag= j | | | | |
| FT | /note= "f1 origin of replication" | | | | |
| FT | 5249..6616 | | | | |
| FT | /*tag= k | | | | |
| FT | /note= "Neo r expression cassette" | | | | |
| FT | 7027..7887 | | | | |
| FT | /*tag= l | | | | |
| FT | misc_feature | | | | |


```

QY 456 AspGluLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnIySserSerLeu 475
      |||||:::|||||
DB 2546 GATGAGCTGATGCGAGCGCTGGAATTTCACAGTACGACTGTGCCACAAAATCTCCCTT 2605
QY 476 GluGluProAspPheTrpIySThrIySLeuGlnCysIleLeuLeuHisAlaPheArg 495
      |||||
DB 2606 GAAGAACCAGGATTTTATTAATACTAAATCAAGCTCGCACTTCTTCATYGGCTTCAGA 2665
QY 496 IleArgAlaValThrIleAsnArgMetSerTyrIleuAsnSerSer 511
      |||||
DB 2666 ATTCGGCACTGACTATTGATFAGAGTGAAGTACGCTACTGTAATCTTCC 2713

RESULT 4
AAD31547
ID AAD31547 standard; DNA: 8623 BP.
XX
XX AAD31547;
AC
XX 18-JUN-2002 (first entry).
XX
XX PIRRES-hb7-1-IL12.3 vector DNA.
DE
XX Expression system; interleukin-12; cancer therapy; cellular vaccine;
KM immunotherapeutic response; IL-12.3; chimeric; human; Simian virus 40;
KM SV40; cytomegalovirus; CMV; ds.
XX
XX Chimeric - Cytomegalovirus.
OS
XX Chimeric - Bacteriophage T7.
OS
XX Chimeric - Homo sapiens.
OS
XX Chimeric - Bacteriophage T3.
OS
XX Chimeric - Rhesus macaque polyoma virus.
XX
XX Chimeric - Unidentified.
FH
FH Key Location/Qualifiers
FT 1..750
FT /tag= a
FT /note= "CMV enhancer; Also serves as a promoter"
FT misc_feature
FT 890..1002
FT /tag= b
FT /note= "Intervening sequence"
FT promoter
FT 1067..1085
FT /tag= c
FT /note= "T7 RNA polymerase promoter"
FT misc_feature
FT 1090..1984
FT /tag= d
FT /note= "Human B7-1 DNA"
FT misc_feature
FT 1090..1956
FT /tag= e
FT /note= "Human B7-1 coding region"
FT RBS
FT 2013..2593
FT /tag= f
FT /note= "IRES sequence"
FT misc_feature
FT 2627..4278
FT /tag= g
FT /note= "Human IL-12.3 DNA"
FT CDS
FT 2640..4268
FT /tag= h
FT /product= "Human IL-12.3 protein"
FT misc_feature
FT 3606..3690
FT /tag= i
FT /note= "Flexible linker of human IL-12.3 sequence"
FT promoter
FT 4398..4407
FT /tag= j
FT /note= "T3 RNA polymerase promoter"
FT polyA_signal
FT 4408..4629
FT /tag= k
FT /note= "SV40 fragment containing polyadenylation signal"
FT rep_origin
FT 4724..5179
FT /tag= l
FT /note= "f1 origin of replication"
FT misc_feature
FT 5243..6610
FT /tag= m

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FT /note= "Neo r expression cassette"
FT misc_feature 7021..7881
FT /tag= n
FT /note= "Ampicillin resistance"
XX
XX US2002018767-A1.
XX
XX 14-FEB-2002.
XX
XX 10-APR-2001; 2001US-0828825.
XX
XX 27-JUL-2000; 2000KR-0043498.
XX
XX (LEES/) LEE S.
XX PA (KIMH/) KIM H.
XX
XX Lee S, Kim H;
XX
XX WPI; 2002-239247/29.
XX P-SDB; AAE19819.
XX
XX New expression system, useful as vaccine for treating cancer, comprises
PT DNA molecule encoding interleukin-12 and costimulatory molecule,
PT operably linked to promoter that directs the expression of DNA molecule
XX
XX Example 1; Page 24-29; 76pp; English.
XX
XX The invention relates to an expression system which comprises a DNA
XX molecule encoding interleukin (IL)-12 and a costimulatory molecule,
XX operably linked to a promoter that directs the expression of the DNA
XX molecule. Expression vectors of the invention are useful for in vitro
XX generation of genetically modified human cancer cells for cancer
XX therapy. These cells share phenotypes of both antigen presenting cells
XX and cancer cells and are suitable as a cellular vaccine for certain
XX types of cancer. Expression vectors are useful for eliciting an anti
XX tumour immune response in a individual. They are useful for activating
XX T cells for immunotherapeutic responses against primary or metastatic
XX cancers. The present sequence is PIRRES-hb7-1-IL12.3 vector DNA.
XX This vector comprises cytomegalovirus (CMV) promoter and enhancer,
XX bacteriophage T7 RNA polymerase promoter, human B7-1 DNA, IRES sequence,
XX human IL-12.3 DNA, bacteriophage T3 RNA polymerase promoter,
XX Simian virus 40 (SV40) fragment containing polyadenylation signal, f1
XX origin of replication, Neo r expression cassette and ampicillin
XX resistance sequence.
XX
XX Sequence 8623 BP; 2182 A; 2128 C; 2147 G; 2166 T; 0 other;
XX
XX Alignment Scores:
XX Pred. NO.: 1,45e-193 Length: 8623
XX Score: 2306.50 Matches: 439
XX Percent Similarity: 89.44% Conservative: 27
XX Best Local Similarity: 84.26% Mismatches: 44
XX Query Match: 85.65% Indels: 11
XX DB: 24 Gaps: 3
XX
XX US-09-917-265-67 (1-511) x AAD31547 (1-8623)
QY 1 IleTPrGluLeuGlnIySAspValTyrValIaGluLeuAspTrpHisProAspAlaPro 20
      |||||
DB 2706 ATATGGCAACTGAGAAAGATGTTTATGTCGTGAATTGGATTCGATCCGATGCCCTT 2765
QY 21 GlyGluMetValIleuThrCysHisThrProGluIAspAspIleThrTrpThrSer 40
      |||||
DB 2766 GCAGAAATGCTGCTCCTACCTGTGACCCCGGAGAGATGATGATCAGTGCAGCTTG 2825
QY 41 AlaGlnSerSerGluValIleuGlnGlySerGlyIySThrIleuThrIleGlnValIySgluPhe 60
      |||||
DB 2826 GACCAAGACGAGTGGCTTGAAGCTGTGCAAAACCTCAACATCCAAAGAGTTT 2885
QY 61 GlyAspAlaGlyGlnIyThrCysHisIySgluGlyValIleuSerArgSerLeuLeu 80
      |||||
DB 2886 GGAGATGCTGGCCAGTACACCTGTCAAAAGAGGCGAGGTTCTTAAGCCATTGCTCTG 2945

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QY      81  Leu1Leu1sLysLysGluAspGly1Leu1rPserThrAsp1LeuLeuLysGluGlnLysGlu 100
Db      2946 CTGCTTACAAAAGAAAGATGGAATTTGGTCCATGATATTAAAGACACAAAGAA 3005
QY      101 SerLysAsnLys1LeuLeuLysCysGluAlaLysAsnTySerGlyArgPheThrCys 120
Db      3006 CCCCAAAATGAACCTTCTTAAGATGCGAGCCCAAGATATTATCTGCAGCTTTGACCTGCG 3065
QY      121 Trf1rPleuThrAla1LeuSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
Db      3066 TGGTGGCTGACGACAAATCAGACTGATTTGACATTCAGTGCACAAACACAGAGGCTCT 3125
QY      141 SerAspProGlnGlyVal1ThrCysGlyAlaVal1rLeuSerAlaGluArgVal1rVal 160
Db      3126 TCTGACCCCAAGGGGAGAGCTGGGAGCTGCTCACTCTCTGCAGAGACAGTACAGAGG 3185
QY      161 AspAsnArgAspTy1rLysTy1rThrVal1GluCysGlnGlySerAlaCysProSer 180
Db      3186 GACAACAGAGAGTAT---GAGTACTCAGTGCAGTGCAGAGACAGTGCCTGCCACGCT 3242
QY      181 AlaGlnGluSerLeuP1rGlnGlyVal1Val1AspAla1Leu1sLysLysLysTy1rGlu 200
Db      3243 GCTGAGGAGAGTCTGCCATTGAGTATGAGTGCATGCTGATCCGTTCAAGCTCAAGTATGAA 3302
QY      201 AsnTy1rThrSerSerPhePhe1LeuArgAsp1Leu1sLysProAspPro1rPheAsnLeu 220
Db      3303 AACTACACCCAGCAGCTCTTCTCATGAGGACATCTCAACCTGACCCACCAACACTTG 3362
QY      221 GlnLeuLysP1rLeuLysAsnSerArgHisVal1GluVal1Ser1rP1rGluTy1rProAspThr 240
Db      3363 CACCTGAAGCCATTAAAGATTTCTCGCAGCTGAGAGTGCAGCTGCAGTACCTGACACACC 3422
QY      241 Trf1rPserThrProHisSerTy1rPheSerLeuThrPheCys1LeuGlnAlaGlnGlyLysAsn 260
Db      3423 TGGAGTACTCCACATTTCTACTTCTCCCTGACATTCGCTGCGTCAAGTCCAGGCAAGAGC 3482
QY      261 AsnArgGluLysLysAspArgLeuCysVal1AspLysThrSerAlaLysVal1CysHis 280
Db      3483 AAGAGCAAAAGAAAGTACAGTCTTCACGACAAAGACTCAGCAGCGTATATGTGCCGC 3542
QY      281 LysAspAlaLys1LeuArgVal1GlnAlaArgAspArgTy1rTy1rSerSerSerTy1rP1rSerAsp 300
Db      3543 AAAAATGCCAGCATTTACGCTGCGGCCAGACGCGCTACTATATCTCATCTTGGAGCGAA 3602
QY      301 TrpAlaSerVal1SerCysSerGlyGly-----GlyGlyGly 312
Db      3603 TGGGCATCTGTGCCCTTCAGTGGTGGCGTGCAGACGCGTGGCGTGCAGCGGTGGCGCT 3662
QY      313 GlySer-----ArgAsnLeuPro1rP1rPro1rP1rProSerProGlyMetPheGlnCysLeu 330
Db      3663 GCAAGGCCCATGAGAAACCTCCCGTGGCCATCTCAACACCAGAAATGTTCCATGCTT 3722
QY      331 AsnHisSerGlnThrLeuLeuArgAlaVal1SerAsnThrLeuGlnLysAlaArgGlnThr 350
Db      3723 CACCACATCCCAAAAACCTGCTGAGGGCCGTCAAGCAATGCTCCAGAAAGCCAGCAAACT 3782
QY      351 LeuGlnLeuTy1rSerCysThrSerGluGlu1LeuAspHisGluAsp1LeuThrLysAspLys 370
Db      3783 CTAGAATTTTACCTTCACCTTCTGGAAGATTCATCATGAAATATCACAAAAGATAAA 3842
QY      371 ThrSerThrVal1GluAlaCysLeuProLysGlnLeuThrMetAsnGlnLysSerCysLeuAla 390
Db      3843 ACCAGCAGCATGGAGGCTGTTTACCATTTGCAATTAACCAAGATGAGAGTGGCTTAAT 3962
QY      391 SerArgGlu1LeuSerLeu1LeuThrAsnGlySerCysLeuAlaSerCysLysAlaSerPhe 410
Db      3903 TCCAGAGAGACCTCTTTCATTAACATATGAGAGTGGCTGCTCCAGAAAGACCTCTTTT 3962
QY      411 MetThrValLeuLysLeuSerSer1LeuTy1rGluAspLeuLysMetTy1rGlnMetGluPhe 430
Db      3963 ATGATGGCCCTGTGCTTACTAGATTATGAACACTTGAAGATGTACAGAGTGGAGTTC 4022

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QY      431  LysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln1LeuLeuAspGlnAsn 450
Db      4023 AAGACCATGATGCAAAAGCTTCTGATGATCTTAAGAGCGAGATCTTTAGATCAAAAC 4082
QY      451  MetLeuThrAla1LeuAspGluLeuGlnAlaLeuAsnPheAsnSerVal1rVal1Pro 470
Db      4083 ATCTGGCAGATTATGATGAGCTGATGCAGCCCTGAAATTTCAACAGTGCAGACTGTCGA 4142
QY      471  GlnLysSerSerLeuGluGluProAspPheTy1rLys1rLys1rLysLysCys1rLeu 490
Db      4143 CAAAATCTCTCCTTGAAGAACCGGATTTTATAACTAAATCAAGCTCTGCATCTT 4202
QY      491  LeuHisAlaPheArg1LeuArgAlaVal1Thr1LeuAsnArgMetSerTy1rLeuAsnSer 510
Db      4203 CTTCATGCTTTCACAATTTGGGCGAGTGCATATGATAGAGTATGACTATCTGAAATGCT 4262
QY      511  Ser 511
Db      4263 TCC 4265

RESULT 5
AAD31551
ID      AAD31551 standard; DNA; 8644 BP.
XX      AC
XX      AAD31551:
XX      18-JUN-2002 (first entry)
DE      pIRES-IL12.3-hb7-1 vector DNA.
XX      DE
XX      Expression system: interleukin-12; cancer therapy; cellular vaccine;
KW      immunotherapeutic interse; IL-12.3; chimeric; human; Simian virus 40;
KW      SV40; cytomegalovirus; CMV; ds.
XX      OS
XX      Chimeric - Cytomegalovirus.
OS      Chimeric - Bacteriophage T7.
OS      Chimeric - Homo sapiens.
OS      Chimeric - Bacteriophage T3.
OS      Chimeric - Rhesus macaque polyoma virus.
OS      Chimeric - unidentified.
XX      XX
FH      Key
FT      enhancer
FT      1..750
FT      /tag= a
FT      /note= "CMV enhancer. Also serves as a promoter."
FT      1067..1085
FT      /*tag= b
FT      /note= "T7 RNA polymerase promoter."
FT      1090..2731
FT      /*tag= c
FT      /note= "Human IL-12.3 DNA"
FT      1103..2731
FT      /*tag= d
FT      /product= "Human IL-12.3 protein"
FT      2087..2131
FT      /*tag= e
FT      misc_feature
FT      2767..3347
FT      /tag= f
FT      /note= "Linker of human IL-12.3 sequence"
FT      3384..4278
FT      /tag= g
FT      /note= "Human B7-1 DNA"
FT      4398..4419
FT      /tag= h
FT      /note= "T3 RNA polymerase promoter"
FT      4429..4650
FT      /tag= i
FT      /note= "SV40 fragment containing polyadenylation signal"
FT      4745..5200
FT      /*tag= j
FT      /note= "f1 origin of replication"
FT      5264..5681
FT      misc_feature

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FT      /*tag= k
FT      /note= "Neo r expression cassette"
FT      misc_feature
FT      7042..7902
FT      /tag= 1
FT      /note= "Ampicillin resistance"
XX      US2002018767-A1.
XX      14-FEB-2002.
XX      10-APR-2001; 2001US-0828825.
XX      27-JUL-2000; 2000KR-0043498.
XX      (LEES/) LEE S.
XX      (KIMH/) KIM H.
XX      Lee S, Kim H;
XX      WPI; 2002-239247/29.
XX      P-PSDB; AAE19823.
XX      New expression system, useful as vaccine for treating cancer, comprises
PT      DNA molecule encoding interleukin-12 and costimulatory molecule,
PT      operably linked to promoter that directs the expression of DNA molecule
XX      Example 1; Page 52-57; 76pp; English.
XX      The invention relates to an expression system which comprises a DNA
XX      molecule encoding interleukin (IL)-12 and a costimulatory molecule,
XX      operably linked to a promoter that directs the expression of the DNA
XX      molecule. Expression vectors of the invention are useful for in vitro
XX      generation of genetically modified human cancer cells for cancer
XX      therapy. These cells share phenotypes of both antigen presenting cells
XX      and cancer cells and are suitable as a cellular vaccine for certain
XX      types of cancer. Expression vectors are useful for eliciting an anti
XX      tumour immune response in a individual. They are useful for activating
XX      T cells for immunotherapeutic responses against primary or metastatic
XX      cancers. The present sequence is pIRES-IL12.3-hb7-1 vector DNA.
XX      This vector comprises cytomegalovirus (CMV) promoter and enhancer,
XX      bacteriophage T7 RNA polymerase promoter, human B7-1 DNA, IRES sequence,
XX      human IL-12.3 DNA, bacteriophage T3 RNA polymerase promoter,
XX      Simian Virus 40 (SV40) fragment containing polyadenylation signal, fl
XX      origin of replication, Neo r expression cassette and ampicillin
XX      resistance sequence.
XX      Sequence 8644 BP; 2187 A; 2134 C; 2152 G; 2171 T; 0 other:
XX
XX      Alignment Scores:
XX      Pred. No.: 1,46e-193 Length: 8644
XX      Score: 2306.50 Matches: 439
XX      Percent Similarity: 89.44% Conservative: 27
XX      Best Local Similarity: 84.26% Mismatches: 44
XX      Query Match: 85.65% Indels: 11
XX      DB: 24 Gaps: 3
XX
XX      US-09-917-265-67 (1-511) x AAD31551 (1-8644)
XX      QY      11leTropolueuglulysAspValTYrValValGluLeuAspTRPHisProAspAlaPro 20
XX      Db      1169 ATATGGAACTGAAGAAAGATGTTTATGTGTGTAATTTGGATTGCGGATGCCCT 1228
XX      QY      21 GlyLueValValleuthrCysSHisThrProGluGluAspAspIleThrTrpThrSer 40
XX      Db      1229 GGAGAAATGCTGCTCACCTGTGACACCCCTGAAGAAAGATGATATCACCCTG 1288
XX      QY      41 AlGlnSerSerGluValleuGlySerGlyLysThrleuThrIleGlnValLysGluPhe 60
XX      Db      1289 GACCGAGCAGTGAAGCTTGTAGGCTGTGCAAAACCTGACATCCAAAGTCAAGAGTTT 1348
XX      QY      61 GlyAspAlaGlyGlnTrpThrCysHisLysGlyGlyValleuSerArgSerleuLeu 80

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Db      1349 GGAGATGCTGGCCAGTACACCTCTGTCAAAAGAGCGGAGTTCTTAAGCATTCGCTCCG 1408
QY      81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGlu 100
Db      1409 CTGCTTCACAAAAAGAAAGATGGAATTTGGTCCACATGATATTTTAAAGACCAAGAAAGA 1468
QY      101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTrpSerGlyArgPheThrCys 120
Db      1469 CCAAAAAATTAAGACCTTTCTTAAGATGCGAGGCCAAGAAATTAATTCGAGCTTACACTGC 1528
QY      121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
Db      1529 TGGTGGCTGACGCAATTCAGTACTGATTTGACATTCAGTCAAAAGCAGCAGAGGCTCT 1588
QY      141 SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgVal 160
Db      1589 TCTGACCCCAAGAGGTGACGTGCGGAGCTGCTGACACTCTGACAGAGAGTCAAGAGG 1648
QY      161 AspAsnArgAspTrpLysLysTrpThrValGluCysGlnGluGlySerAlaCysProSer 180
Db      1649 GACAAACAGAGATAT--GAGTACTCAGTGGAGTCCAGAGAGACAGTCCCTGCCAGCT 1705
QY      181 AlaGluGluSerLeuProIleGluValValAlaLysAlaIleHisLysLeuLysTrpGlu 200
Db      1706 GCTGAGGAGAGTGTGCTTCATGAGTCAATGAGTGGATGCGCTTCACAGCTCAAGTATGAA 1765
QY      201 AsnTrpThrSerSerPhePheIleArgAspIleIleLysProAspProThrAsnLeu 220
Db      1766 AACTACACAGCAGCTTCTTCATCAGGAGCATCATCATCAACCTGACCCCAACACTTG 1825
QY      221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTrpProAspThr 240
Db      1826 CACCTAAGCCATTAAGAAATTCGCGAGGTGGAGTCAAGCTGGAAGTCACTCCGACAC 1885
QY      241 TrpSerThrProHisSerTrpPheSerLeuThrPheCysIleGlnAlaGlnLysLysAsn 260
Db      1886 TGGAGTACTCCATTCCTACTTCTCCGACATTTGGCTTCAGAGTCCAGGCAAGAAC 1945
QY      261 AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValLysHis 280
Db      1946 AAGAGGAAAGAAAGAAATGAGAGTTCACCGCAACAAACCTCAGCCAGCTCTCTCCGC 2005
QY      281 LysAspAlaLysIleArgValGlnAlaArgAspArgTrpLysSerSerArgProAsp 300
Db      2006 AAAAATGCCAGCTTGTAGCTGCGGCGCCAGGACCGCTACTATGATCTTGTGACAGAA 2065
QY      301 TrpAlaSerValSerCysSerGlyGly-----GlyGlyGly 312
Db      2066 TGGGCAATCTGTGCTGCACTGTGGCGGTGGAAGCGGTGCGGTGGAAGCGGTGGCGGT 2125
QY      313 GlySer-----ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeu 330
Db      2126 GGAAGGCCATGCGAAGAACTCCCGCGGCGACCTCCAGACAGGAATGTTCCCATCCCT 2185
QY      331 AsnHisSerGlnThrLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThr 350
Db      2186 CACCACTCCCAAAACCTGCTGAGGCGCGTGAACATGCTCCAGAAAGGCGMACAAACT 2245
QY      351 LeuGluLeuTrpSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLys 370
Db      2246 CTGAATTTTACCTTGCACCTTCTGAAAGATTTGATCATGAAGATTCACAAAAAGATTA 2305
QY      371 ThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAla 390
Db      2306 ACCAGCAGAGTGAAGCGCTGTTACCATTTGAATTAACCAAGATGAAGAGTTGCCATAAT 2365
QY      391 SerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerLysAlaSerPhe 410
Db      2366 TCCAGAGAACACCTTTTCAATTAATGAGATGCTGCTGCGCTCCGAAAGACCTCTTT 2425
QY      411 MetThrValLeuLeuSerSerIleTrpGluAspLeuLysMetTrpLysGlnMetGluPhe 430
Db      2426 ATGATGCGCCCTGTGCTTGTAGTATTTATGAAGACTGAACATGTACCAAGGTGGAGTT 2485

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| | | | |
|----------|--|---|------|
| OY | 431 | Lysalamelcnaalalysleuleuemetaspbrolysarglinllepheleuaspghasn | 450 |
| | | | |
| Db | 2486 | AAGACCATGATGCAAGAGCTTCTGATGATCCTTAAGAGCCAGATCTTCTGATCAAAAC | 2545 |
| OY | 451 | Metteurhralaileaspghleuleuglnlaleuasnphneaservalththvalpro | 470 |
| | | | |
| Db | 2546 | ATGCTGGCAGCTATTATGATCAGCTGATGAGCCCTGCAATTTCAACAGTGAGATGTGCCA | 2605 |
| OY | 471 | GlnysserSerleuglucIuPProaspPheTyrLysThrLysIleLysleuCysIleleu | 490 |
| | | | |
| Db | 2606 | CAAAATTCCTCCCTTGGAAGAACCGGATTTTATAAACTAAATCAACGCTGTGATACTT | 2665 |
| OY | 491 | LeuHisaIaIhearglleatrgAlaValThrIleasnAargMetSerTyrLeuAsnSer | 510 |
| | | | |
| Db | 2666 | CTTCATCTCTTCAGAAATTCGGCAGTGACTATGTGATGAGATGATGACCTATCTGAATCCT | 2725 |
| OY | 511 | Ser 511 | |
| | | | |
| Db | 2726 | TTC 2728 | |
| RESULT 6 | | | |
| AAD31549 | | | |
| ID | AAD31549 | standard; DNA; 8638 BP. | |
| XX | | | |
| AC | AAD31549: | | |
| XX | | | |
| DT | 18-JUN-2002 | (first entry) | |
| XX | | | |
| DE | PIRES-hb7-1-IL12.4 | vector DNA. | |
| XX | | | |
| KW | Expression system: interleukin-12; cancer therapy; cellular vaccine; | | |
| KW | Immunotherapeutic response; IL-12.4; chimeric; human; Simian virus 40; | | |
| XX | SV40; cytomegalovirus; CMV; ds. | | |
| OS | Chimeric - Cytomegalovirus. | | |
| OS | Chimeric - Bacteriophage T7. | | |
| OS | Chimeric - Homo sapiens. | | |
| OS | Chimeric - Bacteriophage T3. | | |
| OS | Chimeric - Rhesus macaque polyoma virus. | | |
| OS | Chimeric - Unidentified. | | |
| XX | | | |
| Key | | Location/Qualifiers | |
| FT | enhancer | 1..750 | |
| FT | | /*tag= a | |
| FT | | /note= "CMV enhancer; Also serves as a promoter" | |
| FT | misc_feature | 890..1002 | |
| FT | | /*tag= b | |
| FT | | /note= "Intervening sequence" | |
| FT | promoter | 1067..1085 | |
| FT | | /*tag= c | |
| FT | | /note= "T7 RNA polymerase promoter" | |
| FT | misc_feature | 1090..1984 | |
| FT | | /*tag= d | |
| FT | | /note= "Human B7-1 DNA" | |
| FT | misc_feature | 1090..1954 | |
| FT | | /*tag= e | |
| FT | | /note= "Human B7-1 coding region" | |
| FT | RBS | 2013..2593 | |
| FT | | /*tag= f | |
| FT | | /note= "IRES sequence" | |
| FT | misc_feature | 2627..4293 | |
| FT | | /*tag= g | |
| FT | | /note= "Human IL-12.4 DNA" | |
| FT | CDS | 2640..4283 | |
| FT | | /*tag= h | |
| FT | | /product= "Human IL-12.4 protein" | |
| FT | misc_feature | 3606..3706 | |
| FT | | /*tag= i | |
| FT | | /note= "Linker of human IL-12.4 sequence" | |
| FT | promoter | 4392..4413 | |
| FT | | /*tag= j | |
| FT | | /note= "T3 RNA polymerase promoter" | |
| FT | | | |

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FT      polyA-signal      4423..4644
FT      /*tag=      k
FT      /note= "SV40 fragment containing polyadenylation signal"
FT      rep-origin      4739..5194
FT      /*tag=      l
FT      /note= "fl origin of replication"
FT      misc-feature      5258..6625
FT      /*tag=      m
FT      /note= "Neo r expression cassette"
FT      misc-feature      7036..7896
FT      /*tag=      n
FT      /note= "Ampicillin resistance"
FT
XX      US2002018767-A1.
XX
XX      14-FEB-2002.
XX
XX      10-APR-2001; 2001US-0828825.
XX
XX      27-JUL-2000; 2000KR-0043498.
XX
XX      (LEES/) LEE S.
XX      (KIMH/) KIM H.
XX
XX      Lee S, Kim H;
XX
XX      WPI: 2002-239247/29.
XX      P-PSDB; AME19821.
XX
XX      New expression system, useful as vaccine for treating cancer, comprises
XX      DNA molecule encoding interleukin-12 and costimulatory molecule,
XX      operably linked to promoter that directs the expression of DNA molecule
XX
XX      Example 1; Page 38-43; 76pp; English.
XX
XX      The invention relates to an expression system which comprises a DNA
XX      molecule encoding interleukin (IL)-12 and a costimulatory molecule,
XX      operably linked to a promoter that directs the expression of the DNA
XX      molecule. Expression vectors of the invention are useful for in vitro
XX      generation of genetically modified human cancer cells for cancer
XX      therapy. These cells share phenotypes of both antigen presenting cells
XX      and cancer cells and are suitable as a cellular vaccine for certain
XX      types of cancer. Expression vectors are useful for eliciting an anti
XX      tumour immune response in a individual. They are useful for activating
XX      T cells for immunotherapeutic responses against primary or metastatic
XX      cancers. The present sequence is pIRS-hb7-1-IL12.4 vector DNA.
XX      This vector comprises cytomegalovirus (CMV) promoter and enhancer,
XX      bacteriophage T7 RNA polymerase promoter, human B7-1 DNA, IRES sequence,
XX      human IL-12.4 DNA, bacteriophage T3 RNA polymerase promoter,
XX      Simian virus 40 (SV40) fragment containing polyadenylation signal, fl
XX      origin of replication, Neo r expression cassette and ampicillin
XX      resistance sequence.
XX
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XX      Query Match:      85.56%      Indels:      16
XX      DB:      24      Gaps:      3
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XX
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QY 41 AlaglnserSerGluValLeuGlySerGlyLysThrThrLeuThrIleGlnValLysGluPhe 60
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 QY 121 TrpTyrLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArGlyPhe 140
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 Db 3066 TGGTGGCTGACGACAAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGCTCT 3125
 QY 141 SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArGValArGVal 160
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 QY 161 AspAsnArGAspTyrLysLysTyrThrValGluCysGlnGlnLysSerAlaCysProSer 180
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 Db 3186 GACAAACAAGAGATAT--GAGTACTCAGTGGAGTGCAGAGGAGCAGTGCCTGCCAGCT 3242
 QY 181 AlaglnGlnSerLeuProIleGlnValValValAspAlaIleHisLysLeuLysTyrGlu 200
 |||||
 Db 3243 GCTGAGAGAGTGTGCCCATTTGAGTGTATGTTGATGCTCCGTCAAGCTCAAAATATAGAA 3302
 QY 201 AsnTyrThrSerSerPhePheIleArGAspIleIleLysProAspProProThrAsnLeu 220
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 Db 3843 ATCACAAAAGATAAACACAGCAGCTGAGGCCCTGTTTACATTTGAATTAACCAAGAT 3902

QY 386 GluSerCysLeuAlaSerArGlnLysSerLeuIleThrAsnGlySerCysLeuAlaSer 405
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 QY 406 GlyLysAlaSerPheMetThrValLeuCysLeuSerSerIleTyrGlnLysPheLysMet 425
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 QY 426 TyrGlnMetThrLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIle 445
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 Db 4023 TACAGGTGAGTTCAGAACATGATGCAAACTTCTGATGATCTTAAGAGCAGATC 4082
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 ID AAD31550 standard; DNA: 8659 BP.
 AC AAD31550;
 XX 18-JUN-2002 (first entry)
 DE pIRES-TL12.4-hb7-1 vector DNA.
 XX Expression system; interleukin-12; cancer therapy; cellular vaccine;
 KW immunotherapeutic response; IL-12.4; chimeric; human; Simian virus 40;
 KW SV40; cytomegalovirus; CMV; ds.
 XX Chimeric - Cytomegalovirus.
 OS Chimeric - Bacteriophage T7.
 OS Chimeric - Homo sapiens.
 OS Chimeric - Bacteriophage T3.
 OS Chimeric - Rhesus macaque polyoma virus.
 OS Chimeric - Unidentified.
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 FT enhancer
 FT 1..750
 FT /tag= a
 FT /note= "CMV enhancer; Also serves as a promoter"
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 FT /tag= b
 FT /note= "T7 RNA polymerase promoter"
 FT 1090..2756
 FT /tag= c
 FT /note= "Human IL-12.4 DNA"
 FT 1103..2746
 FT /tag= d
 FT /product= "Human IL-12.4 protein"
 FT 2087..2146
 FT /tag= e
 FT /note= "Linker of human IL-12.4 sequence"
 FT 2782..3362
 FT /tag= f
 FT /note= "IRES sequence"
 FT 3399..4293
 FT /tag= g
 FT /note= "Human B7-1 DNA"
 FT 4413..4434
 FT /tag= h

QY 1 ILETPGILuLeuGluLysAspValTyrValValGluLeuAspTrpHisProAspAlaPro 20
 Db 2706 ATATGGGAACCTAAGAAAGATGTTATATGCTAGAAATTGGATTGGATCCGAGTCCCT 2765
 QY 21 GlyIuMetValValLeuThrCysHisThrProGluGluAspAspIleThrTrpHisSer 40
 Db 2766 GCAGAAATGGTGCTCTCCTACCTGTGCACCCCTGAAGAAGATGGATTCACCTGGACCTTG 2825
 QY 41 AlaGlnSerSerGluValLeuGluSerGlyLysThrLeuThrIleGlnValLysGluPhe 60
 Db 2826 GACCAGAGCAGTGGAGCTTTAGCTGTGCAGAAACCCTGCACCATTCACAGTCAAGAGATT 2885
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 Db 3126 TCTGACCCCAAGAGGGTGCAGCTGCGAGCTGCTACACTCTGTGCAGAGAGACGAGAGG 3185
 QY 161 AspaAsnArgAspTyrLysLysTyrThrValIleGlyGlnGlySerIleAcysProSer 180
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 QY 181 AlaGluGlnSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
 Db 3243 CCGTAGAGAGAGTCTCCCATTCAGTGCATGAGTGCAGTCCGTTCCACAGCTCAAGTATGAA 3302
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 Db 3303 AACTCACCAGCAGCTTCTTCATCAGGACATCATCAAACTGACCCCAACAACCTTG 3362
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 QY 261 AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValValCysHis 280
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QY 361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
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 QY 381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
 Db 3828 GAATTACCAAGAAATAGAGTGGCTTAATTCAGAGAGACCTCTTTCATTAACATAATGGG 3887
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 QY 421 GluAspLeuLysMetGlyGlnMetGluPheLysAlaMetAsnAlaLysLeuMetAsp 440
 Db 3948 GAGACTTAAGATGTACACAGGTGGAGTTCCAGACCATGATTAATGCCAAGCTTGTGATGAT 4007
 QY 441 ProLysArgGlnIlePheLeuAspGluAsnMetLeuThrAlaIleAspGluLeuGln 460
 Db 4008 CCTAAGAGCAGACTTCTTCTAGATCAAAACATGCTGCGAGTTATGATGAGCTGATGACG 4067
 QY 461 AlaLeuAsnPheAsnSerValThrValProGlnLysSerSerLeuGluLysProAspPhe 480
 Db 4068 GCCCTGAATTTCAACAGTGAAGTGTGCCACAAAATCCTCCCTGAAGACCGGATTTT 4127
 QY 481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
 Db 4128 TATTAACCTAAATCAAGCTCTGCATCTTCTTCATGCTTTCAGAAATTTGGCGCAGTACT 4187
 QY 501 IleAsnArgMetMetSerTyrLeuAsnSerSer 511
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 AC AAD31546;
 XX
 DF 18-JUN-2002 (first entry)
 XX
 DE PIRRES-hb7-1-11L12.0 vector DNA.
 XX
 KW Expression system; interleukin-12; cancer therapy; cellular vaccine;
 KW immunotherapeutic response; IL-12; chimeric; human; Simian virus 40;
 KW SV40; cytomegalovirus; CMV; ds.
 XX
 OS Chimeric - Cytomegalovirus.
 OS Chimeric - Bacteriophage T7.
 OS Chimeric - Homo sapiens.
 OS Chimeric - Bacteriophage T3.
 OS Chimeric - Rhesus macaque polyoma virus.
 OS Chimeric - Unidentified.
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XX      14-FEB-2002.
XX      10-APR-2001; 2001US-0828825.
XX      27-JUL-2000; 2000KR-0043498.
XX      (LEES/) LEE S.
XX      (KIMH/) KIM H.
XX      Lee S, Kim H:
XX      WPI: 2002-239247/29.
XX      P-PSDB; AAE19818.
XX      New expression system, useful as vaccine for treating cancer, comprises
XX      DNA molecule encoding interleukin-12 and costimulatory molecule,
XX      operably linked to promoter that directs the expression of DNA molecule
XX      Example 1; Page 17-22; 76pp; English.
XX      The invention relates to an expression system which comprises a DNA
XX      molecule encoding interleukin (IL)-12 and a costimulatory molecule,
XX      operably linked to a promoter that directs the expression of the DNA
XX      molecule. Expression vectors of the invention are useful for in vitro
XX      generation of genetically modified human cancer cells for cancer
XX      therapy. These cells share phenotypes of both antigen presenting cells
XX      and cancer cells and are suitable as a cellular vaccine for certain
XX      types of cancer. Expression vectors are useful for eliciting an anti
XX      tumour immune response in an individual. They are useful for activating
XX      T cells for immunotherapeutic responses against primary or metastatic
XX      cancers. The present sequence is pIRES-hb7-1-IL12.0 vector DNA.
XX      This vector comprises cytomegalovirus (CMV) IE promoter and enhancer,
XX      bacteriophage T7 RNA polymerase promoter, human B7-1 DNA, IRES sequence,
XX      human IL-12.0 DNA, bacteriophage T3 RNA polymerase promoter,
XX      Simian virus 40 (SV40) fragment containing polyadenylation signal, f1
XX      origin of replication, Neo r expression cassette and ampicillin
XX      resistance sequence.
XX      Sequence 8578 BP; 2176 A; 2122 C; 2120 G; 2160 T; 0 other;

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 Percent Similarity: 89.82% Conservative: 27

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DB      |||||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
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DB      |||||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
DB      TGGTGGCTGACGAAACACTACTGATTTACATTCAGTCCAAAGACCAAGAGGCTCT 3125
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DB      |||||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
DB      AACTACACGACGACCTTCTTATCAGGAGCATATCAAACTGACCCACCAACMACTTG 3362
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Db 3768 ATTGATCATGAAGATATCATCAAAAGATAAACACACAGACAGAGCCCTGTTTACCATTG 3827
QY 381 GluLeuThrMetLanGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
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Db 3828 GAATTAACCAAGATGAGAGTTGGCTTAATTCCACAGACACCTCTTTCATTAATATGGG 3887
QY 401 SerCysLeuAlaSerGlyLysAlaSerPheMetThrValIleCysLeuSerSerIleTyr 420
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3888 AGTTGGCTGGCTCCAGAAACACCTCTTTATGATGAGCCCTGTGCTTATGATATTTAT 3947
QY 421 GluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3948 GAAGACTTGAGAGATGTACAGGTGAGTTCAAGACATGAATGCAAAAGCTTCTGATGAT 4007
QY 441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuGln 460
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4008 CCTAAGAGCGAGATCTTTCTAGATCAAAACATGCTGGCAGTTATTGATCAGCTGATGAG 4067
QY 461 AlaLeuAsnPheAsnSerValThrValProGlnLysSerSerLeuGluProAspPhe 480
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4068 GCCCTGAATTTCAACAGTACAGTCTGTGCACAAAATCTCCCTTGAAGAACCGATTTT 4127
QY 481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4128 TATTAACCTAAATCAACCTCTGCATCTTCTTCATGCTTTCACAAATTCGGGACAGTACT 4187
QY 501 IleAsnArgMetMetSerTyrLeuAspSerSer 511
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4188 ATGTATGAGTGTAGTACTATCTGATGCTTCC 4220

RESULT 10
AAV13817
ID AAV13817 standard: cDNA to mRNA: 990 BP.
XX
AC AAV13817:
XX
DT 14-MAY-1998 (first entry)
XX
DE Canine IL-12 P40 subunit cDNA.
XX
KW Canine: Interleukin-12 P40 subunit; IL-12 P40 subunit; antitumour;
KM antiviral; vaccine adjuvant; ds.
XX
OS Canis sp.
XX
FH
FT Key Location/Qualifiers
FT CDS 1..990
FT /tag= a
FT /product= interleukin-12_P40_subunit

JPI0036397-A.
PD 10-FEB-1998.
XX
XX 08-NOV-1996: 96JP-0296789.
PF
XX 23-MAY-1996: 96JP-0128104.
PR 08-NOV-1995: 95JP-0289729.
XX
XX (TORA ) TORAY IND INC.
PA WPI: 1998-174914/16.
XX P-PSDB: AAM41791.
DR
XX Canine interleukin 12 - comprises P40 and p35 subunits; useful in
PT veterinary medicine, e.g. antitumour, antiviral and vaccine adjuvant
```

```
PT activities are expected
XX
XX Claim 10: Pages 10-11; 12pp: Japanese.
XX
CC The present sequence encodes a canine interleukin-12 (IL-12) P40
CC subunit. A canine IL-12 comprising a P40 and p35 subunit is capable
CC of inducing an antiviral activating factor and the expression of
CC class II MHC molecules in canine tumour cells, stimulating
CC proliferation of canine blastogenic lymphocytes and activating
CC canine leukocytes to inhibit canine tumour cells. The canine IL-12
CC can be used in veterinary medicines, e.g. antitumour, antiviral and
CC vaccine adjuvant activities are expected.
XX
SQ Sequence 990 BP: 279 A; 244 C; 249 G; 218 T; 0 other:

Alignment Scores:
Pred. No.: 5,72e-137 Length: 990
Score: 1653.00 Matches: 307
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 61.38% Indels: 0
DB: 19 Gaps: 0

US-09-917-265-67 (1-511) x AAV13817 (1-990)
QY 1 IletFPGIuLeuGluLysAspValTyrValIleGluLeuAspTPRHisProAspAlaPro 20
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 67 ATATGGAACTGGAAGAAAGATGTTATATGTTGATGACTGGACCCCTGATCCCCC 126
QY 21 GlyIuMetValIleLeuThrCysHisThrProGluGluAspAspIleThrTPRHisSer 40
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 127 GGAGAAATGGTGGTCCCTCACCTGCATCCCTGAAGAAAGATGACATCCTGGACCTCA 186
QY 41 AlaGlnSerSerGluValLeuGluSerGlyLysThrLeuThrIleGlnValLysGluPhe 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 187 GCGGACACAGTGAAGTCTTAGTCTGTAAACCTGACCATCCAGTCAAAAGATTT 246
QY 61 GlyAspAlaGluGlnTyrThrCysHisLysGlyGlyLysValLeuSerArgSerLeuLeu 80
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 247 GGAGATGCTGGCCAGTATACCTGCCATTAAGAGGCAAGGTTCTGACCCGCTACTCTCG 306
QY 81 LeuIleHisLysLysGluAspGlyIleTPRSerThrAspIleLeuLysGluGlnLysGlu 100
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 307 TTGATTTCAAAAAAAGAAAGATGGAATTTGGTCCATCATATCTTAAGGAACAGAAAGA 366
QY 101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 367 TCCAAAAATTAAGATCTTCTGAAATGTAGGCAAGAAATTAATTCGACGTTTCACATGC 426
QY 121 TRPTRPLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerArgGlyPhe 140
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 427 TGTGGCTGACGGCAGATCAGTACGATTTTGAATTCAGTTCAAAAGTACGAGAGGCTTC 486
QY 141 SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgVal 160
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 487 TCTGACCCCAAGGAGGTGACATGTGAGACAGTACATTTCAGAGAGGAGGTGAGAGTG 546
QY 161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProSer 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 547 GACAACAGGAGATTAATAGAGTACAGTGTGAGTGTGAGAGGAGGAGTCCGCCCTCT 606
QY 181 AlaGluGlnSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 607 GCCGAGGAGAGGCTTACCATCGAGTCTGCTGCTGCTGCTATTTCACAGCTCAAGTATGAA 666
QY 201 AsnTyrThrSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeu 220
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 667 AACTACACACAGAGCTTCTTCATCAGACATCATCAACACAGACCCACCAACCTG 726
QY 221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTTPGluTyrProAspThr 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 727 CAGTGAAAGCCATTGMAAAATTCGCGCAGCGTGGAGGTGAGTGGGAATACCCGACACCC 786
```

QY 241 TrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 260
 DB 787 TGGAGCACCACCATTCCTACTCTCTCCGACATTTTGCAATACAGCCGAGGCAAGAAC 846
 QY 261 AsnArgGlnLysLysAspArgLeuGlyValAspLysThrSerAlaLysValAlaCysHis 280
 DB 847 AATAGAGAAAAGAAAGATAGACTCTGCTGACAAAGCCTCAGCCAAAGTCTGTGCCAC 906
 QY 281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTyrPseAsp 300
 DB 907 AAGGATGCCAAGATCCCGCTGCAGCAAGCCGACCGCTATAGTTCATCTCTGAGAGCAG 966
 QY 301 TrpAlaSerValSerCysSer 307
 DB 967 TGGGCATCTGTCTCTCCACT 987
 RESULT 11
 AAX35625
 ID AAX35625 standard; cDNA to mRNA; 990 BP.
 AC AAX35625;
 XX
 DT 09-JUL-1999 (first entry)
 XX
 DE Nucleic acid encoding canine Interleukin-12 (IL-12).
 XX
 KM Interleukin-12; IL-12; dog; cat; immune disease; CatIL12; heterodimer;
 KM tumour; skin disease; infectious disease; allergic disease; ds.
 XX
 OS Canis sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..990
 FT /*tag= a
 FT
 XX
 PN JP11106350-A.
 XX
 PD 20-APR-1999.
 XX
 PF 15-MAY-1998; 98JP-0133345.
 XX
 PR 07-AUG-1997; 97JP-0213755.
 PR 16-MAY-1997; 97JP-0127690.
 XX
 PA (TORA) TORAY IND INC.
 XX
 DR WPI; 1999-308068/26.
 DR P-PSDB; AAY02342.
 XX
 PT A prevention and treating agent containing interleukin 12 (CatIL12) -
 XX for prevention and treatment of dog and cat immune diseases
 PS Claim 1; Page 14-15; 16pp; Japanese.
 XX
 CC The present sequence encodes canine interleukin-12 (IL-12). The
 CC specification describes a method for the prevention and treatment
 CC of dog and cat immune diseases. The treatment used an agent comprising
 CC dog IL-12 (CatIL12) proteins to form a heterodimer. The agent is
 CC useful for preventing and treating dog and cat immune diseases,
 CC including tumours, skin diseases, infectious diseases and allergic
 CC diseases.
 XX
 SQ Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 other;
 Alignment Scores:
 Pred. No.: 5.72e-137 length: 990
 Score: 1653.00 Matches: 307
 Percent Similarity: 100.008 Conservative: 0
 Best Local Similarity: 100.008 Mismatches: 0
 Query Match: 61.38% Indels: 0
 DB: 20 Gaps: 0
 US-09-917-265-67 (1-511) x AAX35625 (1-990)

QY 1 IleTrpGluLeuGlnLysAspValTyrValValGlnLeuAspTrpHisProAspAlaPro 20
 DB 67 ATATGGGAAGTGGAGAAAGATGTTTATGTTGTAAGAGTGGACCTGATGCCCC 126
 QY 21 GlyGluMetValValLeuThrCysHisThrProGlnGluAspAspIleThrTrpThrSer 40
 DB 127 GGAGAAATGGTGGTCTCCACCTCCATACCCCTGAAGAAAGATGACATCATCTTGACCTCA 186
 QY 41 AlaGlnSerSerGlnValLeuGlnLysSerGlyLysThrLeuThrIleGlnValLysGluPhe 60
 DB 187 GCCCAGACGAGTAAAGTCCCTAGCTTCTGGTAAACTCTGACCATTCAGATGCAAGATTT 246
 QY 61 GlyAspAlaGlyGlnTyrThrCysHisLysGlyGlyLysValLeuSerArgSerLeuLeu 80
 DB 247 GGAGATGCTGGCCAGATATACCTGCATTAAGAGGCAAGGTTCTGAGCCGCTCAGTCTG 306
 QY 81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnGly 100
 DB 307 TTGATTCACAAAAAGAAAGATGGAAATTTGGTCCACTGATATCTTAAAGCAACGAAAGAA 366
 QY 101 SerLysAsnLysIlePheLeuLysCysGlnAlaLysAsnTrpSerGlyArgPheThrCys 120
 DB 367 TCCAAAATATAGATCTTTTCTGAAATGTGAGGCANAGATTTATCTGACGCTTTCACATGC 426
 QY 121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
 DB 427 TGGTGGGTGACGGCATACACTGACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGCTTC 486
 QY 141 SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgVal 160
 DB 487 TCTGACCCCAAGAGGGGTGACATGTGAGCAGTGCACCTTCCACAGAGAGGCAAGAGTG 546
 QY 161 AspAsnArgAspTyrLysLysTyrThrValGlnCysGlnGlnLysSerAlaCysProSer 180
 DB 547 GACAAACAGGATTTATAAGAAAGTACAGAGTGAAGTGCAGAGGCGAGTGCCTCTCT 606
 QY 181 AlaGlnLysLeuLeuProIleGlnValValAlaLysPalaIleHisLysLeuLysTyrGlu 200
 DB 607 GCCGAGAGAGCCTACCCATCGAGTGTGTGTGATGTATCAACAAGCTCAAGTATGAA 666
 QY 201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPheTrpAsnLeu 220
 DB 667 AACTTACACGACAGCTTCTTCATCAGACATCATCAAAACCAAGCCCAAAACCTG 726
 QY 221 GlnLeuLysProLeuLysAsnSerArgHisValGlnValSerTrpGlnTyrProAspTrp 240
 DB 727 CAGCTGAGGCATTTGAAAAATTTCTCGCAGCTGAGAGTCAAGTGGGAATACCCGACACC 786
 QY 241 TrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 260
 DB 787 TGGAGCACCACCATTCCTACTCTCTCCGACATTTTGCAATACAGCCGAGGCAAGAAC 846
 QY 261 AsnArgGlnLysLysAspArgLeuGlyValAspLysThrSerAlaLysValAlaCysHis 280
 DB 847 AATAGAGAAAAGAAAGATAGACTCTGCTGACAAAGCCTCAGCCAAAGTCTGTGCCAC 906
 QY 281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTyrPseAsp 300
 DB 907 AAGGATGCCAAGATCCCGCTGCAGCAAGCCGACCGCTATAGTTCATCTCTGAGAGCAG 966
 QY 301 TrpAlaSerValSerCysSer 307
 DB 967 TGGGCATCTGTCTCTCCACT 987
 RESULT 12
 AAX03162
 ID AAX03162 standard; cDNA to mRNA; 990 BP.
 AC AAX03162;
 XX
 DT 30-MAR-1999 (first entry)
 XX

DE Nucleic acid encoding canine interleukin 12.
XX
XX Canine: interleukin 12; IL-12; feline: immunological disease: tumour:
KM skin disease: viral infection: allergic disease: breast tumour:
KM oesinophilic granuloma: epidermoid tumour; skin tumour; lipoma:
KM othematoma; pneumoedema; skin soft pedicled soft tumour; anal tumour;
KM otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KM allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KM dog parvovirus infection: distemper virus: cat plaque virus infection:
KM feline leukemia; allergy: pollinosis; ds.
XX
OS Canis sp.
XX
XX Key Location/Qualifiers
FH CDS 1..990
FT /*tag= a
FT /product= interleukin_12
XX
XX MO9851327-A1.
XX
XX 19-NOV-1998.
XX
XX 07-MAY-1998; 98MO-JP02031.
XX
XX 16-MAY-1997; 97JP-0127690.
XX
XX (TORA) TORAY IND INC.
XX
XX Okano F, Satoh M, Yamada K:
XX
XX WPI: 1999-070100/06.
XX P-PSDB: AAW84373.
XX
XX New therapeutic and prophylactic agents - comprise
PT genetically-engineered canine interleukin 12, used to treat, e.g.
PT canine and feline immunological diseases
XX
XX Claim 1; Page 30-32; 45pp: Japanese.
XX
XX The present sequence encodes a canine interleukin 12 (IL-12) protein.
CC The IL-12 protein can be used in therapeutic or prophylactic agents.
CC The agents can be used to prevent and treat canine and feline
CC immunological diseases including dog and cat tumours, skin diseases,
CC viral infections and allergic diseases, especially tumours, breast
CC tumour, oesinophilic granuloma, epidermoid tumour, skin tumour, lipoma,
CC othematoma, pneumoedema, skin soft pedicled soft tumour and anal
CC tumour; skin diseases, otitis externa, dermatitis, eczema, fungal
CC diseases of the skin, pyoderma, allergic dermatitis, nettle rash,
CC traumatic dermatitis and hair loss; infections: dog parvovirus infection
CC and distemper virus, cat plaque virus infection and feline leukemia, and
CC allergic diseases, e.g. pollinosis.
XX
XX Sequence 990 BP: 279 A; 244 C; 249 G; 218 T; 0 other:
SO
Alignment Scores:
Pred. No.: 5,72e-137 Length: 990
Score: 1653.00 Matches: 307
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 61.38% Indels: 0
DB: 20 Gaps: 0
US-09-917-265-67 (1-511) x AAX03162 (1-990)
QY 1 11etTtG1uLeuCluLysAspValTYrValValG1uLeuAspTrpHisProAspAlaPro 20
DB 67 ATATGGAACTGAGAAAGATCTTATGTTGTAGACTTGACCTGCACCTCGATGCCCC 126
QY 21 G1AG1MeiValValLeuThrCysHisThrProGluGluAspSpleThrTrpThrSer 40
DB 127 GGAAGAAATGGTGCTCTCCATCCCATCCCTGGAAGAGATGACATCTGACCTCA 186
QY 41 AlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60

DB 187 GCCGAGAGCAGTGAAGTCTAGGTTCTGTGAAAACTCGACCATCTCAAGTCGAAGAATT 246
QY 61 GlyAspAlaGlyGlnTYrThrCysHisLysGlyValLysValLeuSerArgSerLeuLeu 80
DB 247 GGAGATGCTGGCCAGTATACCTGCCATTAAGGAGGCAAGGTTTCGACCCGCTCACTCTG 306
QY 81 LeuIleHisLysLysGlyAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGlu 100
DB 307 TTGATTACAAAAAGAAAGATGAAATTTGGTCCCTATATCTTTAAAGGAACAGAAAGAA 366
QY 101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTYrSerGlyArgPheThrCys 120
DB 367 TCCAAAAATTAAGATCTTCTGAAATGTGAGCAAAAGAAATTAATCTGACGCTTCACATGC 426
QY 121 TrpTrpLeuThrAlaIleSerThrAspLeuLysTheserValLysSerSerArgGlyPhe 140
DB 427 TGGTGCTGACGGCAATCAGTACGATTTGAAATTCAGTGCAAAGTACGAGAGGCTTC 486
QY 141 SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgVal 160
DB 487 TCTGACCCCCCAAGGGGTGACATGTGGAGCACTGACACTTTCAGCAGAGAGGCTCAGAGTG 546
QY 161 AspAsnArgAspTYrLysTYrThrValGluCysGlnGlnGlySerAlaCysProSer 180
DB 547 GACACACAGGATTTAAGAAAGTACACAGTGAAGTGCAGAGGGCAGTGCCTGCCCTCT 606
QY 181 AlaGluLysLeuProIleGluValValAlaLysAlaIleHisLysLeuLysTYrGlu 200
DB 607 GCCGAGGAGAGCCATCCATCGAGTGTGGTGTGCTATTCAAGCTCAAGCTCAAGTATGAA 666
QY 201 AspTrpThrSerSerPhePheIleArgAspIleIleLysProAspProThrAspLeu 220
DB 667 AACTACACCGACACTTCTTCATCAGACATCAACAACCGACACCAACCAACCTG 726
QY 221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTYrProAspThr 240
DB 727 CAGCTGAAGCATTTGAAAAATTCCTGGCAGCTGGAGGTCAAGCTCGAATACCCGACACC 786
QY 241 TrpSerThrProHisSerTYrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 260
DB 787 TGGAGCACCCACCATTTCTTACTCTCCCTGACATTTTGCAATACAGGCCAGGCGCAAGAC 846
QY 261 AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValCysHis 280
DB 847 AATGAGAAAAAGAAAGATAGACTGCTGGTGAAGACCTAGCCAAAGTGTGTGCGAC 906
QY 281 LysAspAlaLysIleArgValGlnAlaArgAspArgTYrTYrSerSerSerTrpSerAsp 300
DB 907 AAGCATGCCAAAGATCCGCGTGCAGACCCGAGACCGGTACATATACTTCATCTGAGAGGAC 966
QY 301 TrpAlaSerValSerCysSer 307
DB 967 TGGGCATCTGTCTCTCCAGT 987
RESULT 13
AA164388
ID AA164388 standard; DNA; 990 BP.
XX
AC AA164388:
XX
XX 23-NOV-2001 (first entry)
XX
DE Canine coding sequence #3.
XX
DE Canine: dog: immunostimulant; interleukin 12; IL12; immunopathy; ds.
XX
XX Canis familiaris.
XX
XX key Location/Qualifiers
FH CDS 1..990
FT /*tag= a
FT /product= "Canine protein #1"

FT sig_peptide 1..66
 FT mat_peptide /tag- b
 FT 67..987
 FT /tag- c
 PN JP2001161378-A.
 PD 19-JUN-2001.
 XX 26-SEP-2000: 2000JP-0292946.
 PF 01-OCT-1999: 99JP-0281234.
 PR (TORA) TORAY IND INC.
 PA WPI: 2001-592466/67.
 DR P-PSDB: AAG66482.
 XX
 XX Preparation of a highly pure protein, interleukin 12, a protein
 PT inhibiting the activity of interleukin 12, and a treating agent and a
 PT treating method for immunopathy of mammalian
 PS Claim 6: Page 16-17; 21pp; Japanese.
 CC The present invention relates to a method for the preparation of a highly
 CC pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
 CC the activity of IL12 is contacted to an ion exchanging carrier and/or a
 CC pigment carrier to get IL12 and/or a protein inhibiting the activity of
 CC IL12. The protein is used as a preventive agent for dog immunopathy. The
 CC present sequence was used in the method of the present invention.
 XX
 SO Sequence 990 BP: 279 A; 244 C; 249 G; 218 T; 0 other:

Alignment Scores:
 Pred. No.: 5,72e-137 Length: 990
 Score: 1653.00 Matches: 307
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 61.38% Indels: 0
 DB: 22 Gaps: 0

US-09-917-265-67 (1-511) x AAI64388 (1-990)

QY 1 ILETTPGILUENGILULYSASPYALTYRVALGLULEUASPTRPDISPROASPALAPRO 20
 DB 67 AATGGGAAGTGGAGAAAGATGTTATGTGTAGAGTTGGACGACCCCTGATGCCCCC 126
 QY 21 GLYGLUMETVALLEUTHRCYSHSTRPRROGLUGLASAPSLLEHTRTPHRSER 40
 DB 127 GGAGAAATGGTGTCTCACTGCTGACCTGACCTGAAAGAAAGATGACATCACTTGACCTCA 186
 QY 41 ALAGINSERSERGLUVALLEUGLYSERGLYSTRLEUTHRIEGLINVALYSGIUPHE 60
 DB 187 GCGCAGACGACGAGAAAGTCTAGGTCTGTGTAAGCTGACCATCCAAAGCAAGATTT 246
 QY 61 GLYASPALAGLYGINTYRTHRCYSHSLYSGLYGLYVALLEUSERASERGLULEU 80
 DB 247 GGAGATGCTGGCCAGATACCTGCTCCATTAAGGAGGCAAGTCTGACGCTCCTCTG 306
 QY 81 LEULIEHLSLYSLYSLUASPGLYLLETTPSERTHASPILEULEUYSGLUGLNUYSGLU 100
 DB 307 TTGATTCACAAAAGAAAGATGAATTTGCTCCACGATATCTTAAGGAGCAAGAAAGAA 366
 QY 101 SERLYASNLYSILEPHELEULYSCYGLUALALYASNTYSERGLYRGPHEHRCYS 120
 DB 367 TCCAAAATAATAGATCTTTCTGAAATGTGAGGCAAGAAATATTCTGAGCTTTACATGC 426
 QY 121 TTPTPLEUTHRALALESERTHASPLEULYSPHESEVALYSSERASERGLYPHE 140
 DB 427 TGGTGGCTGACGCAATCAGTACTGATTTGAATTCAGTCAAAAGTGCAGAGGCTTC 486
 QY 141 SERASERPROGLINGLYVALTHRCYSGLYALAVALTHREUSERALAGLUARYVAL 160

DB 487 TCTGACCCCCAAGGGGTGACATGTGAGCAGATGACACTTTTCAGCAGAGAGGGTCAAGTGG 546
 QY 161 ASPASNARGASPTYRTHRYSTYRTHRVALLGLUCYSGINGLYSERALACYSPROSER 180
 DB 547 GACACAGGAGATTATAGAAAGTACACAGTGGAGTGCAGAGAGGAGTGCCTGCCCTCT 606
 QY 181 ALAGLUISERLEUPROILEGLUVALVALASPALALEHLSLYSLEULYSTYRGLU 200
 DB 607 GCCGAGAGAGCTTACCCATCGACGCTGTGTGATGTATTACAAAGCTCAAGTATGAA 666
 QY 201 ASNTYTRHRSERPHAEHLEARGAPLIELELYSPROASPROPROTHRSANLEU 220
 DB 667 AACTTACACAGAGCTTTTCATTCAGACATATCAAAACAGACCCCAACACCTG 726
 QY 221 GINLEULYSPROLEULYSANSEARGHISVALGLUVALISERTRP5LUYTRPROASPTHR 240
 DB 727 CAGCTAACCCATGTGAAAATTTCTGCGACGTRGAGAGTCAAGTGGGAATACCCCGACAC 786
 QY 241 TRPSETRTHPROHISSETRYPHESERLEUTHRPHECYSILEGLNALAGLNUYLSAN 260
 DB 787 TGGAGCAGCCCACTTCCTCTCTCCATTTTCATACAGGCGCCAGGCAAGAAC 846
 QY 261 ASNARGGLULYSLYSPARGLEUCYSVALASPLYSTRSERALALYVALCYSHS 280
 DB 847 AATAGAGAAAGAAAGATAGACTCTGCTGGACAAAGACCTCAAGGTGCTGCTCAC 906
 QY 281 LYSASPALALYSILEARGVALGNAIARASPARITYRYSERSETRTPSERASP 300
 DB 907 AAGGATGCCAAGATCCGCTGCAGAACGCCGAGACCGCTACTATAGTTCATTCGAGACGAC 966
 QY 301 TRPALASERVALSERCYSSER 307
 DB 967 TGGCATCTGTGTCTCTGCACT 987

RESULT 14
 ID AAV13816 standard; cDNA to mRNA. 990 BP.
 AC AAV13816;
 DT 14-MAY-1998 (first entry)
 DE Canine IL-12 P40 subunit cDNA.
 XX
 XX Canine; interleukin-12 P40 subunit; IL-12 P40 subunit; antitumour;
 KW antiviral; vaccine adjuvant; ds.
 XX
 OS Canis sp.
 FH
 FT Key Location/Qualifiers
 FT CDS 1..990
 FT /tag- a
 FT /product- interleukin-12_P40_subunit
 PN JP10036397-A.
 PD 10-FEB-1998.
 XX
 XX 08-NOV-1996: 96JP-0296789.
 PF 23-MAY-1996: 96JP-0128104.
 PR 08-NOV-1995: 95JP-0289729.
 XX
 PA (TORA) TORAY IND INC.
 DR WPI: 1998-174914/16.
 DR P-PSDB: AAM41790.
 XX
 XX Canine interleukin 12 - comprises P40 and P35 subunits; useful in
 PT veterinary medicine, e.g. antitumour, antiviral and vaccine adjuvant
 PT activities are expected
 PS Claim 8: Page 8; 12pp; Japanese.


```
Db 67 ATATGGGAACGTGAGAAAGATGTTATGTTGTAGAGTTGAGCTGGACCGACCCGTGATGCCCCC 126
QY 21 GlyIuMetValValLeuThrCysHisThrProGluGluAspAspIleThrTrpThrSer 40
Db 127 GGAGAAATGGTGTCTCCTGACCTGCGATACCCCTGAAGAGATGACATCCTTGACCTCA 186
QY 41 AlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
Db 187 GCGCAGAGACGTGAGTGAAGTCTGAGTAAAGCTGACCATCCAAAGTCAAGAAATTT 246
QY 61 GlyAspAlaGlyGlnThrCysHisLysGlyGlyLysValLeuSerArgSerLeuLeu 80
Db 247 GGAGATGCGGGCCAGTATACCTGCGCATAAAGAGGCAAGGTTCTGAGCGGCTCCTCG 306
QY 81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGlu 100
Db 307 TTGATTCCACAAAAGAACAGATGGAATTTGGTCCACTGATATCTTAAGAGACAGAAAGAA 366
QY 101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
Db 367 TCCAAAATATAGATCTTCTGAAATGTGAGCCAAAGAAATTAATCTGACGTTTCACATGC 426
QY 121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
Db 427 TGGTGCGTGCAGCGCAATCAGTACTGATTGAAATTCAGTCAAAAGTAGCAGAGGCTTC 486
QY 141 SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgVal 160
Db 487 TCTGACCCCAAGGGGTGACATGTGAGCAGAGTGCACCTTCAGCAGAGAGGGTCAGAGTG 546
QY 161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProSer 180
Db 547 GACACACAGGATTAATGAAGATACACAGTGCAGTGCAGAGGCGAGTGCCTGCCCTCT 606
QY 181 AlaGluGluSerLeuProIleGluValValAlaAspAlaIleHisLysLeuLysTyrGlu 200
Db 607 GCGGAGGAGAGCCCTACCATCGAGGTGCGTGGATGCTATTCACAAAGCTCAAGTATGAA 666
QY 201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeu 220
Db 667 AACCTACACGACGAGCTTCTTCATCAGACATCATCAACACAGCCACCAAAACCTG 726
QY 221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
Db 727 CAGCTGAAAGCCATTGGAATAATTCTCGCACGTCGAGTGCAGTGGGAATACCCCGACACC 786
QY 241 TrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 260
Db 787 TGGAGACCCCAATTCTCTACTCTCCCTGACATTTTGGCATACAGGCCCAAGGCAAGAAC 846
QY 261 AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValValCysHis 280
Db 847 AATAGAGAAAGAAAGATAGACTCTGCGTGGACAGACCTCAGCCAAAGTCTGTGCGCAC 906
QY 281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsp 300
Db 907 AAGGATGCCAAGATCCGCGTCAAGCCGAGACCGCTACTATATGTTCACTCATCTGAGCGAC 966
QY 301 TrpAlaSerValSerCysSer 307
Db 967 TGGGCATCTGTGCGCTGCAGT 987
```

Search completed: July 16, 2003, 20:25:18
Job time : 393.279 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: July 16, 2003, 19:41:51 ; Search time 2430.6 Seconds

(without alignments)
3404.880 Million cell updates/sec

Title: US-09-917-265-67
Perfect score: 2693
Sequence: 1 IMLEKDVYVELDMHPDP.....HAFRIAVTIRNMSTYLNSS 511

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n model -DEV=xlh
-O=/cgn2.1/USPRO/spool/US09917265/tunat_15072003_092107_1610/app.query.fasta_1_3114
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human4.0.cdi -LIST=45
-DOCALIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09917265.ecgn.1.1.6304.gunat.15072003.092107.1610 -NCPU=6 -ICPU=3
-NO.MMAP -LARGOQUERY -NEG.SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOC
-DEV.TIMEOUT=130 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
EST :
1: em_estba:*
2: em_esthum:*
3: em_estcin:*
4: em_estlmu:*
5: em_estlov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estcl:*
10: gb_estl2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estlin:*
16: em_estlom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_dln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_fod:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB | ID | Description |
|------------|-------|-------|--------|----|----------|---------------------|
| 1 | 497.5 | 18.5 | 475 | 12 | BF704417 | BF704417 MI-P-E6-a |
| 2 | 406 | 15.1 | 812 | 12 | BG702253 | BG702253 602683459 |
| 3 | 394 | 14.6 | 589 | 9 | A1050362 | A1050362 ub30a07..r |
| 4 | 379 | 14.1 | 1099 | 13 | B1523344 | B1523344 603175938 |
| 5 | 354 | 13.1 | 535 | 17 | A2441303 | A2441303 1M0232M24 |
| 6 | 340 | 12.6 | 333 | 12 | BF552757 | BF552757 UI-R-CO-i |
| 7 | 324 | 12.0 | 569 | 17 | A2853726 | A2853726 2M0157M01 |
| 8 | 321.5 | 11.9 | 832 | 13 | B1523369 | B1523369 603175938 |
| 9 | 172.5 | 6.4 | 342 | 13 | BM257856 | BM257856 521721 MA |
| 10 | 170 | 6.3 | 668 | 17 | AC079702 | AC079702 Pan trogl |
| 11 | 156 | 5.8 | 509 | 12 | BG554242 | BG554242 dab70a07. |
| 12 | 153.5 | 5.7 | 875 | 9 | AL537375 | AL537375 AL537375 |
| 13 | 152.5 | 5.7 | 882 | 14 | BQ223533 | BQ223533 AGENCOURT |
| 14 | 150.5 | 5.6 | 997 | 9 | AL528607 | AL528607 AL528607 |
| 15 | 144.5 | 5.4 | 873 | 9 | AL518132 | AL518132 AL518132 |
| 16 | 141 | 5.2 | 938 | 12 | BE901933 | BE901933 601676878 |
| 17 | 139 | 5.2 | 700 | 14 | BQ749057 | BQ749057 UI-M-FB0- |
| 18 | 138.5 | 5.1 | 511 | 12 | BG359887 | BG359887 dab88a05. |
| 19 | 135.5 | 5.0 | 591 | 14 | BM685621 | BM685621 UI-E-C10- |
| 20 | 134 | 5.0 | 324 | 17 | A0981401 | A0981401 RPCT-23-3 |
| 21 | 133.5 | 5.0 | 481 | 14 | BM710190 | BM710190 UI-E-CQ1- |
| 22 | 133.5 | 5.0 | 769 | 14 | BM719097 | BM719097 UI-E-EQ1- |
| 23 | 129.5 | 4.8 | 683 | 10 | AM950312 | AM950312 EST362382 |
| 24 | 127.5 | 4.7 | 912 | 13 | B1760931 | B1760931 603043131 |
| 25 | 127 | 4.7 | 1082 | 14 | BM919605 | BM919605 AGENCOURT |
| 26 | 126 | 4.7 | 447 | 13 | B1824638 | B1824638 603033580 |
| 27 | 124.5 | 4.6 | 361 | 14 | T28073 | T28073 EST26562 Hu |
| 28 | 124.5 | 4.6 | 779 | 13 | B1333959 | B1333959 602997231 |
| 29 | 123.5 | 4.6 | 421 | 14 | D78905 | D78905 H0M526C04B |
| 30 | 123.5 | 4.6 | 502 | 10 | BE650170 | BE650170 UI-M-BH3- |
| 31 | 123.5 | 4.6 | 624 | 12 | BG713383 | BG713383 Pq1ln PK0 |
| 32 | 123 | 4.6 | 412 | 9 | A1629081 | A1629081 FC09401.Y |
| 33 | 123 | 4.6 | 846 | 9 | AL525319 | AL525319 AL525319 |
| 34 | 123 | 4.6 | 906 | 12 | BG754874 | BG754874 602714263 |
| 35 | 123 | 4.6 | 918 | 9 | AL550798 | AL550798 AL550798 |
| 36 | 123 | 4.6 | 927 | 9 | AL553060 | AL553060 AL553060 |
| 37 | 123 | 4.6 | 948 | 9 | AL545121 | AL545121 AL545121 |
| 38 | 123 | 4.6 | 950 | 9 | AL551603 | AL551603 AL551603 |
| 39 | 123 | 4.6 | 973 | 9 | AL548148 | AL548148 AL548148 |
| 40 | 122 | 4.5 | 859 | 12 | BG434397 | BG434397 602506409 |
| 41 | 121 | 4.5 | 742 | 9 | AL549396 | AL549396 AL549396 |
| 42 | 120 | 4.5 | 916 | 9 | AL576559 | AL576559 AL576559 |
| 43 | 119.5 | 4.4 | 666 | 14 | BM935910 | BM935910 UI-M-CG0P |
| 44 | 119.5 | 4.4 | 947 | 14 | BQ939522 | BQ939522 AGENCOURT |
| 45 | 119 | 4.4 | 975 | 12 | BG621100 | BG621100 602616982 |

ALIGNMENTS

RESULT 1
BF704417
LOCUS BF704417 475 bp mRNA linear EST 22-DEC-2000
DEFINITION MI-P-E6-acc-g-09-1-UM.s1 MI-P-E6 Sus scrofa cDNA clone
ACCESSION BF704417
VERSION BF704417.1 GI:11989825
KEYWORDS EST.
SOURCE
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
1 (bases 1 to 475)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene

JOURNAL
MEDLINE
COMMENT

discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
Contact: Tuggle CK
Molecular Genetics Laboratory, Department of Animal Science
Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
Tel: 5152944252
Fax: 5152942401
Email: cktuggle@iastate.edu
Oligo-dT track not found, Not 1 site shown in beginning of sequence
is likely internal to the message. CDNA Library Preparation: RJ
Woods, JA Green, RS Prather S142 Animal Science Research Center,
Department of Animal Science, University of Missouri-Columbia,
65211 Clone distribution: clones will be available through Research
Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA-No.

FEATURES
source

Location/Qualifiers
1..475
/organism="Sus scrofa"
/strain="crossbred"
/db_xref="taxon:9823"
/clone="MI-P-E6-acc-g-09-1-UM"
/clone_lib="MI-P-E6"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not 1; Site_2: EcoRI. The MI-P-E6
library is derived from fetus at gestational day 20. For
a detailed description of the library from which this
clone was derived, please visit our web site at
http://piglet.genome.iastate.edu/
TAG_SEQ=None found"

BASE COUNT 129 a 120 c 121 g 104 t 1 others

ORIGIN

Alignment Scores:

Pred. No.: 9.78e-45 Length: 475
Score: 497.50 Matches: 94
Percent Similarity: 82.93% Conservative: 8
Best Local Similarity: 76.42% Mismatches: 18
Query Match: 18.47% Indels: 3
DB: 12 Gaps: 1

US-09-917-265-67 (1-511) x BF704417 (1-475)

QY 1 ILETRPGLUENGULYSASPVAlTYrValValGluLeuAspTRPHISPROAspAlaPro 20
DB 112 ATGTGGAGCTGGAGAAAGAGCTTATGTTGTAGAGGTGGAGCTGCCGATGCCCT 171
QY 21 G1yGluMetValValLeuThrCysHisThrProGluLysAspAlaLeuThrPThrSer 40
DB 172 GGAAGAAACAGTGAACCTCACCTGTGACACGCTGAAGAGATGACATCACTGACCTCA 231
QY 41 AlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
DB 232 GACCAGACATGAGCATAGGCTGTGAAAGACCTGACCATCATGTCACAAAGAGTTT 291
QY 61 GLYASPAAGLysGlnTYrThrCysHisLysGlyLysValLeuSerATrSerLeuLeu 80
DB 292 CTAGATCTGCTGCCAGTACCTGACCAAGAGGCGAGCTCTGAGGCACTCACTCATCTG 351
QY 81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluLysGlu 100
DB 352 CTGCTCCACAAAGAGAAATGGAATTTGCTCCACTGAATTTTA-----AAAAT 402
QY 101 SerLysAnLysIlePheLeuLysCysGluAlaLysAnTYrSerGlyATrGPhrThCys 120
DB 403 TTCAAAACAAAGACTTCTGTAAGTGAAGACCAAAATTAATCTCGGACGGTTCACTGC 462
QY 121 TrpTrpLeu 123
DB 463 TCATGGGTG 471

RESULT 2
BG702253 812 bp mRNA linear EST 07-MAY-2001
LOCUS 602683459F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4816118 5',
DEFINITION mRNA sequence.

ACCESSION BG702253
VERSION BG702253.1 GI:13973409
KEYWORDS EST.
SOURCE Human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 812)
NIH-MGC http://mhc.nci.nih.gov/.

TITLE

JOURNAL

COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@rsf@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shihrai
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Inceye Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
plate: LHAM0714 row: e column: 15
High quality sequence stop: 804.

FEATURES
source

Location/Qualifiers

1..812
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4816118"
/clone_lib="NIH_MGC_95"
/tissue_type="hippocampus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcag
); Oligo-dT primed using primer 5'-TTTCTTTTCTTTTCTTT-3',
size-selected for average insert size 2.5 kb and
normalized to R0.5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC library."

BASE COUNT 188 a 249 c 226 g 149 t

ORIGIN

Alignment Scores:

Pred. No.: 3.47e-34 Length: 812
Score: 406.00 Matches: 107
Percent Similarity: 65.12% Conservative: 5
Best Local Similarity: 62.21% Mismatches: 35
Query Match: 15.08% Indels: 29
DB: 12 Gaps: 4

US-09-917-265-67 (1-511) x BG702253 (1-812)

QY 253 CysIleGlnAlaGlnGlyLysAsnAsnArgGluLysAspArgLeuCysValAspLys 272
DB 373 TGCATCCAG-----CGGCTCGCCCTGTGTCCC 399
QY 273 ThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAlaArgAspArg 292
DB 400 TGCAGTCCGCGCAGCATGT-----GTCCAG-----CGC 429
QY 293 TyrTrpSerSerTrpSerAspTrpAlaSerValSerCysSerGlyGlyGlyGly 312
DB 430 GCACCTCCTCTGTGTGCTACCTGTGCTCTGACGACACCTCA-----GTG 477
QY 313 GlySerArgAsnLeuProThrProThrProSerProGluMetPheGlnCysLeuAsnHis 332
DB 332

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: L1605 row: 1 column: 09
High quality sequence start: 40
High quality sequence stop: 727.

FEATURES

Source

1. 1099

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_image="5240216"

/clone_lib="NIH_MGC_121"

/lab_host="DH10B"

/note="Organ: brain; Vector: pCMV-SPORT6; Site: 1; NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 017. Note:
this is a NIH_MGC library."

BASE COUNT 359 a 244 c 218 g 276 t 2 others

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-09-917-265-67 (1-511) x B1523344 (1-1099)

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

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QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

/M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 565 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0232 row: M column: 24
Seq primer: CACACAGGAACACGCTATGACC
Class: Plasmid ends
High quality sequence stop: 535.

FEATURES

Source

1. 535

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone_image="U00C1M0232M24"

/clone_lib="Mouse 10kb plasmid U00C1M library"

/sex="Male"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PMD42ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g147321141b/AP12072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT

132 a 135 c 130 g 137 t 1 others

ORIGIN

US-09-917-265-67 (1-511) x AZ441303 (1-535)

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

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QY

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QY

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QY

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QY

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QY

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QY

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QY

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QY

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QY

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QY

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QY

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Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

source

1. 569
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0157M01"
/clone_lib="Mouse 10Kb plasmid UUCG1M library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 143 a 137 c 153 g 136 t
ORIGIN

Alignment Scores:
Pred. No.: 2.52e-25 Length: 569
Score: 324.00 Matches: 66
Percent Similarity: 82.56% Conservative: 5
Best Local Similarity: 76.74% Mismatches: 15
Query Match: 12.03% Indels: 2
DB: 17 Gaps: 0

US-09-917-265-67 (1-511) x A2853726 (1-569)

QY 8 ValTyrValValGluLeuAspTyrPHisProAspAlaProGluGluMetValValLeuThr 27
Db 283 GTTTATGTTGAGAGGTGAGCTGACCTCCGATCCCTGGAGAAACAGTGAACCTGACC 224

QY 28 CysHisThrProGluGluAspAspPleThrTyrPHisSerAlaGlnSerSerGluValLeu 47
Db 223 TGTGACACGGCTGAGAGAGATGACATCACCCTGACCTGACACGACATGAGCTGATA 164

QY 48 GlySerGlyLysThrLeuThrIleGlnValLysGluPheGlyAspAlaGlyGlnTyrThr 67
Db 163 GGCCTCTGGAAGACCCGACCATCCTCAAGAGTTTCTAGATGCTGGCCAGTACACC 104

QY 68 CysHisLysGlyGlyLysValLeuSerArgSerLeuLeuIleHisLysGluAsp 87
Db 103 TGCACAAAGAGAGGAGCTGAGCCACTGACATCTGCTGCCACAAAGAGAGAAA- 45

QY 88 GlyIleTyrSerThrAsp 93
Db 44 GGAAT-TGCTCAGCAGCAT 28

RESULT 8
B1523569 832 bp mRNA linear EST 29-AUG-2001
LOCUS 603175938F1 NIH_MGC_121 Homo sapiens cDNA IMAGE:5240216 5',
DEFINITION mRNA sequence.
ACCESSION B1523569
VERSION B1523569.1 GI:15348361
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 832)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: L1AM1605 row: 1 column: 09
High quality sequence start: 23
High quality sequence stop: 821.
Location/Qualifiers

FEATURES
source
1. 832
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5240216"
/clone_lib="NIH_MGC_121"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH-MGC library."

BASE COUNT 220 a 233 c 200 g 179 t
ORIGIN

Alignment Scores:
Pred. No.: 8.89e-25 Length: 832
Score: 321.50 Matches: 76
Percent Similarity: 61.07% Conservative: 4
Best Local Similarity: 58.02% Mismatches: 26
Query Match: 11.94% Indels: 25
DB: 13 Gaps: 4

US-09-917-265-67 (1-511) x B1523569 (1-832)

QY 253 CysIleGlnAlaGlnGlyLysAsnAsnArgGluLysLysAspArgLeuCysValAspLys 272
Db 277 TGCATCCAG-----CGGCTCCGCCCTGTGTCC 303

QY 273 ThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAlaArgAspArg 292
Db 304 TGCAGTCCCGCTCAGCATGT-----GTCCAG-----CGC 333

QY 293 TyrTyrSerSerSerTyrPAspTyrPAlaSerValSerCysSerGlyGlyGlyGly 312
Db 334 GCAGCCCTCCCTGTTGCTACCCCTGCTCTCCGACCACTCA-----GTT 361

QY 313 GlySerArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHis 332
Db 382 TGGCCATGAACCTCCCGCTGGCCACTCCAGACCAAGATGTTCCATGCCCTTCACAC 441

QY 333 SerGlnThrLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGlu 352
Db 442 TCCCAAAACCTGCTGAGGCGCGTCAGCAACATCCTCCACAAAGCCAGACAACTAGAA 501

QY 353 LeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSer 372
Db 502 TTTTACCTTGCACTCTGGAAGAGATTGATCAAGAGATTACAAAGATAAACACAGC 561

QY 373 ThrValGlnAlaCysLeuProLeuGlnLeuThr 383
Db 562 ACAGTGAGGCGCTTTTACCATTTGAAATTAC 594

```

RESULT 9
LOCUS      BM257856                      342 bp    mRNA    linear    EST 17-DEC-2001
DEFINITION 521721 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION  BM257856
VERSION     BM257856.1  GI:17893455
KEYWORDS   EST.
SOURCE      cow.
ORGANISM   Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovidae; Bovinae; Bos.
REFERENCE   1 (bases 1 to 342)
AUTHORS    Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
            Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,
            G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
            Perlea,G., Holt,L., Karameycheva,S., Liang,F., Quackenbush,J. and
            Keefe,J.W.
            Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
            Genome Res. 11 (4), 626-630 (2001)
TITLE       JOURNAL
MEDLINE     21180013
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt-trimmed with phred
            v0.980904.e. Vector identified by cross-match with the -minscore 18
            and -mismatch 12 options.
            PCR Primers
            FORWARD: AGGAACAGCTATGACCAT
            BACKWARD: GTTTTCCAGTCACGACG
            Plate: 125 row: E column: 18
            Seq primer: ATTAGCTGACACTATAG.
FEATURES
            source
            1..342
            /organism="Bos taurus"
            /db_xref="taxon:9913"
            /clone_lib="MARC 3BOV"
            /tissue_type="pooled"
            /lab_host="DH10B"
            /note="Vector: pCMV SPORT6; Site.1: NotI; Site.2: SalI;
            Library made from pooled tissue from marrow, alveolar
            macrophage, ovary, fetal semitendinosus muscle, and fetal
            longissimus muscle."
BASE COUNT  67 a 135 c 74 g 66 t
ORIGIN
Alignment Scores:
Pred. No.: 7.51e-09                      Length: 342
Score: 172.50                            Matches: 43
Percent Similarity: 73.13%                Conservative: 6
Best Local Similarity: 64.18%              Mismatches: 14
Query Match: 6.41%                       Indels: 5
DB: 13                                     Gaps: 3
US-09-917-265-67 (1-511) x BM257856 (1-342)
OY 295 serseerfppserasptp---Alaservalsercysserglyglyglyglygly 313
DB 151 TCCCTCCATATTCACACCTGTTCTCTCCACACACCTCCACCTCAGTTTG-GGC--- 206
OY 314 SerarqanleuProthProthProserProglyMetphglnCysleuAsnHisser 333
DB 207 ---AGGAGCCCTCCACACACACAGCAAGCCAGAGAG---ACCTGCTCGACTACTCC 260
OY 334 GlnhrleuauargAlaValserAsnthrlleuGlnlyAlaIarglnThrleuGlnleu 353
DB 261 CAAAACCTGGTACGAGCGCTGACGCAACACGCTACAGAGAGCCAGCAAACTCTAGAAATT 320
OY 354 TyrserscythrsergluGlu 360

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DB 321 TACTCTGCACTTGTGAGGAG 341
|||||
RESULT 10
LOCUS      AG079702/c                      668 bp    DNA    linear    GSS 03-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-075107.R, genomic survey sequence.
ACCESSION  AG079702.1  GI:16631504
VERSION     AG079702.1  GI:16631504
KEYWORDS   GSS.
SOURCE      Pan troglodytes male lymphoblast DNA, clone_11b:PTB Chimpanzee Male
            PAC library clone: PTB-075107.R.
            Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
REFERENCE   1
AUTHORS    Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Matanabe,H. and Sakaki,Y.
            BAC end sequences of library PTB
            Unpublished
            2 (bases 1 to 668)
            Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suenho-chou, Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:chimpes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
            Clones are derived from the chimpanzee BAC library PTB This BAC end
            was generated during the R&D process and may have higher chance of
            clone tracking errors.
            PRIMERS
            Sequencing: M13Rev
            LIBRARY
            Vector : pKS145
            R.Site 1 : SacI
            R.Site 2 : SacI.
            Location/Qualifiers
            1..668
            /organism="Pan troglodytes"
            /db_xref="taxon:9598"
            /clone="PTB-075107.R"
            /sex="male"
            /cell_type="lymphoblast"
            /clone_lib="PTB Chimpanzee Male BAC library"
BASE COUNT  180 a 138 c 137 g 213 t
ORIGIN
Alignment Scores:
Pred. No.: 4.26e-08                      Length: 668
Score: 170.00                            Matches: 30
Percent Similarity: 82.50%                Conservative: 3
Best Local Similarity: 75.00%              Mismatches: 7
Query Match: 6.31%                       Indels: 0
DB: 17                                     Gaps: 0
US-09-917-265-67 (1-511) x AG079702 (1-668)
OY 100 GtuserlysasnllyllepheleuyscysguAlaValserAsnthrlleuGlnly 119
DB 542 GAACCAAGACGTACACCTTTGTAAGATGCGAGCAACAAATATTTCAGAGCTTTCACC 483
OY 120 CystpTpPleuthrAlaIleserThraspleuysPheSerVallySerSerargly 139
DB 482 TCGTGTGGTGGACGACATCAGTACTGATTGACATTCAGTCAAAAGCAGCAGAGG 423
RESULT 11
LOCUS      BG554242                      509 bp    mRNA    linear    EST 09-APR-2001
DEFINITION dab70a07.y2 NICHD XGC Emb4 Xenopus laevis cDNA IMAGE:4203388
            5' similar to TR:016542 Q16542 INTERLEUKIN-11 RECEPTOR. ;, mRNA
            sequence.

```



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Db      543 GCGAAGCGTCAAGACATTCAACACATGATGTCAGACACCTCCAGCATCATGTGTC 602
OY      271 AspLysThrSerAlaLysValValCysHisLysAspAlaLysLeuArgValGlnAlaArg 290
Db      603 ATCCAGCAGCGCCGCGGAGCGCCCTGAGGCAC-----GTGGTGCAGCTTCGTCGCCAG 653
OY      291 AspArgTyrLysSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 310
Db      654 GAGAGATTCCGGCAGGACGAGTGCAGAGTGC-----AGCCC-GGAGGC 697
OY      311 GtlyGlyLysSerArgAsnLeuProThrProThrProSerProGly 325
Db      698 CATGGCAGCGCTTGAGACAGCTTCTCTCCACAGACCATCCGCG 742

RESULT 14
AL528607 997 bp mRNA linear EST 13-FEB-2001
LOCUS    AL528607 LTI_NFL001_NBC4 Homo sapiens cDNA clone CS0DD001YE13 5
DEFINITION
prime, mRNA sequence.
ACCESSION
AL528607
VERSION  AL528607.1 GI:12792100
KEYWORDS EST.
SOURCE   human.
ORGANISM Homo sapiens
           Chordata; Craniata; Vertebrata; Euteleostomi;
           Eukaryota; Metazoa;
           Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 997)
AUTHORS  Li,W.B., Gruber,C., Jesse,J. and Polyes,D.
TITLE    Full-length cDNA libraries and normalization
JOURNAL  Unpublished (2001)
COMMENT  Contact: Genoscope
         Genoscope - Centre National de Sequencage
         BP 191 91006 EVRY cedex - France
         Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
Source
1.997
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DD001YE13"
/clone_lib="LTI_NFL001_NBC4"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/notes="Organ: Brain; Vector: PCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the PCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 180 a 331 c 290 g 184 t 12 others
ORIGIN

```

Alignment Scores:

```

Pred. No.:      1.21e-05      Length:      997
Score:          150.50      Matches:      67
Percent Similarity: 36.13%      Conservative: 32
Best Local Similarity: 24.45%      Mismatches: 94
Query Match:      5.59%      Indels:      83
DB:              9      Gaps:      12

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US-09-917-265-67 (1-511) x AL528607 (1-997)

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OY      19 AlaProGlyGluMetValValLeuThrCysHisThrProGluGlu----- 33
Db      192 GCCGCGCCGCGAGTTGCTACGCCACAGACACAGTCCACAGGAGCACCACCATGTCAG 251
OY      34 -----AspAspIleThr-----TrrThrSerAla 41
Db      252 TAGGAGCGCGCTGGGCTCTGACGTGACACTGCCATGTGGAGACAGMAAACTGGATCTGCG 311

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OY      42 GlnSerSerGluValLeuGly-----SerGlyLysThrLeu 53
Db      312 GTGACCTGGCGGGGTAATGCGACAGACACCGCCCTGACCTGCTCAAGCGCTTCAGCTG 371
OY      54 ThrIleGlnValLysGluPheGlyAspAlaGlyGlnTyrThrCysHisLysGlyLys 73
Db      372 GTTCTTCATGAGCTGGAACCTGGCCACAGTGGCTCTCCAGCTTCACCGTCAGTCC 431
OY      74 ValLeuSerArgSerLeuLeuLeuIleHisLysLysGlnAspGlyIleThrSerThrAsp 93
Db      432 TGGCAGCTGGCGCACCAAGTCTGCTGCAATG-----GGCTTG----- 470
OY      94 IleLeuLysGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGlnAlaLysAsn 113
Db      471 -----CCGCGCGGAGCGCTGCTGCTCAGCTCAGCTGCGCGTCAAACT 509
OY      114 TyrSerGlyArgPheThrCysTrpTrpIleThrAlaIleSerThrAspLeuLysPheSer 133
Db      510 TACCCCAAGGCGCTTCTACTGACAGTGGCAATGCCACCCCGACCTTACAT----- 560
OY      134 ValLysSerSerArgGlyPheSerAspProGlnGlyValThrCysGlyAlaValThrLeu 153
Db      561 -----CCCAAC-----ACCTTCATGTCAGCTGCTG 587
OY      154 SerAlaGluArgValArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGln 173
Db      588 CATGGCTCCAAATATTTGCTC-----TGTCGA- 613
OY      174 GluGlySerAlaCysProSerAlaGluGluSerLeuProIleGluValValAlaAspAla 193
Db      614 GAAGGA-----CCGAGCCCTCAAGAACCGCTGCACATTCGCTACATGCACCTGTT 664
OY      194 IleHisLysLeuLysTyrGlu-----AsnTyr 202
Db      665 CTCACAC--ATCAGACACAAGGCTCCATAGTGCAGACATGCCCTGGCGCCACATGCC 722
OY      203 ThrSerSerPhePheIleArg--AspIleIleLysProAspProProThrAsnLeuGln 221
Db      723 ACAGCTATCAGCTTTCAGCAGTTCACCAATGTGAACCTCGACCTCCACAAATATGTGTA 782
OY      222 LeuLysProLeu---LysAsnSerArgHisValGlnValSerTrpIleTyrProAspThr 240
Db      783 GCCCGGCGAGTGGCCAGCAACCTCGCGGCTGGAGGTACGTGGCAGACCCCTTGACC 842
OY      241 TrpSerThrProHis--SerTyrPheSerLeuThrPheCys 253
Db      843 TGGCCTGACCCCTGAGTGTCTTCTCTCAAGTCTTCTGCG 882

RESULT 15
AL518132 873 bp mRNA linear EST 13-FEB-2001
LOCUS    AL518132 LTI_NFL011_NBC1 Homo sapiens cDNA clone CS0DA010YM20 5
DEFINITION
prime, mRNA sequence.
ACCESSION
AL518132
VERSION  AL518132.1 GI:12781625
KEYWORDS EST.
SOURCE   human.
ORGANISM Homo sapiens
           Chordata; Craniata; Vertebrata; Euteleostomi;
           Eukaryota; Metazoa;
           Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 873)
AUTHORS  Li,W.B., Gruber,C., Jesse,J. and Polyes,D.
TITLE    Full-length cDNA libraries and normalization
JOURNAL  Unpublished (2001)
COMMENT  Contact: Genoscope
         Genoscope - Centre National de Sequencage
         BP 191 91006 EVRY cedex - France
         Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
Source
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/organism="Homo sapiens"
/db_xref="taxon:9606"

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/clone="CS0DA010YM20"  
/clone_id="LT1_NFLO11_NBC1"  
/sex="male"  
/tissue_type="neuroblastoma cells"  
/lab_host="DH10B"  
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA  
was primed with a NotI-oligo(dT) primer. Five prime end  
enriched, double-stranded cDNA was digested with Not I and  
cloned into the Not I and Eco RV sites of the pCMVSPORT 6  
vector. Library is not normalized, but is the control for  
the normalized libraries. Library was constructed by Life  
Technologies. Contact : Feng Liang Life Technologies, a  
division of Invitrogen 9800 Medical Center Drive Rockville  
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :  
Fliang@lifetech.com URL :  
http://fulllength.invitrogen.com"  
BASE COUNT 148 a 298 c 251 g 165 t 11 others  
ORIGIN
```

Alignment Scores:

| Pred. No.: | 4.51e-05 | Length: | 873 |
|------------------------|----------|---------------|-----|
| Score: | 144.50 | Matches: | 62 |
| Percent Similarity: | 36.63% | Conservative: | 27 |
| Best Local Similarity: | 25.51% | Mismatches: | 96 |
| Query Match: | 5.37% | Indels: | 60 |
| DB: | 9 | Gaps: | 11 |

US-09-917-265-67 (1-511) x AL518132 (1-873)

```
OY 21 GlycylmethylevalleuthrcysHisThrProGluLysPheAspIleThrTrp--- 38  
Db 264 GCCTCTGACGTGACATKCCATCTGGAGACGACAACTGGATGCTGCGTGCACCTGGCGG 323  
OY 39 ---ThrserAlaGlnserSerGluValleuGlyserGlyLysThrLeuThrIleGlnVal 57  
Db 324 GTAATKKGACAGACCTGGCCCTGACCTCTGCACGCGCTCYAGCTGCTGCATCGC 383  
OY 58 LysGlnPheGlyAspAlaGlyGlnIleThrCysHisLysGlyGlyLysValLeuSerArg 77  
Db 384 CTGCAACTGGGCCACACACTKGCCTTACGCGCTCTCCACCGCTGACTCTGGACCTGGCG 443  
OY 78 SerLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGlu 97  
Db 444 CACCAAGTCTGCTGCATGK-----CGCTTG----- 470  
OY 98 GlnLysLysSerLysAsnLysIlePheLeuLysCysGlnAlaLysAsnTyrSerGlyArg 117  
Db 471 -----CCGCCCGCGAGCGCTKTTCTCAGCTGCCGCTCCACACTTACCCCAAGGC 521  
OY 118 PheThrCysTrpIleuThrAlaIleSerThrAspLeuLysPheSerValLysSerSer 137  
Db 522 TTCTACTGACGCTGGCATCTGCCACCCCACTTCACT----- 560  
OY 138 ArgGlyPheSerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArg 157  
Db 561 -----CCCAAC-----ACCTTCAATGTTACTGTCGTCGATGCTGCCAA 599  
OY 158 ValArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAla 177  
Db 600 ATTATGCTC-----TGTGA-GAAGCA----- 619  
OY 178 CysProSerAlaGluGlnSerLeuProIleGluValValAlaAspAlaIleHisLysLeu 197  
Db 620 ---CCCGAGCCCTCAAGACCGCTGCCCATTTCCATGACGACCTGTTCTCCACC-ATC 674  
OY 198 LysTyrGlu-----AsnTyrThrSerSerPhe 206  
Db 675 AAGTACAGAGCTTCATAGCTCAGCATGCTGCCACCATGCGCACAGCATATCACC 734  
OY 207 PheIleArg---AspIleIleLysProAspProThrAsnLeuGlnLeuLysProLeu 225  
Db 735 TTTCAGCAGTTCCACCATTTGTGAAGCCTGATCTTCAGAAATATGTGTAGCCCGCGACGTG 794
```

```
OY 226 ---LysAsnSerArgHisValGluValSerTrpIleuTyrProAspTrpThrSerThrPro 244  
Db 795 CCAGACAAACCTCGCGCGCTGAGAGTGACGTGGCAGACCCCTGACCTGGCTGAMCCT 854  
OY 245 HisSerTyr 247  
Db 855 GAGTCTTTT 863
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Search completed: July 17, 2003, 09:27:22
Job time : 2434.6 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 16, 2003, 19:43:49 : Search time 72.061 Seconds
(without alignments)
2174.711 Million cell updates/sec

Title: US-09-917-265-67
Perfect score: 2693
Sequence: 1 IWELEKDVYVVELDHPADP.....HAFRIRAVTINRMSTYLNSS 511

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153336381 residues
Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame-p2n.model -DEV=xlh
-O=/cgn2_1/USPTO.spool/US0917265/rnat_15072003_092107_1619/app-query.fasta-1.3114
-DB=Issued_Patents_NA -OFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOCPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human4.0.cdi
-LIST=45 -DOCALLIGN=200 -THR.SCORE=pcr -THR.MAX=100 -THR.MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptlo -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USRR=US0917265.@CGN_1_119.grunat_15072003_092107_1619 -NCPU=6 -ICPU=3
-NO_MMAPP -LARGEODTRY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOC
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents_NA: *
1: /cgn2_6/prodata/1/ina/5A.COMB.seq: *
2: /cgn2_6/prodata/1/ina/5B.COMB.seq: *
3: /cgn2_6/prodata/1/ina/6A.COMB.seq: *
4: /cgn2_6/prodata/1/ina/6B.COMB.seq: *
5: /cgn2_6/prodata/1/ina/PCtus.COMB.seq: *
6: /cgn2_6/prodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------------------------------|
| 1 | 2309.5 | 85.8 | 1560 | 2 | US-08-751-767A-11 Sequence 11, Appl |
| 2 | 2309.5 | 85.8 | 1523 | 2 | US-08-751-767A-9 Sequence 9, Appl |
| 3 | 2309.5 | 85.8 | 6139 | 2 | US-08-751-767A-7 Sequence 7, Appl |
| 4 | 1653 | 61.4 | 990 | 4 | US-08-079-984A-11 Sequence 11, Appl |
| 5 | 1640 | 60.9 | 990 | 4 | US-09-079-984A-1 Sequence 1, Appl |
| 6 | 1420.5 | 52.7 | 1870 | 4 | US-09-310-842-4 Sequence 4, Appl |
| 7 | 1419.5 | 52.7 | 987 | 4 | US-08-848-760B-24 Sequence 24, Appl |
| 8 | 1419.5 | 52.7 | 2318 | 4 | US-09-851-062-3 Sequence 3, Appl |
| 9 | 1418.5 | 52.7 | 987 | 1 | US-08-186-529-1 Sequence 1, Appl |
| 10 | 1418.5 | 52.7 | 987 | 1 | US-08-640-386A-1 Sequence 1, Appl |
| 11 | 1418.5 | 52.7 | 1018 | 2 | US-08-184-009-194 Sequence 14, App |
| 12 | 1418.5 | 52.7 | 1018 | 2 | US-08-458-356-194 Sequence 14, App |

| | | | | | |
|----|--------|------|------|---|--|
| 13 | 1418.5 | 52.7 | 1018 | 4 | US-08-460-736-194 Sequence 194, App |
| 14 | 1418.5 | 52.7 | 1399 | 2 | US-08-751-767A-3 Sequence 3, Appl |
| 15 | 1418.5 | 52.7 | 2362 | 1 | US-08-265-087-1 Sequence 1, Appl |
| 16 | 1418.5 | 52.7 | 2362 | 1 | US-08-621-493-1 Sequence 1, Appl |
| 17 | 1418.5 | 52.7 | 2362 | 2 | US-08-965-668-1 Sequence 1, Appl |
| 18 | 1418.5 | 52.7 | 2362 | 4 | US-09-260-173-1 Sequence 1, Appl |
| 19 | 1058.5 | 39.3 | 1061 | 2 | US-08-385-335A-13 Sequence 13, Appl |
| 20 | 1049.5 | 39.0 | 6295 | 2 | US-08-655-206A-4 Sequence 4, Appl |
| 21 | 1049.5 | 39.0 | 7287 | 2 | US-08-655-206A-1 Sequence 1, Appl |
| 22 | 970 | 36.0 | 669 | 4 | US-09-079-984A-12 Sequence 12, Appl |
| 23 | 965 | 35.8 | 669 | 4 | US-09-079-984A-2 Sequence 2, Appl |
| 24 | 881.5 | 32.7 | 1364 | 1 | US-08-265-087-3 Sequence 3, Appl |
| 25 | 881.5 | 32.7 | 1364 | 1 | US-08-621-493-3 Sequence 3, Appl |
| 26 | 881.5 | 32.7 | 1364 | 4 | US-08-965-668-3 Sequence 3, Appl |
| 27 | 881.5 | 32.7 | 1364 | 4 | US-09-260-173-3 Sequence 3, Appl |
| 28 | 878.5 | 32.6 | 762 | 4 | US-08-848-760B-21 Sequence 21, Appl |
| 29 | 878.5 | 32.6 | 1316 | 2 | US-08-684-687-3 Sequence 3, Appl |
| 30 | 878.5 | 32.6 | 1316 | 4 | US-09-851-520-3 Sequence 3, Appl |
| 31 | 878.5 | 32.6 | 1645 | 4 | US-09-310-842-2 Sequence 2, Appl |
| 32 | 877 | 32.6 | 660 | 1 | US-08-186-529-3 Sequence 3, Appl |
| 33 | 877 | 32.6 | 660 | 1 | US-08-640-386A-3 Sequence 3, Appl |
| 34 | 875.5 | 32.5 | 1026 | 2 | US-08-751-767A-1 Sequence 1, Appl |
| 35 | 871 | 32.3 | 721 | 2 | US-08-184-009-199 Sequence 199, App |
| 36 | 871 | 32.3 | 721 | 2 | US-08-458-356-199 Sequence 199, App |
| 37 | 871 | 32.3 | 721 | 4 | US-08-460-736-199 Sequence 10, Appl |
| 38 | 549 | 20.4 | 713 | 2 | US-08-385-335A-10 Patent No. 5171840-8 |
| 39 | 211.5 | 7.9 | 1404 | 6 | 5480796-8 Patent No. 5480796 |
| 40 | 211.5 | 7.9 | 1404 | 6 | 5480796-8 Patent No. 5480796 |
| 41 | 211.5 | 7.9 | 1486 | 4 | US-08-795-473B-3 Sequence 3, Appl |
| 42 | 211.5 | 7.9 | 1486 | 4 | US-09-439-856-3 Sequence 3, Appl |
| 43 | 211.5 | 7.9 | 2061 | 6 | 5171840-1 Patent No. 5171840 |
| 44 | 211.5 | 7.9 | 2061 | 6 | 5480796-1 Patent No. 5480796 |
| 45 | 211.5 | 7.9 | 3319 | 4 | US-08-795-473B-2 Sequence 2, Appl |

ALIGNMENTS

RESULT 1
US-08-751-767A-11
Sequence 11, Application US/08751767A
Patent No. 5994104
GENERAL INFORMATION:
APPLICANT: ANDERSON, ROBERT J.
APPLICANT: GRANT, HUGH
APPLICANT: MACDONALD, IAN D.
TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,767A
FILING DATE: 08-NOV-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 117-221
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164091
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1560 base pairs

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1557
US-08-751-767A-11

Alignment Scores:
Pred. No.: 1,46e-252
Score: 2309.50
Percent Similarity: 89.60%
Best Local Similarity: 84.39%
Query Match: 85.76%
Length: 1560
Matches: 438
Conservative: 27
Mismatches: 45
Indels: 9
Caps: 2

US-09-917-265-67 (1-511) x US-08-751-767A-11 (1-1560)

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QY 21 GtAGluMetValValLeuThrCysHisThrProGluLysAspIleThrTrpThrSer 40
DB 64 GGAAGAAATGGTGGTCTCCTGACCTGTGACACCCCTGAAAGATGATGATCCTGACCTTG 123
QY 41 AlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
DB 124 GACACAGCAGTGGAGTCTTAGGCTGGCAAAACCTGACATCCAAAGTCAAGATTT 183
QY 61 GtAspAlaGlyGlnTyrThrCysHisLysGlyGlyLysValLeuSerArgSerLeu 80
DB 184 GGAGATGCTGGCAGTACACCTGTCAAAAGAGGAGGCTTAAACCATTCGCTCTG 243
QY 81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGlu 100
DB 244 CTGCTTCACAAAAGAGAGATGGAATTTGGTCCACTATATTTTAAAGGCCAGAAAGAA 303
QY 101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
DB 304 CCAAAAATTAAGACCTTTTAAGATGCGAGCCCAAGAAATTTCTGAGCTTCACCTGC 363
QY 121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
DB 364 TGGTGGCTGAGCAACACACTGATGATTTGACATTCAGTGTCAAAACACAGAGGCTCT 423
QY 141 SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgVal 160
DB 424 TCGACCCCAAGAGGGGTGAGCTGCGAGCTGCTACACTCTCTGACAGAGAGTCAAGAGG 483
QY 161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluLysSerAlaCysProSer 180
DB 484 GACACAGAGAGATAT--GAGTACTCAGTGAATGCGAGAGAGAGACAGTCCGCCAGCT 540
QY 181 AlaGlnGluSerLeuProIleGluValAlaValAspAlaIleHisLysLeuLysGlu 200
DB 541 GCTGAGAGAGTGTGCCCATGAGTGCATGTGATGCCCTTCAACAGCTCAAGTAAAGAA 600
QY 201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspPropTrpAsnLeu 220
DB 601 AACTACACCGAGAGCTTCTTCATCAGGACATCATCAACCTGACCCACCAAGAACTTG 660
QY 221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
DB 661 CACCTGAAGCATTAAGAATTCCTCGCAGAGTGAGAGTACGTGGAGTACCTGACACAC 720
QY 241 TrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 260
DB 721 TGGAGTACTCCAACTTCCTCCTCCCTGACATTTCTGCTTCAAGGTCCAGGCAAGAGC 780
QY 261 AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValLysCysHis 280

DB 781 AAGAGAGAAAAGAAATAGACTCTTCAGCGAGACAAACCTCAGCCAGGCTCATCTGCCG 840
QY 281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsp 300
DB 841 AAAAATGCCAGCATTTAGCGTGGCGGCCAGACCGGCTACTATATGCTCATCTTGAGCAGA 900
QY 301 TrpAlaSerValSerCysSerGlyGly-----GlyGlyGly 312
DB 901 TGGGCATCTGTGCTCCCTGACATGCTGCGCGTGAAGCGCGGTGCGGAGACCGCGGTGCG 960
QY 313 GlySerArgAsnLeuProThrProThrProSerProGlyMetPheGlnLeuAsnHis 332
DB 961 GGCAGAGAAAGACTCCCGCCGACCTCCAGACCCAGAGATGTTCCTACCTTCACAC 1020
QY 333 SerGlnThrLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGlu 352
DB 1021 TCCCAAAACCTGCTGAGGCGCGTCAAGCAATGCTCCAGAGAGCCAGACAAACTATAGA 1080
QY 353 LeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSer 372
DB 1081 TTTTACCTTGGCACTCTCTGAAGAGATTGATCATGAAGATATCAAAAGTAAAGCAC 1140
QY 373 ThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGlnSerCysLeuAlaSerArg 392
DB 1141 ACAGTGGAGGCTGTTTACCATTTGGAATTTACCAAGATGAGAGTGGCTTAATTCAGA 1200
QY 393 GlnIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThr 412
DB 1201 GAGACCTCTTTCATCAATGAGAGTGGCTGCTGCTCCAGAAAGACCTTTTATGATG 1260
QY 413 ValLeuCysLeuSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAla 432
DB 1261 GCCCTGTGCTTGTGATTTATTTAAAGACTTGAACATGATACAGGTGAGTCAAGACC 1320
QY 433 MetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeu 452
DB 1321 ATGAATGCAAGCTTGTGATGATCTTAAGAGCAATCTTCTTAATCAAAACATGCTG 1380
QY 453 ThrAlaIleAspGluLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLys 472
DB 1381 GCATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
QY 473 SerSerLeuGlnGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 492
DB 1441 TCTCTCCCTGAAGACCGGATTTTATTAACATAAATCAAGCTGCTGCACTTCTTCAT 1500
QY 493 AlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnSerSer 511
DB 1501 GCTTGAAGATTTGGGCGAGTACTATTGACAGAGTACAGAGCTATCTGAATGCTTCC 1557

RESULT 2
US-08-751-767A-9
Sequence 9, Application US/08751767A
Patent No. 5994104
GENERAL INFORMATION:
APPLICANT: ANDERSON, ROBERT J.
APPLICANT: GRANT, HUGH
APPLICANT: MACDONALD, IAN D.
TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHIVE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

```

: APPLICATION NUMBER: US/08/751,767A
: FILING DATE: 08-NOV-1996
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: SADOFF, B.J.
: REGISTRATION NUMBER: 36,663
: REFERENCE/DOCKET NUMBER: 117-221
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 7038164091
: TELEFAX: 7038164100
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1623 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..1620
:
US-08-751-767A-9

Alignment Scores:
Pred. No.: 1,56e-252 Length: 1623
Score: 2309.50 Matches: 438
Percent Similarity: 89.60% Conservative: 27
Best Local Similarity: 84.39% Mismatches: 45
Query Match: 85.76% Indels: 9
DB: Gaps: 2

US-09-917-265-67 (1-511) x US-08-751-767A-9 (1-1623)
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QY 21 GLYLUMETVALLEUTHRCYSHISThrProGluGluASPSP1LEThrTrpSer 40
DB 127 GGAGAAATGCTGTCCTACCTGTGACACCCCTGAAGAATGATACCTGGACCTTG 186
QY 41 AlaInserSerGluValLEUGLYSergLYSThrLeuThrIleGlnValLYSGluPhe 60
DB 187 GACACAGACGACGTGAGCTTTAGGCTGTGGCAAAACCCTGACCATCAAGTCAAGAGCTTT 246
QY 61 GLYSPALAGLYGINTYRThRCYSHISLYSGLYGILYSVALLEUSerArgSerLeuLeu 80
DB 247 GGAATGCTGCCGACGTACACCTGTACAAAGAGCGAGTTCTAAGCCATTGCTCTG 306
QY 81 LEUILEHISLYSGIULASPGIYIETRPserThrAspIleLeuLYSGluGlnYSGLu 100
DB 307 CTGCTTCACAAAAGCAAGATGCAATTGCTCCACTGATATTTAAAGACCACAGAA 366
QY 101 SerLYSAnLYSLeIlePheLeuLYSCYGLUALALYSAnTYRSerGlyArgPheThrCys 120
DB 367 CCCAAAATAAGACCTTTCTAAGATGCCAGGCCAAAGATTATTCTGGACGTTTCACCTGC 426
QY 121 TrpTrpLeuThrAlaIleSerThrAspLeuLYSPheSerValLYSserSerArgLYPhe 140
DB 427 TGGTGGCTGACGACAAATCAGTACTGATTGACATTCACTGTCAAAAAGCAGAGAGCCCT 486
QY 141 SerASPProGlnGlyValThRCYSGLYALALValThrLeuSerAlaGlnValArgVal 160
DB 487 TCTGACCCCAAGCGCGTACGCTGGCAGCTCTACACTCTCTCGACAGAGAGTCAAGAGG 546
QY 161 ASPAnArgASPTrpLYSLYSSTYRThrValGluCYSGlnGlySerAlaCysProSer 180
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QY 181 AlaGlnGluSerLeuProIleGlnValValAlaValAspAlaIleHISLYSLeuLYSTyrGlu 200
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QY 241 TrpSerThrProHISSerTYRPhSerLeuThrPheCYSIleGlnAlaGlnLYSAsn 260
DB 784 TGGACTACTCCACATTCTACTCTCCCTGACATTCTCGTYCACGTCCAGGCAAGAGC 843
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DB 844 AAGACAGAAAAGAAAGATAGAGTCTTCACAGGACCAAGACTCAGCCAGCTATCTGCCGC 903
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DB 904 AAAAATGCCACACTAGCGGTGGGCGCCAGACCCCTACTATAGCTCATCTTGGACGGAA 963
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DB 1084 TCCCAAAACGCTGAGGGCCGTCAGCAACATGCTCGAGAAAGCCAGCAAACTTAA 1143
QY 353 LeuTYRserCYSThrSerGluGlnIleAspHISGluASP1LEThrLYSASPTrpSer 372
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QY 393 GluIleSerLeuIleThrAsnGlySerCYSLeuAlaSerGlyLYSAlaSerPheMetThr 412
DB 1264 GAGACCTCTTTCATACTAATAGGGAGTTGCCCTGCCCTCACAAMACCTCTTTATGATG 1323
QY 413 ValLeuCYsLeuSerSerIleTYRGLuSPLeuLYSMETTYRGLMetGlnPheLYSAla 432
DB 1324 GCCCTGCTCTTACTAGTATTATGACACCTTGAAGATGTACACAGTGGAGTTCAAGACC 1383
QY 433 MetAsnAlaLYSLeuLeuMetASPProLYSArgGlnIlePheLeuASP1AsnMetLeu 452
DB 1384 ATGAATGCCAAAGCTTCTGATGATCTTAAGAGCGCAGATCTTTGATCAAAACATGCTG 1443
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DB 1444 GCAGTTATTGATGAGCTGATCAGGCCCTCGAATTTCACACAGTGAAGCTGCCCAAAAA 1503
QY 473 SerSerLeuGluGluProASPPhetyrLYSThrLYSIIeLYSLeuCYsIIleLeuHIS 492
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RESULT 3
US-08-751-767A-7
: Sequence 7, Application US/08751767A
: Patent No. 5994104
: GENERAL INFORMATION:
: APPLICANT: ANDERSON, ROBERT J.
: APPLICANT: GRANT, HUGH
: APPLICANT: MACDONALD, IAN D.
: TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN
: NUMBER OF SEQUENCES: 80
```

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHUE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,767A
FILING DATE: 08-NOV-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 117-221
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164091
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 6139 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 322..4841
US-08-751-767A-7

Alignment Scores:
Pred. No.: 1,496-251 Length: 6139
Score: 2309.50 Matches: 438
Percent Similarity: 89.60% Conservative: 27
Best Local Similarity: 84.39% Mismatches: 45
Query Match: 85.76% Indels: 9
DB: Gaps: 2

US-09-917-265-67 (1-511) x US-08-751-767A-7 (1-6139)
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QY 21 G1yG1uMe1Val1LeuThrCysHisThrProG1uG1uAspS11eThrTrpThrSer 40
DB 3348 GGAGAAATGGTGCCCTGACCTGACACCCCTGAAGAAAGATGATACCTGACCTG 3407
QY 41 AlG1SerSerG1uVal1LeuG1SerG1yLysThrLeuThrLeuG1Val1SerG1uPhe 60
DB 3408 GACCAGAGCGAGTGGGCTTGAAGCTGCGCAAAACCTGACCAATCCAAAGTCAAGAGTTT 3467
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DB 3468 GGAGATCTGCGCAGTACCTGTCACAAAGAGCGAGGTTCACCAATTCGCTCTG 3527
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QY 121 TrpTrpLeuThrAla1LeSerThrAspLeuLysPheSerVal1LysSerSerArG1yPhe 140
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QY 181 AlG1uG1uSerLeuPro1LeG1uVal1Val1AspAla1LeHisLysLeuLysTyrG1u 200
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DB 4245 GGCAGCAGAAACCTCCCTCCGCGCCAGCTCCGACCCAGCAAGATGTTCCTACCTCCAC 4304
QY 333 SerG1uThrLeuLeuArGAlaValSerAsnThrLeuG1uLysAlaArG1uThrLeuG1u 352
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DB 4365 TTTTACCTTGCACCTTCTGAAGATTTGATGATGATGATGATCAAAAGATTAACACAG 4424
QY 373 ThrValG1uAlaCysLeuProLeuG1uLeuThrMetAsnG1uSerCysLeuAlaSerArG 392
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QY 393 G1u1LeSerLeu1LeThrAsnG1ySerCysLeuAlaSerG1yLysAlaSerPheMetThr 412
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QY 413 ValLeuCysLeuSerSer1LeTyrG1uAspLeuLysMetTyrG1uMetG1uPheLysAla 432
DB 4545 GCCCTGCGCTTGTAGTATTATTAAGAACTTGAAGATGTAACAGAGTGGAGTTCAGAGCC 4604
QY 433 MetAsnAlaLysLeuLeuMetAspProLysArG1u1LePheLeuAspG1uAsnMetLeu 452
DB 4605 ATGAATGCAAAAGCTTCTGATGATGATCTTAAGAGCAATCTTCTTACATCAAAACATG 4664
QY 453 ThrAla1LeAspG1uLeuG1uAlaLeuAsnPheAsnSerVal1ThrVal1ProG1uLys 472
DB 4665 GCGATTATTGATGATGATGATGAGCGCCCTGAATTTTAAACAGTGAAGCTGCGCACAAA 4724
QY 473 SerSerLeuG1uG1uProAspPheTyrLysThrLys1LeLysLeuCys1LeLeuLeuHis 492
DB 4725 TCTCTCCCTTGAACAAACGGATTTTATTAACATCAAGCTGTCGATCTTCTCAT 4784
QY 493 AlaPheArG1LeArGAlaVal1Thr1LeAsnArGMetLeuSerTyrLeuAsnSerSer 511

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Db 4785 GCTTCAGAAATTCGGCAGTGCATGTGACAGACGACGACCTATCATCTTC 4841
RESULT 4
US-09-079-984A-11
Sequence 11, Application US/09079984A
Patent No. 6231850
GENERAL INFORMATION:
APPLICANT: Okano, Fumiyoshi, Satoh, Masahiro,
APPLICANT: Yamada, Katsushige
TITLE OF INVENTION: Canine interleukin 12, a production method
TITLE OF INVENTION: thereof, an immune disease treatment method and preventive
TITLE OF INVENTION: method using it
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Miller & Christenbury Intellectual Property
Department of Schnader, Harrison, Segal and Lewis, LLP
STREET: 1600 Market Street, 39th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079, 984A
FILING DATE: 15-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Austin R. Miller
REGISTRATION NUMBER: 16,602
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-1810
TELEFAX: (215) 568-6946
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 990 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: Canine IL12
LOCATION: 1 to 987
IDENTIFICATION METHOD: Similarity
US-09-079-984A-11
Alignment Scores:
Pred. No.: 3e-178 Length: 990
Score: 1653.00 Matches: 307
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 61.38% Inserts: 0
Gaps: 0
DB: 4
US-09-917-265-67 (1-511) x US-09-079-984A-11 (1-990)
QY 1 ILETRPGIULEGULYSASPVALTFRVALGULEUASPTTRPISPROASPLAPRO 20
DB 67 ATATGGGAAGTGGAGAAAGATGTTATCTTGTAGAGTTGGACTGGACCTGATGCCCCC 126
QY 21 GYGLUETVALVALLIETHRCYSHISTHPRGUGLUASPSPILETHTTRPHTSER 40
DB 127 GGAGAAATGCGTGCTCCTACCTGCATACCCCTGAGAGAAATGACATCATTTGACCTCA 186
QY 41 AAGInSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
DB 187 GCGGAGACACTGAAGTCTAGTTCGTGTAAGAACTTGACCAATCCAAAGCAAGATT 246

QY 61 GLYASPALAGLYGINTYTRTHRCYSHISTHPRGUGLUASPSPILETHTTRPHTSER 80
DB 247 GGAGATGCTGGCCATATACCTGCCATTAAGAGGCAAGGTTCTAGCCGCTCATCTCTG 306
QY 81 LEUILEHISLYSLYSGLUASPSPILETHTTRPHTSERHISPLEULEULYSGLUINLYSGU 100
DB 307 TTGATTTCACAAAAAAGAAAGATGAGATTGGTCCACTGATATCTTAAGGAACAGAAAGAA 366
QY 101 SERLYSASNLYSIIEPHELEULYSCGTLUALYASNTYRSERYLAARGPHERCY 120
DB 367 TCCAAAATAATGATCTTCTGMAATGAGGCAAGAAATTAATTCGGACGTTTCACATGC 426
QY 121 TRPTRLPLAETHRALIISERTHRSPLEULYSPHESERVALYSSERARGLTY 140
DB 427 TGGTGCTGACGGCAGATCACTGATTTGAAATTCAGTGTCAAAAGTAGACGAGGCTTC 486
QY 141 SERASPPROGLINGLYVALTHRCYSLYALAYALTRPLSERALAGLYARGVAL 160
DB 487 TCTGACCCCAAGGGGTGACATGTGACAGACGACCTTTCAGCAGAGGGGTGACAGTG 546
QY 161 ASPASNAARGSPTRYLYSLYSTYTRVALGLUCYSGINGLUYSERALACYPROSER 180
DB 547 GACAACAGGAGATTATTAAGAGACAGACAGTGAGTGTGAGAGGGCAGTGCCTGCTCT 606
QY 181 ALAGLUGUSERLEUPROILLEUVALVALASPALALIEHISLYLEULYSTYRG 200
DB 607 GCCGAGAGAGCTTACCATCGAGTGTGGGTGATGCTATTTCACACACTCAAGATGAA 666
QY 201 ASNTYTRHTSERSEPHLEARGSPILLELYSLEYSLEYSLEYSLEYSLEYSLEYS 220
DB 667 AACTACACAGAGAGTCTTCTATCAGACACATCATCAACAGACCCCAACCAAGCTG 726
QY 221 GINLEULYSPROLEULYSASNTARGHISVALGLUVALSETTRPGIUTYTRPROASPHR 240
DB 727 CAGCTGAAGCCATTGMAAATTCCTCGCACGCGGAGTGTGAGATACCCGACAC 786
QY 241 TRPSETRTHPRHISSETRYPHESERLEUPHRYEYIIEGHLAIGLYLYSASN 260
DB 787 TGGAGACCCCAACATCTCTACTCTCCCTCGACATTTTCATACAGCCCGAGGCAAGAAC 846
QY 261 ASNARGGLULYSASPARGLUCYVALASPLYSTRHSERLALYSVALVALCYSHIS 280
DB 847 AATAGAGAAGAAAGATAGACTCTGCTGGACAGACTCAGCCAAAGCTGTGTGCCAC 906
QY 281 LYSASPALALYSILEARGVALGLNLAARGASPARGYTRYRSERSETTRPHTSERASP 300
DB 907 AAGATGCCAAGATCCGCTGCAAGCCGACAGCCGCTACTATGATTCCTGAGCGCAC 966
QY 301 TRPALASERVALSERCYSSER 307
DB 967 TGGCATCTGTGCTCGCAGT 987
RESULT 5
US-09-079-984A-1
Sequence 1, Application US/09079984A
Patent No. 6231850
GENERAL INFORMATION:
APPLICANT: Okano, Fumiyoshi, Satoh, Masahiro,
APPLICANT: Yamada, Katsushige
TITLE OF INVENTION: Canine interleukin 12, a production method
TITLE OF INVENTION: thereof, an immune disease treatment method and preventive
TITLE OF INVENTION: method using it
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Miller & Christenbury Intellectual Property
Department of Schnader, Harrison, Segal and Lewis, LLP
STREET: 1600 Market Street, 39th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/079,984A
 FILING DATE: 15-MAY-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Austin R. Miller
 REGISTRATION NUMBER: 16,602
 REFERENCE/DOCKET NUMBER: 1051-98
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 563-1810
 TELEFAX: (215) 568-6946
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 990 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 ORIGINAL SOURCE:
 ORGANISM: Canis familiaris
 FEATURE:
 NAME/KEY: Canine IL12
 LOCATION: 1 to 987
 IDENTIFICATION METHOD: Similarity
 US-09-079-984A-1

Alignment Scores:

| Pred. No.: | 9.03e-177 | Length: | 990 |
|------------------------|-----------|---------------|-----|
| Score: | 1640.00 | Matches: | 304 |
| Percent Similarity: | 99.67% | Conservative: | 2 |
| Best Local Similarity: | 99.02% | Mismatches: | 1 |
| Query Match: | 60.90% | Indels: | 0 |
| DB: | 4 | Gaps: | 0 |

US-09-917-265-67 (1-511) x US-09-079-984A-1 (1-990)

QY 11letrpqluenglubysaspa1lyrvala1gluleuasprrph1sproaspala1pro 20
 DB 67ATATGGAACTGGAGAAAGATGTTTATGTTAGTAGTGGACGGCCCTGATGCCCCC 126
 QY 21GlyGluMetValValLeuThrCysHisThrProGluGluAspSerIleThrPrlrSer 40
 DB 127GGAGAAATGGTGGTCTCCACCTCCATACCCCTGAAGAAGATGACATCAGCTTGACCTCA 186
 QY 41AlaGlnSerSerGluValLeuGlySerGlyLysThrIleuThrIleGlnValLysGluPhe 60
 DB 187GGCAGAGCAGTGAATCTCTAGSTTCTGTAAACTCTGACCATCCAGTCAGCAAGATTT 246
 QY 61GlyAspAlaGlyLysIleThrCysHisLysGlyLysValLeuSerArGserLeu 80
 DB 247GGAGATGCTGGCAGATATACCTCCATTAAGAGGCAAGTCTTGAGCCGCTCAGTCTG 306
 QY 81LeuIleHisLysLysGluAspGlyIleThrPrlrSerThrAspIleLeuLysGluGlu 100
 DB 307TTATTCACAAAAAGAGATGAATTTGGTCCACGATATCTTAAAGAGAAACAGAAAGAA 366
 QY 101SerLysAsnLysIlePheLeuLysCysGluAlaLysAspTrpSerGlyArgPheThrCys 120
 DB 367TCCAAAAATAGATCTTCTGAAATGTAAGGCAAGAAATATTTCTGACGCTTTCACATGC 426
 QY 121TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArGlyPhe 140
 DB 427TGGTGGCTGAGCCCATCATCTACTGATTTGAAATTCAGTGTCAAAAGTACAGAGCTTC 486
 QY 141SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgVal 160
 DB 487TCTGACCCCAAGAGGGGTGACATGTGAGCAGTGTACACTTTCACAGAGAGAGGTGAGAGTG 546
 QY 161AspAsnArgAspTrpTrpLysLysTrpThrValGluCysGlnGluGluSerAlaCysProser 180

DB 547GACACAGGAGTTATGAAGATACAGACGTGACAGGCGCAGTCCCTCT 606
 QY 181AlaGluLysLeuPheProIleGluValAlaValAspAlaIleHisLysLeuLysTrpGlu 200
 DB 607GGCAGAGAGAGCTTACCCTACGAGTGGTGGTGGATGATTCACAAAGCTCAAGTATGAA 666
 QY 201AsnTrpThrSerSerPhePheIleArgAspIleIleLysProAspProProthrAsnLeu 220
 DB 667AACTACACAGCAGCTTCTTCATCAGACATCATCAACACACACCACCAACACCTG 726
 QY 221GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTrpProAspTrp 240
 DB 727CAGCTAAGCAGTGAATAATTTCCGACGTTGAGAGTCAAGTGGGAATATCCCGACACC 786
 QY 241TrpSerThrProHisSerTrpPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 260
 DB 787TGGAGACCCCAATTCCTACTCTCTCCGACATTTTGCATACAGCCCAAGGCAAGAAC 846
 QY 261AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValAlaCysHis 280
 DB 847AATAGAGAAAGAAAGATGACTCTCGTGCACAGACCTCAGCCCAAGGTCGTGTCAC 906
 QY 281LysAspAlaLysIleArgValGlnAlaArgAspArgTrpTrpSerSerSerTrpSerAsp 300
 DB 907AAGGATGCCAGATCCCGCTGCAAGCCCGAGACCGCTACTATATGTTCACTCTGAGCGAC 966
 QY 301TrpAlaSerValSerCysSer 307
 DB 967TGGCAGTCTGTGCTCCCTGCAAGT 987

RESULT 6

US-09-310-842-4
 Sequence 4, Application US/09310842A
 Patent No. 6451593

GENERAL INFORMATION:
 APPLICANT: Wiltig, Prof. Burghardt
 APPLICANT: Jungmans, Claas
 TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Ge
 FILE REFERENCE: XI 597/99
 CURRENT APPLICATION NUMBER: US/09/310,842A
 CURRENT FILING DATE: 1999-05-12
 EARLIER APPLICATION NUMBER: DE 196 48 625.4
 EARLIER FILING DATE: 1996-11-13
 NUMBER OF SEQ ID NOS: 13
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 4

LENGTH: 1870

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

NAME/KEY: gene

LOCATION: (1)..(1870)

OTHER INFORMATION: Interleukin-12 (IL-12, p40-subunit); Oligo DNA Dumbbell

FEATURE:

NAME/KEY: misc.binding

LOCATION: (1)..(2)

OTHER INFORMATION: Intramolecular binding site: the T-nucleotides at position 1 t

OTHER INFORMATION: Intramolecular binding site: the T-nucleotides at position 186

FEATURE:

NAME/KEY: misc.binding

LOCATION: (1869)..(1870)

OTHER INFORMATION: Intramolecular binding site: the T-nucleotides at position 186

OTHER INFORMATION: to 1870 can be modified with amino or caroxy features

OTHER INFORMATION: Description of Artificial Sequence: Strandness: both; nuclei

OTHER INFORMATION: acid (linear), hypothetical: No. 6451593 anti-sense: No

US-09-310-842-4

Alignment Scores:

| Pred. No.: | 2.41e-151 | Length: | 1870 |
|---------------------|-----------|---------------|------|
| Score: | 1420.50 | Matches: | 267 |
| Percent Similarity: | 86.83% | Conservative: | 23 |

Best local Similarity: 79.94% Mismatches: 33
 Query Match: 52.75% Indels: 12
 DB: 4 Gaps: 2

US-09-917-265-67 (1-511) x US-09-310-842-4 (1-1870)

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QY 1 ILETRPGILEUGCLULYSASPVALTYRVALGLULEUASPTTRPHISPROASPALAPRO 20
   |||
Db 699 ATATGGCACTGAGCAAGAAAGATGTTATGTCTGACATTTGGATTGGTATCCGCGATGCCCT 758
QY 21 GLYGLUETVALVALLLEUTHCYSHISTHRPROGLUINUASPAPILETHTTRPTHTSER 40
   |||
Db 759 GGAGAAATGCTGCTCCTCCTGACCTGTGACACCCCTGAGAGATGATATCCTGACCTTG 818
QY 41 ALAGINSEISERGLUVALLEUGLYSERGLYSTRHLEUTHRLLEGINVALVGLUPLHE 60
   |||
Db 819 GACCAGAGCAGTGGCTTATAGCTGTGGCAAAACCCCTGACCATTCAGTCAAGAGATT 878
QY 61 GLYASPALAGLYGINTYRTHRCYSHISLYSGLYLYSVALLLEUSERARGSERLEU 80
   |||
Db 879 GGAGATCTGGCCGCTACCTGTGACCAAGAGCCAGGTTCTAAGCCATTCGCTCTG 938
QY 81 LEUITLEHISLYSGLYUASPGLYLETTPSERTHRASPILLEULYSGLULNLSGLU 100
   |||
Db 939 CTGCTTCACAAAAGCAAGATGCAATTGTGTCACATGATTTTAAAGACCAAGAA 998
QY 101 SERLYSASNYSLIEPHELEULYSCYGLUVALYASNTYRSERGILYARGPHTHCYS 120
   |||
Db 999 CCCAAAATAGACCTTTCTAAGATGCGAGGCCAAGATTTCTTGACGTTTCACTGC 1058
QY 121 TRPTPLEUTHRALALIESERTHRASPLEULYSSEERVALYSSERSEARGLYPHE 140
   |||
Db 1059 TGGTGGCTGACGACAAATCAGTACTGATTTGACATTCAGTCCAAAGACGAGAGGCTCT 1118
QY 141 SERASPRONGINLYVALTHRCYSGLYALVALTHLEUSERVALAGLARGVALARGVAL 160
   |||
Db 1119 TCTGACCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTCCAGAGAGATGAGAGG 1178
QY 161 ASPASPARGASPTLYSLYSTYRTHVALGLUCYSGINLUYSEARGLACYSER 180
   |||
Db 1179 GACACACAAGGATAT---GAGTACTCAGTGGAGTGCCAGGAGGAGGAGGCTGCCAGCT 1235
QY 181 ALAGLUULSERLEUPROLEGUVALVALVALASPALALEHISLYSLEULYSGLU 200
   |||
Db 1236 GCTGAGAGAGTCTGCCCATTTGAGGTCATGCTGATGCCCTTCCAAAGCTCAAGTATCAA 1295
QY 201 ASNTYRTHRSERSERPHEPHEILEARGASPILEILEULYSPROASPROPTHTASNULEU 220
   |||
Db 1296 AACACACACGACGCTTCTTCATCAGGACATCATCAAACTTGACCCACCAACACTTG 1355
QY 221 GLULEULYSPROLEULYSASNSERARGHISVALGLUVALSETTPGLUTYTPROASPTHR 240
   |||
Db 1356 CAGCTGAGGCCATTAAAGAAATCTCGCAGGTGGAGGTGACCTGGAGTACCTGACACC 1415
QY 241 TRPSETRHPROHISSETRYRPHSESERLEUTHRPHECYSYSLLEGINAGLILYSASN 260
   |||
Db 1416 TTGGAGTCTCCACACTTCTACTTCTCCCTGACATTCCTGCGTTACAGGTCCAGGCAAGAGC 1475
QY 261 ASNARGGLULYSLYSASPARGLEUCYSVALASPIYSTRSERALALYSVALCYSHIS 280
   |||
Db 1476 AAGGCAAAAAGAAAGATAGAGTCTCACCGCAAGACCTCAGCCAGGTCATCTGCCGC 1535
QY 281 LYSASPALALYSILEARGVALGLNALIARGASPARGRYTRYRSESERSETTRPSERASP 300
   |||
Db 1536 AAAAATGCCACGACTTACGCTGGGGCCAGAGACCGCTACTACTATCTTGGAGCGAA 1595
QY 301 TRPALASERVALISERYSERGLYGLYGLYGLYGLYSEARARGANLEU----- 317
   |||
Db 1596 TGGGCACTCTGCGCCCTGCACATTA-GGAGCTCATTAATAGCCATACCATTTGTAGAGCT 1654
QY 318 -----PROFTHPROTHPROSERPRO 324
   |||
Db 1655 TTACTTCTTTAAAAAACCTCCACACCTCCCTGAGACT 1696

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RESU# 7
US-08-848-760B-24
; Sequence 24, Application US/08848760B
; Patent No. 6248721
; GENERAL INFORMATION:
; APPLICANT: Chang, Lung-Ji
; TITLE OF INVENTION: Animal Model For Evaluation Of Vaccines
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: United States of America
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/848,760B
; FILING DATE: 25-Jan-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/838,702
; FILING DATE: 09-Apr-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PACE, DORAN R.
; REGISTRATION NUMBER: 38,261
; REFERENCE/DOCKET NUMBER: CNG-100C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 987 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-08-848-760B-24

Alignment Scores:
Pred. No.: 1,06e-151 Length: 987
Score: 1419.50 Matches: 261
Percent Similarity: 91.86% Conservative: 21
Best Local Similarity: 85.02% Mismatches: 24
Query Match: 52.71% Indels: 1
DB: 4 Gaps: 1

US-09-917-265-67 (1-511) x US-08-848-760B-24 (1-987)
QY 1 ILETRPGILEUGCLULYSASPVALTYRVALGLULEUASPTTRPHISPROASPALAPRO 20
   |||
Db 67 ATATGGCAACTGAGCAAGAAAGATGTTATGTCTGACAAATTTGGATTGGTATCCGCGATGCCCT 126
QY 21 GLYGLUETVALVALLLEUTHCYSHISTHRPROGLUINUASPAPILETHTTRPTHTSER 40
   |||
Db 127 GGAGAAATGCTGCTCCTCCTGACCTGTGACACCCCTGAAAGAGATGATACCTTGACCTTG 186
QY 41 ALAGINSEISERGLUVALLEUGLYSERGLYSTRHLEUTHRLLEGINVALVGLUPLHE 60
   |||
Db 187 GACCAGAGCAGTGGAGTCTTATAGCTGTGGCAAAACCCCTGACCATTCAGTCAAGAGATT 246
QY 61 GLYASPALAGLYGINTYRTHRCYSHISLYSGLYLYSVALLLEUSERARGSERLEU 80
   |||
Db 247 GGAGATGCTGCGCCGCTGACCTGTGACCAAGAGCGAGGTTCTTAACCATTCGCTCTG 306
QY 81 LEUITLEHISLYSGLYUASPGLYLETTPSERTHRASPILLEULYSGLULNLSGLU 100

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|||||
Db      307 CTGCTTCACAAAAAGAGATGGATTGGTCCAGATATTTTAAAGGACCGAAAGAA 366
QY      101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyAqpPheThrCys 120
Db      367 CCAAAAATAGACCTTTCTTAAGATCGAGGCCAAGATATTTCTGAGCTTTCCACTGC 426
QY      121 TTPTRPLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
Db      427 TGGTGCTGACGACAACTAGTACTGATTGACATTCAGTGTCAAAAGACAGCAGAGCTCT 486
QY      141 SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgVal 160
Db      487 TGTGACCCCAAGGGGTGACGTGCGAGCTGACACTCTGTCAAGAGAGCAAGG 546
QY      161 AspAsnArgAspTyrLysTyrThrValGluCysGlnGluLysSerAlaCysProSer 180
Db      547 GACAAACAGAGAT---GAGTACTCAGTGGAGTGCAGAGAGACAGTGCCTCCAGCT 603
QY      181 AlaGluGluSerLeuProIleGluValValAspAlaIleHisLysLeuLysTyrGlu 200
Db      604 GCTGAGAGAGCTGCTCCCATTTGAGTGCATGTCGATGCGGTCCACAAGCTCAAGTATGAA 663
QY      201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPheProAsnLeu 220
Db      664 AACTACACGACGAGCTTCTTCATCAGGAGCATCATCAACCTGACCCCAACCACTTG 723
QY      221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
Db      724 CAGCTACAGCATTAAGAATTTCTCGGAGGTGAGTGCAGTGCAGGAGTACCTGCAGACC 783
QY      241 TTPSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 260
Db      784 TGGAGTACTCCACATTCCTACTTCTCCGACATTTCTGCGTCCAGTCCAGGCAAGAGC 843
QY      261 AsnArgGlnLysLysAspArgLeuCysValAspLysThrSerAlaLysValValLysHis 280
Db      844 AAGAGAGAAAGAAAGATAGAGTCTTCCACCGACAAGACCTCAGCCAGCTATCTGCCG 903
QY      281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsp 300
Db      904 AAAAATGCCAGCATTTAGCGTGGCGGCCGACGACCGCTACTATAGCTCATCTTGAGACGAA 963
QY      301 TTPAlaSerValSerCysSer 307
Db      964 TGGGCATCTGTGCTCCCTGCAGT 984

RESULT 8
US-09-851-062-3
; Sequence 3, Application US/09851062
; Patent No. 6448081
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTI-SENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
; FILE REFERENCE: RTS-0247
; CURRENT APPLICATION NUMBER: US/09/851,062
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 3
; LENGTH: 2318
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (14)...(1000)
US-09-851-062-3

Alignment Scores:
Pred. No.: 4,5e-151 Length: 2318
Score: 1419,50 Matches: 261
Percent Similarity: 91,86% Conservative: 21
Best Local Similarity: 85,02% Mismatches: 24

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Query Match: 52,718 Indels: 1
DB: 4 Gaps: 1
US-09-917-265-67 (1-511) x US-09-851-062-3 (1-2318)
QY      1 TleTrrGluLeuGlnLysAspValTyrValValGluLeuAspTrpHisProAspAlaPro 20
Db      80 ATATGGGAACGTGAAGAAATGTTATGTCGTAAGAAATTTGATGATCGGATGCCCT 139
QY      21 GlyIleMetValValLeuThrCysHisThrProGlnGluAspIleThrTrpThrSer 40
Db      140 GGAGAAATGTTGCTCTCCTCAGCTGTGACACCCCTGAAAGAAATGATGATTCACCTGACCTTG 199
QY      41 AlaGlnSerSerGluValLeuGlnLysSerGlyLysThrLeuThrIleGlnValLysGluPhe 60
Db      200 GACCAAGAGCAGTGTAGCTTTAGGCTGTGCAAAACCTGACCATTCACAAAGAGTTT 259
QY      61 GlyAspAlaGlyGlnTyrThrCysHisLysGlyGlyLysValLeuSerArgSerLeuLeu 80
Db      260 GGAGATGCTGGCCAGTACCTGTCCAAAGAGGCGGAGTTCTTAAGCCATTGCTGCTCTG 319
QY      81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGlnGlnLysGlu 100
Db      320 CTGCTTCACAAAAAGAAAGATGGAATTTGCTCAGCTGATATTTTAAAGACCAAGAAAGAA 379
QY      380 CCAAAAATTAAGACCTTTCTTAAGATCGAGGCCAAGAAATTAATTCGAGCTTTCACCTGC 439
QY      121 TTPTRPLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
Db      440 TGGTGCTGACGACAAATTCAGTACTGATTTGACATTCAGTGTCAAAAGCGAGAGGCTCT 499
QY      141 SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgVal 160
Db      500 TGTGACCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTTCGACAGAGAGTCAAGAGG 559
QY      161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluLysSerAlaCysProSer 180
Db      560 GACAAACAGAGAT---GAGTACTCAGTGGAGTGCAGAGAGACAGTCCCTGCCAGCT 616
QY      181 AlaGluGluSerLeuProIleGluValValAspAlaIleHisLysLeuLysTyrGlu 200
Db      617 GCTGAGAGAGTGTGCTCCATTTGAGGTGAGTGGCGGTTCACAAAGCTCAAGATGTGA 676
QY      201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPheProAsnLeu 220
Db      677 AACTACACGACGCTTCTTCATCAGGACATCATCAAACTGACCCACCAACCACTTG 736
QY      221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
Db      737 CAGCTGAACCCATTAAGAATTTCTCGGAGGTGAGGTGAGTGGGAGTACCTGACACC 796
QY      241 TTPSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 260
Db      797 TGGAGTACTCCACATTCCTACTTCTCCGACATTTCTGCGAGGTCCAGGAGCAAGAGC 856
QY      261 AsnArgGlnLysLysAspArgLeuCysValAspLysThrSerAlaLysValValCysHis 280
Db      857 AAGAGAGAAAGAAAGATAGAGTCTTCACCGACAAGACCTCAGCCAGCTCATCTGCGCC 916
QY      281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsp 300
Db      917 AAAAATGCCAGCATTTAGCTGCGGCCGACGACCGCTACTATAGCTCATCTTGAGACGAA 976
QY      301 TTPAlaSerValSerCysSer 307
Db      977 TGGGCATCTGTGCTCCCTGCAGT 997

RESULT 9
US-08-186-529-1
; Sequence 1, Application US/08186529
; Patent No. 5573764

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1 NAME: Brown, Scott A.
2 REGISTRATION NUMBER: 32,724
3 REFERENCE/DOCKET NUMBER: GI 55255A
4 TELECOMMUNICATION INFORMATION:
5 TELEPHONE: 617-498-8224
6 TELEFAX: 617-876-5851
7 INFORMATION FOR SEQ ID NO: 1:
8 SEQUENCE CHARACTERISTICS:
9 LENGTH: 987 base pairs
10 TYPE: nucleic acid
11 STRANDEDNESS: single
12 TOPOLOGY: linear
13 MOLECULE TYPE: cDNA
14 ORIGINAL SOURCE:
15 ORGANISM: Homo sapiens
16 CELL TYPE: Lymphoblast
17 CELL LINE: RPMI 8866
18 FEATURE:
19 NAME/KEY: CDS
20 LOCATION: 1..987
21 US-08-640-3864-1

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US-09-917-265-67 (1-511) x US-08-184-009-194 (1-1018)

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Qy 1 IlettrpgluLeuGluLysAspValTyrValValGluLeuAspTrpHisProAspAlaPro 20
Db ATATGGGAACGAGAAAGATGTTATGTCGTAAAGATGGATGGTATCCGATGCCCT 157
Qy 21 GlyLmeValValLeuThrCysHisThrProGluGluAspPleThrTriPthSer 40
Db GGAGAAATGGTGGTCCCTGACCTGTGACACCCCTGACAGAGATGGATACCTGGACCTTG 217
Qy 41 AlaGlnSerSerGluValLeuGlySerGlyThrLeuThrIleGlnValLysGluPhe 60
Db GACCAAGACGAGTGAAGCTTGTAGCTGTGCAAAACCCGTGACCATTCAGTCAAGAGATT 277
Qy 61 GlyAspAlaGlyGlnTyrThrCysHisLysGlyGlyValLeuSerArgSerLeuLeu 80
Db GGAGATGCTGGCGCTGACCTGTGACAAAGAGCGGCTTAAAGCCATTGCGTCTG 337
Qy 81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGlu 100
Db CTGCTTCACAAAAGAGATGGAATTTGGTCCACTGATATTTTAAAGGACAGAAAGAA 397
Qy 101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
Db CCCAAAATAAGACCTTTCTAAGATGCCAGCCCAAGAAATATTCTGACGTTTCACCTGC 457
Qy 121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
Db TGGTGGCTGAGACAACTGATGATGATTTGACATTCACAAAGCAGAGAGAGCGCTCT 517
Qy 141 SerAspProGlnGlyValThrCysGlyValAlaValThrLeuSerAlaGluArgValArgVal 160
Db TCTACCCCAAGAGGAGTGGCTGCGAGCTGCTACACTCTCTCCAGAGAGATCAGAGGG 577
Qy 161 AspaAsnArgAspTyrLysLysTyrThrValGluLysGlnGluLysSerAlaCysProSer 180
Db GACAACAAGAGATAT---GACTACTGAGTGGAGTCCAGAGAGACAGCGCCGCCACT 634
Qy 181 AlaGluGluSerLeuProIleGluValValAlaAspAlaIleHisLysLeuLysTyrGlu 200
Db GCTGAGAGAGCTGCGCCATTCGAGCTGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCT 694
Qy 201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeu 220
Db AACTACACACGACGACTTCTCATCAGGACATCATCAACCTGACCCAGCAGACCTTG 754
Qy 221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
Db CAGCTGAAGCCATTAAAGAAATTCGCGCAGCTGAGCGTCACTGGGACTGACCTGACAC 814
Qy 241 TrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 260
Db TGGAGTACTCCACATTCCTACTCTCCCTGACATTCCTGCTGAGTCCAGTCCAGGCAAG 874
Qy 261 AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValValCysHis 280
Db AAGAGAGAAAGAAAGATAGAGTCTTCACGAGCAAGACCTCAGCCACCGTATCTGCGCC 934
Qy 281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTrpSerSerSerTrpSerAsp 300
Db AAAAATGCCAGCATTTAGCGTCCGCGCCAGAGACCGCTACTATAGCTCATCTTGGAGCG 994
Qy 301 TrpAlaSerValSerCysSer 307
Db TGGGCACTGCTGCCCTGCACT 1015

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RESULT 12
US-08-458-356-194
Sequence 194 Application US/08458356
Patent No. 5942235
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo

```

APPLICANT: Tartaglia, James
APPLICANT: Cox, William I.
TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
NUMBER OF SEQUENCES: 217
CORRESPONDENCE ADDRESS:
ADDRESSER: Curtis, Morris & Safford
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,356
FILING DATE: 02-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/184,009
FILING DATE: 19-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEX: 425066CURTMS
INFORMATION FOR SEQ ID NO: 194:
SEQUENCE CHARACTERISTICS:
LENGTH: 1018 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-458-356-194

Alignment Scores:
Pred. No.: 1,456-151 Length: 1018
Score: 1418.50 Matches: 261
Percent Similarity: 91.86% Conservative: 21
Best Local Similarity: 85.02% Mismatches: 24
Query Match: 52.67% Indels: 1
DB: 2 Gaps: 1

US-09-917-265-67 (1-511) x US-08-458-356-194 (1-1018)
Qy 1 IlettrpgluLeuGluLysAspValTyrValValGluLeuAspTrpHisProAspAlaPro 20
Db ATATGGGAACGAGAAAGATGTTATGTCGTAAAGATGGATGGTATCCGATGCCCT 157
Qy 21 GlyLmeValValLeuThrCysHisThrProGluGluAspPleThrTriPthSer 40
Db GGAGAAATGGTGGTCCCTGACCTGTGACACCCCTGACAGAGATGGATACCTGGACCTTG 217
Qy 41 AlaGlnSerSerGluValLeuGlySerGlyThrLeuThrIleGlnValLysGluPhe 60
Db GACCAAGACGAGTGAAGCTTGTAGCTGTGCAAAACCCGTGACCATTCAGTCAAGAGATT 277
Qy 61 GlyAspAlaGlyGlnTyrThrCysHisLysGlyGlyValLeuSerArgSerLeuLeu 80
Db GGAGATGCTGGCGCTGACCTGTGACAAAGAGCGGCTTAAAGCCATTGCGTCTG 337
Qy 81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGlu 100
Db CTGCTTCACAAAAGAGATGGAATTTGGTCCACTGATATTTTAAAGGACAGAAAGAA 397
Qy 101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
Db CCCAAAATAAGACCTTTCTAAGATGCCAGCCCAAGAAATATTCTGACGTTTCACCTGC 457

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0Y      121TTPPTPLEUHTAlAlIleSerTHrAsPLeUysPhSeSerValLysSerSerArgGlyPhe 140
Db      458 TGTGGCTACCAACAATCATAGTACTGATTGACATTGAAGTCAAAGCACAGAGCGCTCT 517
0Y      141 SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgVal 160
Db      518 TGTGACCACCCCAAGGGGTGACGTGCAGAGCTGTACACTCTCTGCAGAGAAGTCAAGCGG 577
0Y      161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluLysSerAlaCysProSer 180
Db      578 GACAACAAGAGACTAT--GAGTACTCAGTGAGAGTGCAGAGGAGACAGTGGCTCCCAAGCT 634
0Y      181 AlaGlnGluSerLeuProIleGluValAlaValAspAlaIleHisLysLeuLysTyrGlu 200
Db      635 CGTGAAGAGAGCTGCCCATTTAGAGTCATGCTGAGTGAAGCCGTTCAACAAGTCAAGTATGAA 694
0Y      201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProthrAsnLeu 220
Db      695 AACTACACACGACGAGCTTCTTCATCAGGACATCATCAAACTGACCACCCAGAACACTTG 754
0Y      221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
Db      755 CAGCTGAAGCCATTAAGAATTCGTGGCAGGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 814
0Y      241 TrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnLysLysAsn 260
Db      815 TGAGTACTACCCACATTCCTACTCTTCCTCCGACATTTCTGCGTTTAGAGTCCAGGCGAAGC 874
0Y      261 AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValLysHis 280
Db      875 AAGACAGAAAAMAAGATAGACTCTTCACGACAMAGACCTCACCCAGCGCATCTGGCGC 934
0Y      281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsp 300
Db      935 AAAAATGCCAGCATTAAGCTGGGGGCCAGGACCGCTACTAATGCTCATCTTGGAGCAA 994
0Y      301 TrpAlaSerValSerCysSer 307
Db      995 TGGCATCTGTGCCCCGTGCAGT 1015

RESULT 13
US-08-460-736-194
; Sequence 194, Application US/08460736
; Patent No. 6265189
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; APPLICANT: Tartaglia, James
; APPLICANT: Cox, William I.
; TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
; NUMBER OF SEQUENCES: 217
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,736
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/184,009
; FILING DATE: 19-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506

```

| | | |
|---|--------------------------------|---|
| : | REFERENCE/DOCKET NUMBER: | 454310-2530 |
| : | TELECOMMUNICATION INFORMATION: | |
| : | TELEPHONE: | (212) 840-3333 |
| : | TELEFAX: | (212) 840-0712 |
| : | TELEX: | 425066CURTMS |
| : | INFORMATION FOR SEQ ID NO: | 194: |
| : | SEQUENCE CHARACTERISTICS: | |
| : | LENGTH: | 1018 base pairs |
| : | TYPE: | nucleic acid |
| : | STRANDEDNESS: | single |
| : | TOPOLOGY: | linear |
| : | MOLECULE TYPE: | cDNA |
| : | US-08-460-736-194 | |
| Alignment Scores: | | |
| Pidm. No.: | 1,45e-151 | Length: 1018 |
| Score: | 1418.50 | Matches: 261 |
| Percent Similarity: | 91.86% | Conservative: 21 |
| Best Local Similarity: | 85.02% | Mismatches: 24 |
| Query Match: | 52.67% | Indels: 1 |
| DB: | 4 | Gaps: 1 |
| US-09-917-265-67 (1-511) x US-08-460-736-194 (1-1018) | | |
| OY | 1 | IleTrpGluLeuGluLysAspValTyrrValAlaGluLeuAspTrpHisProAspAlaPro 20 |
| Dd | 98 | ATATGGCACTGAAAGAACATGTATTATGCGTAGAATTGGATTGGTATCCGATGCCCT 157 |
| OY | 21 | GLyGlMetValValLeuthrCysHsrThrProGluGuaAspPrlIethTrpThSer 40 |
| Dd | 158 | GGGAAGAATGGTGCTTCACCTGCTGCACACCCTTGAAAGATGATACCTGGACCTTG 217 |
| OY | 41 | AlaGlnSerSerGluValLeuGlySerGlyTythrLeuthrIleGlnValValSgluPhe 60 |
| Dd | 218 | GACCAGAGCGATGAGSTCTTAGCGTCTGGCAAACCTGCACCATCAAGTCAAGAGATT 277 |
| OY | 61 | GLyAspAlaGlyInTrpThrCysHsluSgLyGlyValLeuSerArgSerLeuLeu 80 |
| Dd | 278 | GGAGATGCTGGCCAGTACACTGTCCAAAGGAGCGAGTTCTTAAGCCATTGCTCTCTG 337 |
| OY | 81 | LeuIleHisLysLysGluAspGlyLleTrpSerThrAspIleLeuLysGluGlnLysGlu 100 |
| Dd | 338 | CTGCTTCACAAAAGGAAGATGGAATTGGTGCCTCATGTATTTTAAAGACACAAGAA 397 |
| OY | 101 | SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTYrSerGlyArgPheThrCys 120 |
| Dd | 398 | CCCAAAATAAGACCTTTCTAAGATGCGAGGCCAAAGATTATCTGGACGTTTCACTGTC 457 |
| OY | 121 | TriTPLeuthrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgLYphe 140 |
| Dd | 458 | TGtGTGCTGACGACATTCAGTACTGATTGGACATTCAAGTGCMAAAGCACAGAGGCTCT 517 |
| OY | 141 | SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgVal 160 |
| Dd | 518 | TCAGACCCCCCAAGGGGTGACGTGCGAGGCTGTCACACTCTGTGAGAGAGATGACAGGG 577 |
| OY | 161 | AspAsnArgAspTrpLysTyrrThrValGluCysGlnGluGlySerAlaCysProSer 180 |
| Dd | 578 | GACAAACAAGAGAT--GAGTACTGAGTGGAGTCCAGAGAGACAGGCTGCTGCCAGCT 634 |
| OY | 181 | AlaGlnGluSerLeuProIleGluValValAlaAspAlaIleHisLysLeuLysTyrrGlu 200 |
| Dd | 635 | GCtGAGGAGAGTGTGCCCATTCAGGTCATGGTGGATGGCGTTCCACAAAGCTAAGTAA 694 |
| OY | 201 | AsnTrpThrSerSerPhePheIleArgAspIleIleLysProAspProTrpHisAsnLeu 220 |
| Dd | 695 | AACCTACACAGCGAGCTTCTTCACTACGGGACATCATCAACCTGACCCACCAACAACTTG 755 |
| OY | 221 | GlnLeuLysProLeuLysAsnSerPrghlsvAlaGluValSerTrpGluTyrrProAspThr 240 |
| Dd | 755 | CACCTGAAGCATTTAAAGATTCTGGGACGGGGAGGTACAGCTGGGAATACCTGGACACC 814 |
| OY | 241 | TrpSerThrProHisSerLysTrpPheSerLeuthrPheCysIleGlnAlaGlnGlyLysAsn 260 |

|||||
Db 815 TGGAGTACTCCACATCTCTACTCTCCCTGCATCTTGCGTTCAGGCGCAGGAGGC 874
OY 261 ASNARGLUISLVSASPARGLEUCYSVALASPLYSRHSERIALYSVALCYSHIS 280
Db 875 AAGGAGAAAAGAAAGATAGAGTCTTCAGGACCAAGACCTCAGCGTCATCTGCCGC 934
OY 281 LYSASPALALYSILEARGVALGIALAARGSPARTGYTYRYSERSETRPSERASP 300
Db 935 AAAAATGCCAGCATTTAGCGTCCGGCCAGAGACCGCTACTATAGCTCATCTTGAGCGCAA 994
OY 301 TRPALASERVALSERCYSSER 307
Db 995 TGGGCATCTGTGCCCTGCAGT 1015
RESULT 14
US-08-751-767A-3
Sequence 3, Application US/08751767A
Patent No. 5994104
GENERAL INFORMATION:
APPLICANT: ANDERSON, ROBERT J.
APPLICANT: GRANT, HUGH
APPLICANT: MACDONALD, IAN D.
TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHVE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,767A
FILING DATE: 08-NOV-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B. J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 117-221
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164091
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1399 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 43..1026
US-08-751-767A-3
Alignment Scores:
Pred. No.: 2,49e-151 Length: 1399
Score: 1418.50 Matches: 261
Percent Similarity: 91.86% Conservative: 21
Best Local Similarity: 85.02% Mismatches: 24
Query Match: 52.67% Indels: 1
Gaps: 1
US-09-917-265-67 (1-511) x US-08-751-767A-3 (1-1399)
OY 1 |||TTPGLIULEUGLULYSASPVALTYYVALICILEULSAPTRPHISPROASPAIAPRO 20
Db 109 ATATGGAACTGAAGAAAGATGTTATGTCCTAGAAATTGGATTGCTCCGAGTCCCT 168

OY 21 GLYGLUETVALVALLLEUTHRCYSHISRHPROGLUGLUASAPSLIETHRTPRPSER 40
Db 169 GGAGAAATGCTGGTCTCCTACCTGTGACACCCCTTAAGAGATGGTATCACCCTGGACCTTG 228
OY 41 ALAGLNSERSEGLIUALLEUGLYSERGLYSRTHLEUTHRIEGLINALLYSGLUPHE 60
Db 229 GACCAAGACATGAGGTGTTAGGCTGGCAAAAACCCGTGACCATTCGAAGTCGAAGAGTTT 288
OY 61 GLYSAPALAGLYINTYRTHRCYSHISLYSGLYGLYVALLEUSERARGSERLEULEU 80
Db 289 GGAGATGCTGGCCAGTACACCTGTACAAAAGAGCGCAGGTTCTAAGCATTCCTCCTCG 348
OY 81 LEULIETHSLYSLSYSGLUASPGLYLITRPSERTHRSPILLEULYSGLUGLNUGLU 100
Db 349 CTGCTTCACAAAAGGAAGATGGAATTTGGTCCACTGATATTTAAAGGACACAGAAAGAA 408
OY 101 SERLYSASNLYSILEPHELEULYSGLIUALALYSANTRYSERGLYARGPHETHRYS 120
Db 409 CCCAAAATATAGACCTTTCTAAGATGCGAGGCCAAGAATTCTTGAGCGTTTCACCTGC 468
OY 121 TRPTTRLEUTHRALALIESERTHRASPLEULYSRHSERVALYSSERSEARGLYPHE 140
Db 469 TGGTGGCTGACGACAAATCAGTACGATTTCACATTCAGTGTCAAAAAGCAGCAGAGCTCT 528
OY 141 SERASPPROGLINGLYVALTHRCYGLYVALALATHREUSERALAGLUARGVALARGVAL 160
Db 529 TCTGACCCCAAGGGGTGACGTGGAGCTCTCTACCTCTCTTGAGAGAGAGTACAGAGC 588
OY 161 ASPASNARGASPTRYLYSTYRTHYRVALGLUCYGLINGLUGLYSERIALACYSPROSER 180
Db 589 GACAAACAGAGAT---GAGTACTCACTGAGAGTCCAGAGAGAGAGTCCGCTGCAGCT 645
OY 181 ALACLUGLUSERLEUPROLIEGLIUALVALASPALALIEHISLYSLEULYSTYRGLU 200
Db 646 GCTGAGAGAGTCTGCCCATGTGAGTCATGTGTGATGCCGTTCACAAAGCTCAAGTATGAA 705
OY 201 ASPTYRTHRSERSERPHEPHEILEARGASPILEILEYSPROASPPROPRTHRASLEU 220
Db 706 AACTACACACGACCTCTTATCAGGACATTCATCAAACTGACCCACCCACAGACATGTG 765
OY 221 GLNLEULYSPROLEULYSASNSERFARGHISVALGLUVALSERTPGLUTYRPROASPTH 240
Db 766 CAGCTGAAGCATTAAGAATTCTCGGAGGTGAGAGTGCACCTGGAGTACCCTGACACCC 825
OY 241 TRPSERTHRPROHISSETRYRPHESERLEUTHRPHECYSILEGLINALLGLYLSASN 260
Db 826 TGGAGTACTCCACATCTCTACTCTCCCTGCACATTCGCTTCAGGTCACAGGCCAAGAGC 885
OY 261 ASNARGLUISLVSASPARGLEUCYSVALASPLYSRHSERIALYSVALCYSHIS 280
Db 886 AAGGAGAAAAGAAAGATAGAGTCTTCACGGACAAAGACTAGCCAGCGTATCTGCCGC 945
OY 281 LYSASPALALYSILEARGVALGIALAARGSPARTGYTYRYSERSETRPSERASP 300
Db 946 AAAAATGCCAGCATTTAGCGTCCGGCCAGAGACCGCTACTATCTTGGAGCGAA 1005
OY 301 TRPALASERVALSERCYSSER 307
Db 1006 TGGGCATCTGTGCCCTGCAGT 1026
RESULT 15
US-08-265-087-1
Sequence 1, Application US/08265087
Patent No. 5571515
GENERAL INFORMATION:
APPLICANT: SCOTT, PHILLIP
APPLICANT: TRINCHIERI, GIORGIO
TITLE OF INVENTION: Compositions and Methods for use of
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson

STREET: Spring House Corporate Center, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/265,087
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/229,282
FILING DATE: 18-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST51AUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2362 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 33..1016
US-08-265-087-1
Alignment Scores:
Pred. No.: 6.04e-151 Length: 2362
Score: 1418.50 Matches: 261
Percent Similarity: 91.86% Conservative: 21
Best Local Similarity: 85.02% Mismatches: 24
Query Match: 52.67% Indels: 1
DB: 1 Gaps: 1
US-09-917-265-67 (1-511) x US-08-265-087-1 (1-2362)
QY 1 ILETPrGluLeuGluLysAspValTYrValIValGluLeuAspTrpHisProAspAlaPro 20
DB 99 ATATGGAACTGAGAGAAAGATGTTATGTCGTAGAAATGGATTGGATTCGGATGCCCT 158
QY 21 GlyGluMetValIleuThrCysHisThrProGluGluAspAlaIleThrTrpThrSer 40
DB 159 GGAGAAATGGTGGTCTCACCTGTGACACCCCTGGAAGAAGATGATACCTGGACCTTG 218
QY 41 AlaGlnSerSerGluValIleuGlySerGlyLysThrIleGlnValLysGluPhe 60
DB 219 GACCAAGAGAGTGGCTTACCTGCTGCAAAAACCTGACCATCCAAAGCAAGAGATT 278
QY 61 GLYAspAlaGlyIntyrThrCysHisLysGlyLysValIleuSerArgSerLeuLeu 80
DB 279 GGAAGATGCTGGCCAGTACACTGTCAAAAAGAGGCGGAGGTTCTTAAGCCATTGCTCTG 338
QY 81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGlu 100
DB 339 CTGCTTCACAAAAAGAGAGATGGAATTGCTCCACATATTTTAAAGCAGCAAGAA 398
QY 101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTrpSerGlyArgPheThrCys 120
DB 399 CCCAAAAATAGACCTTTCTTAAGATCGAGGCCAAGAAATATTCTGAGCTTTCACCTGC 458
QY 121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerArgGlyPhe 140
DB 459 TGGTGGCTACGCAATCACTGACTGATTGACATTTGACATTCAGTGTCAAAAAGCAGAGGCTCT 518

QY 141 SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgVal 160
DB 519 TCTGACCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCACAGAGAGTCAAGAGG 578
QY 161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluLysSerLacysProSer 180
DB 579 GACAAACAGAGATAT---GAGTACTGAGTGAAGTCCAGAGAGACAGTCCGCCAGCT 635
QY 181 AlaGluGluSerLeuProIleGluValIleValAspAlaIleHisLysLeuLysTyrGlu 200
DB 636 GCTGAGAGAGATCTGCCCATTTGAGGTCAATGATGATGCCGTTCAACAGCTCAAGTGA 695
QY 201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProthrasnLeu 220
DB 696 AACTACACACAGCAGCTTCTTCATCAGCAGCATCATCAAACTGACCCCAAGAACTTG 755
QY 221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluLysProAspThr 240
DB 756 CAGCTGAACCATTAAGAATTCGCGCAGGTGAGGTGAGGTGAGGAGTACCTGACACC 815
QY 241 TrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 260
DB 816 TGGAGTACTCCACATTCCTACTCTCCCTGACATTTCTGCGTTCAGCTCCAGGCAAGAGC 875
QY 261 AsnArgLysLysLysAspArgLeuCysValAspLysThrSerAlaLysValCysHis 280
DB 876 AAGAGAGAAAGAAAGATAGAGCTTCACGAGCAAGACCTCAGCCAGCTCATCTGCCGC 935
QY 281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTrpSerSerTrpPpsAsp 300
DB 936 AAAAATGCCAGCTTAAGCTGGGGGCCAGGACCGCTACTATAGCTCATCTTGAGCGAA 995
QY 301 TrpAlaSerValSerCysSer 307
DB 996 TGGGCACTGTGTGCCCTGCACT 1016

Search completed: July 17, 2003, 09:32:48
Job time : 87.061 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 16, 2003, 19:59:04 ; Search time 349.106 Seconds
(Without alignments)
3019.692 Million cell updates/sec

Title: US-09-917-265-67
Perfect score: 2693
Sequence: 1 IMLEKDYVVELDHPADP.....HAFRIRAVTINRMSTLNS 511

Scoring table:
BLOSUM62
Xgapop 10.0 , Ygapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1439767 seqs, 1031500376 residues
Total number of hits satisfying chosen parameters: 2879534

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USFTO.spool/US09917265/rnat_15072003_092107_1639/app_query.fasta.1.3114
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-TRANS-human40.csl -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=plc -NORM=ext -HEAPSIZE=500 -MINLEN=0
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-FCGAPOP=6 -FCGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_NA:*

- 1: /cgn2_6/pdata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/pdata/1/pubpna/PCT_NEW_PUB.seq:*
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- 5: /cgn2_6/pdata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/pdata/1/pubpna/PCPUS_PUBCOMB.seq:*
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- 11: /cgn2_6/pdata/1/pubpna/US09_NEW_PUB.seq2:*
- 12: /cgn2_6/pdata/1/pubpna/US09_NEW_PUB.seq3:*
- 13: /cgn2_6/pdata/1/pubpna/US09_PUBCOMB.seq:*
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- 15: /cgn2_6/pdata/1/pubpna/US10_PUBCOMB.seq:*
- 16: /cgn2_6/pdata/1/pubpna/US60_NEW_PUB.seq:*
- 17: /cgn2_6/pdata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------------------------|
| 1 | 2693 | 100.0 | 1533 | 10 | US-09-917-265-66 Sequence 66, Appl |

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|---|----|--------|-------|------|----|-------------------|-------------------|
| C | 2 | 2693 | 100.0 | 1533 | 10 | US-09-917-265-68 | Sequence 68, Appl |
| C | 3 | 2693 | 100.0 | 1599 | 10 | US-09-917-265-61 | Sequence 61, Appl |
| C | 4 | 2693 | 100.0 | 1599 | 10 | US-09-917-265-63 | Sequence 63, Appl |
| C | 5 | 2546 | 94.5 | 1533 | 10 | US-09-917-265-43 | Sequence 43, Appl |
| C | 6 | 2546 | 94.5 | 1533 | 10 | US-09-917-265-45 | Sequence 45, Appl |
| C | 7 | 2546 | 94.5 | 1599 | 10 | US-09-917-265-38 | Sequence 38, Appl |
| C | 8 | 2546 | 94.5 | 1599 | 10 | US-09-917-265-40 | Sequence 40, Appl |
| C | 9 | 2309 | 85.7 | 1608 | 10 | US-09-828-825-15 | Sequence 15, Appl |
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| C | 12 | 2306.5 | 85.6 | 1644 | 10 | US-09-828-825-13 | Sequence 13, Appl |
| C | 13 | 2304 | 85.6 | 1638 | 10 | US-09-828-825-9 | Sequence 9, Appl |
| C | 14 | 2304 | 85.6 | 1639 | 10 | US-09-828-825-11 | Sequence 11, Appl |
| C | 15 | 2275 | 84.5 | 1578 | 10 | US-09-828-825-3 | Sequence 3, Appl |
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| C | 17 | 1653 | 61.4 | 921 | 10 | US-09-917-265-52 | Sequence 52, Appl |
| C | 18 | 1653 | 61.4 | 921 | 10 | US-09-917-265-54 | Sequence 54, Appl |
| C | 19 | 1653 | 61.4 | 987 | 10 | US-09-917-265-58 | Sequence 58, Appl |
| C | 20 | 1653 | 61.4 | 987 | 10 | US-09-917-265-60 | Sequence 60, Appl |
| C | 21 | 1653 | 61.4 | 2267 | 10 | US-09-917-265-107 | Sequence 107, App |
| C | 22 | 1653 | 61.4 | 2267 | 10 | US-09-917-265-109 | Sequence 109, App |
| C | 23 | 1554 | 57.7 | 921 | 15 | US-10-079-616-6 | Sequence 6, Appl1 |
| C | 24 | 1554 | 57.7 | 921 | 15 | US-10-079-616-7 | Sequence 7, Appl1 |
| C | 25 | 1554 | 57.7 | 987 | 10 | US-09-917-265-29 | Sequence 29, Appl |
| C | 26 | 1554 | 57.7 | 987 | 10 | US-09-917-265-31 | Sequence 31, Appl |
| C | 27 | 1554 | 57.7 | 2193 | 15 | US-10-079-616-5 | Sequence 5, Appl1 |
| C | 28 | 1550 | 57.6 | 985 | 10 | US-09-917-265-55 | Sequence 55, Appl |
| C | 29 | 1550 | 57.6 | 985 | 10 | US-09-917-265-57 | Sequence 57, Appl |
| C | 30 | 1546 | 57.4 | 921 | 10 | US-09-917-265-26 | Sequence 26, Appl |
| C | 31 | 1546 | 57.4 | 921 | 10 | US-09-917-265-28 | Sequence 28, Appl |
| C | 32 | 1420.5 | 52.7 | 1870 | 15 | US-10-228-811-4 | Sequence 4, Appl1 |
| C | 33 | 1419.5 | 52.7 | 987 | 15 | US-09-826-025-24 | Sequence 24, Appl |
| C | 34 | 1419.5 | 52.7 | 987 | 15 | US-10-172-399-7 | Sequence 7, Appl1 |
| C | 35 | 1418.5 | 52.7 | 987 | 11 | US-09-754-014-2 | Sequence 2, Appl1 |
| C | 36 | 1418.5 | 52.7 | 987 | 11 | US-09-754-014-3 | Sequence 3, Appl1 |
| C | 37 | 1418.5 | 52.7 | 987 | 11 | US-09-754-014-4 | Sequence 4, Appl1 |
| C | 38 | 1418.5 | 52.7 | 987 | 11 | US-09-836-866-2 | Sequence 2, Appl1 |
| C | 39 | 1418.5 | 52.7 | 2362 | 11 | US-09-924-703-3 | Sequence 3, Appl1 |
| C | 40 | 1058.5 | 39.3 | 1840 | 15 | US-10-172-399-3 | Sequence 3, Appl1 |
| C | 41 | 970 | 36.0 | 666 | 10 | US-09-917-265-46 | Sequence 46, Appl |
| C | 42 | 970 | 36.0 | 666 | 10 | US-09-917-265-47 | Sequence 47, Appl |
| C | 43 | 970 | 36.0 | 1455 | 10 | US-09-917-265-104 | Sequence 104, App |
| C | 44 | 970 | 36.0 | 1455 | 10 | US-09-917-265-106 | Sequence 106, App |
| C | 45 | 969 | 36.0 | 591 | 10 | US-09-917-265-49 | Sequence 49, Appl |

ALIGNMENTS

RESULT 1
US-09-917-265-66
Sequence 66, Application US/09917265
Patent No. US20020052030A1
GENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Borouhns, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
FILE REFERENCE: IN-5
CURRENT APPLICATION NUMBER: US/09/917,265
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 109
SOFTWARE: PatentIn version 3.1
SEQ ID NO 66
LENGTH: 1533
TYPE: DNA
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1533)
OTHER INFORMATION:
US-09-917-265-66

Alignment Scores:

Pred. No.: 1.67e-305 Length: 1533
 Score: 2693.00 Matches: 511
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-09-917-265-67 (1-511) x US-09-917-265-66 (1-1533)

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 QY 21 GlyLmeValValLeuThrCysHisTrpProGluLysAspAlIeThrTrpHisSer 40
 DB 61 GGAGAAATGGTGTCTCCCTCACTCCATCCCTCGAAGAAGATGACATTCATCGACTCA 120
 QY 41 AlaGlnSerSerLysValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
 DB 121 GGCGACAGCAGTGAAGCTGAGTCTGTCTGTAAGAACTCTGACATCCAGTCAAGCAAGATTT 180
 QY 61 GLYAspAlaGlyLysIleThrCysHisLysGlyLysValLeuSerArgSerLeuLeu 80
 DB 181 GGAGATGCTGGCCAGATATACCTCCATMAAGAGCGAAGGTTTGAGCCGCTCCTCTG 240
 QY 81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGlu 100
 DB 241 TTGATTCACAAAAAAGAGATGAGATTTGGTCCACTGATATCTTAAAGAGACAGAAAGA 300
 QY 101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTrpSerGlyArgPheTrpCys 120
 DB 301 TCCAAAAATGAGATCTTTCTGAAATGTGAGGCAAAATATATCTGAGCTTTCACATGC 360
 QY 121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgLysPhe 140
 DB 361 TGGTGGCTGACGGCATACAGTACTGATTTGAATTCAGTCTCAAAAGTACAGAGGCTTC 420
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 DB 421 TCTGACCCCCCAAGGGGTGACATGTGACAGAGTGCACCTTTCACAGAGAGGCTCAGAGT 480
 QY 161 AspAsnArgAspTrpLysLysTrpThrValGluCysGlnGluLysSerAlaCysProSer 180
 DB 481 GACAAAGAGGATTATAGAGATGACAGAGTGAAGTGCAGAGGGCGAGTCCCTCT 540
 QY 181 AlaGluGluSerLeuProIleGluValAlaValAspAlaIleHisLysLysLeuLysTrpGlu 200
 DB 541 GCGAGAGAGAGCTTACCATCCGAGGTCGTGTGATGCTATTTCACAAGCTCAAGTATGAA 600
 QY 201 AsnTrpTrpSerSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeu 220
 DB 601 AACTACACACAGCGCTTCTTCATCAGACATCATCAACACCAACCCACCAACCTG 660
 QY 221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluLysTrpProAspThr 240
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 QY 241 TrpSerTrpProHisSerTrpPheSerLeuThrPheCysIleGlnAlaGlnLysLysAsn 260
 DB 721 TGGAGACCCCACTTCTACTCTCCCTGACATTTTGCATACAGGCCCAAGGCAAGAAC 780
 QY 261 AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValValCysHis 280
 DB 781 AATAGAGAAAGAAAGATAGACTCTGCTGACAAAGACTCAAGGCTCGTGTCCAC 840
 QY 281 LysAspAlaLysIleArgValGlnAlaArgAspArgTrpTrpSerSerSerTrpSerAsp 300
 DB 841 AAGAGATGCCAAGATCCGCTGCAAGCCAGACCGCTACTATAGTTCAATCTGAGACGAC 900
 QY 301 TrpAlaSerValSerCysSerGlyGlyLysGlyLysGlyLysArgAsnLeuProThrPro 320
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QY 321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaVal 340
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 QY 361 IleAspHisGluAspIleThrLysAspLysTrpSerThrValGluAlaCysLeuProLeu 380
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 QY 381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
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 QY 401 SerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeuCysLeuSerIleTrp 420
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 QY 421 GluAspLeuLysMetCysGlnMetGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
 DB 1261 GAGGACTTGAAGATGTACAGATGGAATTCAGAGCCATGACGCAAGCTTTAATGAT 1320
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 DB 1321 CCCAAGAGCAGATCTTCTGTGATCAAAACATGCTGACAGTATGATGAGCTGTTACAG 1380
 QY 461 AlaLeuAsnPheAsnSerValThrValProGlnLysSerSerLeuGlnLysProAspPhe 480
 DB 1381 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCTCCCTTGAAAGAGCGGATTTT 1440
 QY 481 TYrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
 DB 1441 TATATAACTTAATAATCAAGCTGTGCATCTTTCATGCTTCAGAAATGTGTGCGGATGACC 1500
 QY 501 IleAsnArgMetMetSerTrpLeuAsnSerSer 511
 DB 1501 ATCAATATGAAATGATGTCTTCACTTGAACCTCTTCC 1533

RESULT 2
 US-09-917-265-66/c
 ; Sequence 68, Application US/09917265
 ; Patent No. US20020052030A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wonderling, Ramani S.
 ; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
 ; FILE REFERENCE: IM-5
 ; CURRENT APPLICATION NUMBER: US/09/917,265
 ; CURRENT FILING DATE: 2001-07-27
 ; PRIOR APPLICATION NUMBER: 60/223,016
 ; PRIOR FILING DATE: 2000-08-04
 ; NUMBER OF SEQ ID NOS: 109
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 68
 ; LENGTH: 1533
 ; TYPE: DNA
 ; ORGANISM: Canis familiaris
 US-09-917-265-66

Alignment Scores:
 Pred. No.: 1.67e-305 Length: 1533
 Score: 2693.00 Matches: 511
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-09-917-265-67 (1-511) x US-09-917-265-66 (1-1533)
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21 GlyUmeValIValLeuThrCysHisThrProGluGluAspAspIleThrTrpHisSer 40
1473 GGAGAAATGGGTGCTCCTCAGCTGGCCATACCCCTGAAGAAGATGACATCATCTGGAGCTCA 1414
41 AlaGlnSerSerGluValIleuGlySerGlyLysTrpLeuThrIleGluValLysGluPhe 60
1413 GCCGAGACAGCTGAAGTCTCTAGGTTCTGTGTAACACTCTGACCATTCCAAGCAATTTT 1354
61 GlyAspAlaGlyGlnTyrThrCysHisLysGlyGlyLysValLysSerArgSerLeuLeu 80
1353 GGAGATGCTGGCCAGCTATACCTGCGCATTAAGAGAGCAAGGTTCTGAGCCGCTCACTCTG 1294
81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGlu 100
1293 TTGATTCACAAAAAAGAGATGAATTGGTCCACTGATATCTTAAGCAACGAAABAA 1234
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1233 TCCAAAAATAGATCTTCTGAAATGTGAGCCAAAGATTAATTCGAGCGTTTCATGCC 1174
121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
1173 TGTGTGCTGACGGCAATCAGTACTGATTTGAATTCAGTTCAAAAGTACGAGAGCGCTTC 1114
141 SerAspProGlnGlyValIleThrCysGlyValIleValIleLeuSerAlaGluArgValIle 160
1113 TCTGACCCCGCAAGGGGTACATGTGAGACAGTGCACATTTGACGAGAGAGGTGAGCTG 1054
161 AspAsnArgAspTyrTyrLysLysTyrThrValGluGlyGlnGluGlySerAlaCysProSer 180
1053 GACAACACAGGATTTAAGAACTACACACTGAGAGTGTGAGAGGCGAGTCCCTGCCCTCT 994
181 AlaGluGluSerLeuProIleGluValIleValAspAlaIleHisLysLeuLysTyrGlu 200
993 GCCCAGAGAGACCTTACCCATCGAGTCTGCTGCTGATTCACAAACCTCAAGATGAA 934
201 AsnTrpTrpSerSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeu 220
933 AACTACACACAGCTTCTTATCAGACATCATCAACAACGAGCCACCAACAACCTG 874
221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
873 CAGCTGAAGCCATTCAAAAATTTCTGCGCAGCTGAGAGTCACTGGAGTACCCTGCACAC 814
241 TrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 260
813 TGGAGACACCCACATTTCTTACTCTCCCTGACATTTTCATACAGGCCAGGCCAAGAAC 754
261 AsnArgGluLysLysAspArgLeuCysValIleAspLysTrpSerAlaLysValIleCysHis 280
753 AATGAGAGAAAAGAAAGATAGACTCTGCGTGAGACAGACTCAGCCAAAGCTGTGGCCAC 694
281 LysAspAlaLysIleArgValIleAlaIleArgAspArgTyrTyrSerSerSerTrpSerAsp 300
693 AAGGATGCCAAGATCCCGGTGCAAGCCGAGACCCGCTCTATAGTTCATCTCTGAGCGCAC 634
301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
633 TGGGCATCTGTGATCAGTACAGTGGCGGTGGCGCGCATAGAAAACCTTCCCAACCCCT 574
321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnTrpLeuLeuArgAlaVal 340
573 ACTTCATCCCGGGGTATGTTCCAAATGTTTGAACACATCCCAAACTGTTTGAAGACCGCTC 514
341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGlnLeuTyrSerCysThrSerGlyGlu 360
513 AGCAACACGCTTTCAGAAAGCGCACAAACCTCTAGCATTAATATCTCTGACACTTCCGAGAG 454
361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380

453 ATTCATCATGAAGATATCAACAAGATATAAACCACACAGTGGAGCGCTGTTACCACTG 394
381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
393 GAATTAACCATGAAGAAGATGTTGCTGCTGCTTCCAGAGAGATCTCTTTATATACTAACGGG 334
401 SerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeuCysLeuSerSerIleTyr 420
333 ACTTCCCTGGCCCTCTGGAGAAAGCCCTCTTTATAGACGGTCTGTGCTTACGACGATCTAT 274
421 GluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
273 GAGGACTTAAGATGTACAGATGGAATTCAGAGCCATGAAGCAAGCAACTTTAATGAT 214
441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuGln 460
213 CCCAAGACGACAGATCTTCTGTGATCAAAACATGCTGACAGCTATGATGAGACTGTTPACAG 154
461 AlaLeuAsnPheAsnSerValThrValProGlnLysSerSerLeuGluIleProAspPhe 480
153 GCCCGAATTTTCACACAGTGTGACTGTGCCACAGAAATCTCCTTGAAGACCGGATTTT 94
481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
93 TATTAACCTAAATCAACCTCTGCATCTTCTTCTTACAGATTCGTGCGGTGACC 34
501 IleAsnArgMetMetSerTyrLeuAsnSerSer 511
33 ATCAATAGATGATGTCTCTACTTGAACCTCTCC 1

RESULT 3
US-09-917-265-61
: Sequence 61, Application US/09917265
: Patent No. US20020052050A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: APPLICANT: Boroughs, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
: FILE REFERENCE: IM-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: CURRENT FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: PRIOR FILING DATE: 2000-08-04
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO: 61
: LENGTH: 1599
: TYPE: DNA
: ORGANISM: Canis familiaris
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(1599)
: OTHER INFORMATION:
US-09-917-265-61

Alignment Scores:
Pred. No.: 1,79e-305 Length: 1599
Score: 2693.00 Matches: 511
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 10

US-09-917-265-67 (1-511) x US-09-917-265-61 (1-1599)

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21 GlyUmeValIValLeuThrCysHisThrProGluGluAspAspIleThrTrpHisSer 40
127 GGAGAAATGGGTGCTCCTCAGCTGGCCATACCCCTGAAGAAGATGACATCATCTGGAGCTCA 186

QY 41 AlaglnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
 DB 187 GCGGAGGAGCAGTGAAGTCTAGAGTTCTGTGTAAGAACTCTGACCATCTCAAGTCAAGAAATTT 246
 QY 61 GlyAspAlaGlyGlnTyrThrCysHisLysGlyGlyLysValLeuSerArgSerLeuLeu 80
 DB 247 GGAATCTGTGGCCGCTTACCTGCTTAAGAGGCAAGGTTCTGAGCCGCTCTCCTCG 306
 QY 81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGlu 100
 DB 307 TTGATTCACAAAAAAGAAAGATGAAATTTGGTCCCATATATCTTAAGAAACAAAGAA 366
 QY 101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
 DB 367 TCCAAAATAGAACTTCTGAAATGTGAGGCAAGAAATTAATCTGACGTTTCAATGTC 426
 QY 121 TrpThrLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
 DB 427 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 486
 QY 141 SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgVal 160
 DB 487 TCTGACCCCAAGAGGGGTGACATGTGAGCAGTGCACACTTTCAGCAGAGAGGCTCAGAGTG 546
 QY 161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluLysSerAlaCysProSer 180
 DB 547 GACAAACAGGATTTATAAGATACACAGTGTGAGTGTGAGGAGGAGGCTGCTGCTGCTCT 606
 QY 181 AlagluGlnSerLeuProIleGluValValAlaAspAlaIleHisLysLeuLysTyrGlu 200
 DB 607 GCCGAGAGAGCCCTACCATCGAGGCTGTGGTGTGATCTATTCACAAAGCTCAAGTATGAA 666
 QY 201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProThrAsnLeu 220
 DB 667 AACATACACGAGCTTCTTCATCAGACATCATCAACACAGACCCACCAACACCTG 726
 QY 221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
 DB 727 CAGCTGAGGCAATGAAATTCCTCGGACGCTGAGGTGTGAGTGTGAAATCCCGGACACC 786
 QY 241 TrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 260
 DB 787 TGGAGCACCCCACTTCTACTTCTCTGCTGACATTTTGCAATACAGGCCCAAGGCAAAAC 846
 QY 261 AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValCysHis 280
 DB 847 AATAGACAAAAGAAAGATAGACTCTGCTGAGACAGACCTCAGCAAGGTCGTGTGCAC 906
 QY 281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsp 300
 DB 907 AAGGATGCCAAGATCCGCTGACAGCCCGAGACCCGCTACTATATGTTATCTCTGAGCGCAC 966
 QY 301 TrpAlaSerValSerCysSerGlyGlyGlyGlyLysSerArgAsnLeuProThrPro 320
 DB 967 TGGGCACTGTGTATCATCATGTGGGGGGGGGGGAGCTTGAACACTTGCCAAACCCCT 1026
 QY 321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaVal 340
 DB 1027 ACTTCATCCCGGGGTATGTTCATATGTAACCACTCCCAAACTGTGTGAGAGCCGCTC 1086
 QY 341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGlnLeuLysCysThrSerSerGlu 360
 DB 1087 AGCAACACGCTTCAGAAAGCCAGACAACTCTAGAAATTAATATCTCTGACCTCCGAGAG 1146
 QY 361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
 DB 1147 ATTAGCATGATGAAGATATACAAAGGATAAACAGCAGCACTGAGAGGCTCTTACCACTG 1206
 QY 381 GlnLeuThrMetAsnGlnSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
 DB 1207 GAATTAACCATGATGAGAGTCTGCTGCTTCAGAGAGATCTCTTGAATAACTAACGGC 1266
 QY 401 SerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeuCysLeuSerSerIleTyr 420

DB 1267 AGTGGCCCTGGCCCTTGAAAGGCGCTCTTTATGACGGCTCTGTGCTTACAGCATCTAT 1326
 QY 421 GlnAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
 DB 1327 GAGGACTTGAAGATGTCCAGATGTGAATTTAAGGCCCTGAACGCAAACTTTTAATGTAT 1386
 QY 441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuGln 460
 DB 1387 CCCAAGAGGAGATCTTCTTGATCAAAACATGCTGACACTATCATGATGAGCTGTTCAG 1446
 QY 461 AlaLeuAsnPheAsnSerValThrValProGlnLysSerSerLeuGlnGluProAspPhe 480
 DB 1447 GCCCTGAATTTCAACAGTGTGACTGTCCACAGAAATCCCTTGAAGAGCCGATTTT 1506
 QY 481 TyrIleThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
 DB 1507 TATTAACCTAAATCAAGGCTGTGATCTCTTTCATATCTTTCAGAAATTCGTGGGTACC 1566
 QY 501 IleAsnArgMetSerTyrLeuAsnSerSer 511
 DB 1567 ATCAATAGAAATGATGCTCTACTTGAACCTTTC 1599
 RESULT 4
 US-09-917-265-63/c
 : Sequence 63, Application US/09917265
 : Patent No. US20020052030A1
 : GENERAL INFORMATION:
 : APPLICANT: Wonderling, Ramani S.
 : TITLE OR INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
 : FILE REFERENCE: IM-5
 : CURRENT APPLICATION NUMBER: US/09/917,265
 : PRIOR FILING DATE: 2001-07-27
 : PRIOR APPLICATION NUMBER: 60/223,016
 : NUMBER OF SEQ ID NOS: 109
 : SOFTWARE: PatentIn version 3.1
 : SEQ ID NO 63
 : LENGTH: 1599
 : TYPE: DNA
 : ORGANISM: Canis familiaris
 US-09-917-265-63
 Alignment Scores:
 Pred. No.: 1,79e-305 Length: 1599
 Score: 2693.00 Matches: 511
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 0
 DB: 10
 US-09-917-265-67 (1-511) x US-09-917-265-63 (1-1599)
 QY 1 IlettrpLnuLeuGlnLysAspValTyrValGluLeuAspTrpHisProAspAlaPro 20
 DB 1533 ATATGGAACTGGAGAAAGATGTTATGTTGTAGAGTTGACGTGGCAACCTGATGCCCC 1474
 QY 21 GlnGluMetValAlaLeuThrCysHisThrProGlnGluAspIleThrTrpThrSer 40
 DB 1473 GGAAGAAATGGTGTCTCTCAGCTGCCATACCCCTGAAAGAAATGATACATCTTGACCTCA 1414
 QY 41 AlaglnSerSerGluValLeuGlnLysSerGlyLysThrLeuThrIleGlnValLysGluPhe 60
 DB 1413 GCGCAGAGCAGTGAAGCTCTAGGTTCTGTAAAACTCTGACATCCAAAGTCAAGAAATTT 1354
 QY 61 GlyAspAlaGlyGlnTyrThrCysHisLysGlyGlyLysValLeuSerArgSerLeuLeu 80
 DB 1353 GGAAGATGCTGGCCAGATATACCTGCATTAAGAGGCAAGGTTCTGAGCCGCTCAGTCTG 1294
 QY 81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGlnGlnLysGlu 100
 DB 1293 TTGATTCACAAAAAAGAAAGATGAAATTTGGTCCACATGATATCTTAAAGGACAGAAAGAA 1234

| | | | | | | | | | | | | | | | | | | | | | | |
|----|------|-----|-----|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| QY | 101 | Ser | Val | Asn | Lys | Ile | Phe | Leu | Lys | Cys | Val | Ala | Val | Asn | Tyr | Ser | Gly | Arg | Phe | Thr | Cys | 120 |
| DB | 1233 | TC | CA | AA | AA | TA | AG | AT | CT | TC | TG | AA | AT | GT | G | AG | GC | AA | GA | AT | T | 117 |
| QY | 121 | Trp | Phe | Leu | Thr | Ala | Ile | Ser | Thr | Asp | Leu | Lys | Phe | Ser | Val | Lys | Ser | Arg | Gly | Phe | 140 | |
| DB | 1173 | TG | TC | GC | CA | CC | GC | CA | AT | C | AG | T | CA | CA | AT | T | T | G | AA | T | T | 111 |
| QY | 141 | Ser | Asp | Pro | Gln | Ile | Val | Thr | Cys | Gly | Val | Ala | Val | Thr | Leu | Ser | Ala | Gly | Val | Arg | 160 | |
| DB | 1113 | TCT | GA | CCCC | CCCC | AA | GG | GG | GT | CA | TC | AT | GT | GC | AC | CT | T | T | CA | CG | 105 | |
| QY | 161 | Asp | Asn | Arg | Ser | Phe | Tyr | Lys | Tyr | Thr | Val | Glu | Cys | Gln | Gly | Ser | Ala | Cys | Pro | Ser | 180 | |
| DB | 1053 | G | A | C | A | C | A | C | G | A | T | T | A | A | G | A | C | T | T | A | 194 | |
| QY | 181 | Ala | Glu | Glu | Ser | Leu | Pro | Ile | Glu | Val | Val | Ala | Ala | Ile | His | Lys | Leu | Lys | Tyr | Glu | 200 | |
| DB | 993 | G | C | C | G | A | G | G | A | G | A | C | C | T | T | A | C | C | A | T | 934 | |
| QY | 201 | Asn | Tyr | Thr | Ser | Ser | Phe | Phe | Ile | Arg | Asp | Ile | Ile | Lys | Pro | Asp | Pro | Thr | Trp | Ser | 220 | |
| DB | 933 | A | A | C | T | A | C | A | C | A | C | A | C | A | T | C | A | C | A | C | 874 | |
| QY | 221 | Gln | Leu | Lys | Pro | Leu | Lys | Asn | Ser | Arg | His | Val | Glu | Val | Ser | Trp | Gly | Tyr | Pro | Ser | 240 | |
| DB | 873 | C | A | G | C | T | A | G | A | A | A | A | A | T | T | T | C | G | G | A | 814 | |
| QY | 241 | Trp | Ser | Thr | Pro | His | Ser | Tyr | Phe | Ser | Leu | Thr | Phe | Cys | Ile | Gln | Ala | Gln | Gly | Lys | 260 | |
| DB | 813 | T | G | G | A | C | A | C | C | C | A | T | T | C | T | C | T | C | T | C | 754 | |
| QY | 261 | Asn | Arg | Glu | Lys | Lys | Asp | Arg | Leu | Cys | Val | Ala | Ser | Trp | Ser | Ala | Lys | Val | Val | Cys | 280 | |
| DB | 753 | A | A | T | G | A | G | A | A | A | A | A | A | G | A | T | A | G | A | C | 694 | |
| QY | 281 | Lys | Asp | Ala | Lys | Ile | Arg | Val | Gln | Ala | Ala | Arg | Asp | Arg | Tyr | Tyr | Ser | Ser | Ser | Trp | 300 | |
| DB | 693 | A | A | G | A | T | G | C | C | A | A | G | A | T | C | C | G | C | T | A | 634 | |
| QY | 301 | Trp | Ala | Ser | Val | Ser | Cys | Ser | Gly | Gly | Gly | Gly | Ser | Arg | Asn | Leu | Pro | Thr | Pro | 320 | | |
| DB | 633 | T | G | G | C | A | T | C | T | C | A | T | G | C | A | T | G | C | G | C | 574 | |
| QY | 321 | Thr | Pro | Ser | Pro | Gln | Lys | Phe | Gln | Cys | Leu | Asn | His | Ser | Gln | Thr | Leu | Leu | Arg | 140 | | |
| DB | 573 | A | C | T | C | A | T | C | C | C | G | G | A | T | T | C | C | A | A | C | 514 | |
| QY | 341 | Ser | Asn | Thr | Leu | Gln | Lys | Ala | Arg | Gln | Thr | Leu | Glu | Leu | Tyr | Ser | Cys | Thr | Ser | Gln | 360 | |
| DB | 513 | A | G | C | A | A | C | A | G | C | C | C | A | A | C | T | A | G | A | T | 454 | |
| QY | 361 | Ile | Asp | His | Glu | Asp | Ile | Thr | Lys | Asp | Lys | Thr | Ser | Thr | Val | Glu | Ala | Cys | Leu | Pro | 380 | |
| DB | 453 | A | T | T | G | A | T | C | A | T | C | A | T | A | T | C | A | A | C | C | 394 | |
| QY | 381 | Glu | Leu | Thr | Met | Asn | Glu | Ser | Cys | Leu | Ala | Ser | Arg | Glu | Ile | Ser | Leu | Ile | Thr | Asn | 400 | |
| DB | 393 | G | A | A | T | T | A | C | A | T | G | A | T | G | A | T | G | A | T | G | 334 | |
| QY | 401 | Ser | Cys | Leu | Ala | | | | | | | | | | | | | | | | | |

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OY 461 Alaleuanspheasnservaltthrvalprogluyserserleuglucluproasphe 480
      |||||||
Db 153 GCCCTGAATTTCAACAGCTGTGACTGTGCCACAGAAATCCCTTTGAAGACCCGATTTT 94
OY 481 TyrlysrprrlysllelyslaucyslleleuenuhsllapheagjleagAlaValthr 500
      |||||||
Db 93 TATAAACTATAAAATCAAGCTCTGCATCTCTTTCATGCTTTTCAGAAATTCGTGGGTGACC 34
OY 501 lileasnrgmetmetsetrrytleuanserser 511
      |||||||
Db 33 ATCAATAGATGATGTCTCTACTTGACACTCTCC 1

RESULT 5
US-09-917-265-43
: Sequence 43, Application US/09917265
: Patent No. US20020052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: ATTORNEY: Borroughs, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
: FILE REFERENCE: 1M-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: PRIORITY FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: PRIOR FILING DATE: 2000-08-04
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 43
: LENGTH: 1533
: TYPE: DNA
: ORGANISM: Felis catus
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(1533)
: OTHER INFORMATION:
US-09-917-265-43

Alignment Scores:
Pred. No.: 2,93e-288 Length: 1533
Score: 2546.00 Matches: 482
Percent Similarity: 96.67% Conservative: 12
Best Local Similarity: 94.32% Mismatches: 17
Query Match: 94.54% Indels: 0
DB: 10 Gaps: 0

US-09-917-265-67 (1-511) x US-09-917-265-43 (1-1533)
OY 1 lletrrpgluenugluyluaspaValtyrValalguleuasprrphlspioaspAlaPro 20
      |||||||
Db 1 ATATGGCACTCGGAGAAAAACGTTTAGTGTAGAGTTGGACTGGCACCCCTGATGCCCCC 60
OY 21 GlyluuetyAlValleuthrCysHlsThrProglucluaspAspIlethrTrpThrSer 40
      |||||||
Db 61 GGAGAAATGGGTGCTCCACCTCGCATATCTCTGAAGACATGCATCACCTCGACCTCT 120
OY 41 AlaInserSerGlualleuGllySerGlylysrThrleuthrllleInVallysluPhe 60
      |||||||
Db 121 GACCAAGCACTGAAGTCTTAGGCTCTGTATAAACTCTGACCAATCCAAAGTAAAGATT 180
OY 61 GlyspAlaaglyGlnTyrrThrCysHlslyslGlylyslValleuSerArgSerLeuIeu 80
      |||||||
Db 181 GCAATGCTGGCCAGTATACCTGTCATTAAGAGGCGAGGTTCGAGCCATTCCTCTC 240
OY 81 LeuIleHlslyslGluaspGlylletrrSerThrAspIleleuLygluInlyslu 100
      |||||||
Db 241 CTGATACCAAAAAAGGAATGATGAAATTTGGTCCACTATATCTTAAGGAAACAGAAAGAA 300
OY 101 SerlysnlysllePheleuLyCysGluAlaIuAlaysnrrySerGlyArgPheThrCys 120
      |||||||
Db 301 TCCAAAAATAGATCTTTCTTAAGATGGAGGCAAGAAATATCTTGACCGTTTCACCTGC 360
OY 121 TrprrprrprrAlaIleSerThrAspIeuLyPheSerVallyllysserSerArgGlyPhe 140

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Db      361 TGGTGGCTGACGGCAATCAGTACCGATTGGAATTCAGTGTCAAAAGCAGAGGCTCC 420
QY      141 SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgVal 160
      |||||
Db      421 TCTGACCCCAAGAGGTGACTTGTGAGCGGCACACTCTCAGCAGAGAGGTGCAGAGTG 480
QY      161 AspAsnArgAspTyrIleuLysIleuValGluCysGlnGluGlySerAlaCysProSer 180
      |||||
Db      481 GACACAGAGGATTATTAAGAGTACACAGTGCAGAGTGCAGAGGAGGTGCTCCGGCT 540
QY      181 AlaGluGluSerLeuProIleGluValValAlaValAlaIleHisIleuLysIleuVal 200
      |||||
Db      541 GCGGAGAGAGCTTACCCATTGAAGTGTGTGAGCGCTATTTCACAGGCTCAAGTACGAA 600
QY      201 AsnTyrThrSerPhePheIleArgAspIleIleuLysProAspProPheProAsnLeu 220
      |||||
Db      601 AACTACACGACGAGCTTCTTCATCAGGAGCATCATCAACCGGAGCCACCAAGAACCTG 660
QY      221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
      |||||
Db      661 CAACAGAGCCATTAAATAATTCGCGCATGTGGAAGTGCAGTGGGAATACCTGACACC 720
QY      241 TrpSerThrProHisSerIlePheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 260
      |||||
Db      721 TGGAGCAACCCACATTCTACTCTCTCTTAACATTGGCGCTACAGGCTCAAGGCAAGAAC 780
QY      261 AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValAlaCysHis 280
      |||||
Db      781 AACAGAGAAAGAAAGACAGACTCTCGTGAGACAGACCTCAGCCAAAGCTCGTGTGCCAC 840
QY      281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsp 300
      |||||
Db      841 AAGGATGCCAAGATCCGCGTGCAGAGCAGAGCGGTACTATGTGCATCTCTGAGCAAC 900
QY      301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
      |||||
Db      901 TGGGCAATCCGTCTCGCACTGTGGCGGTGGCGGCGGAGTCTGAAACTTGCCAAACCCCT 960
QY      321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaVal 340
      |||||
Db      961 ACTCCATCCCGGGGGATGTCCAGTCCATCAACCATCCCAACCCCTGCGGAGCGCATC 1020
QY      341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyrSerCysThrSerGluGlu 360
      |||||
Db      1021 AGCAACACGCTTCAGAGGCGCAGACAACTAGAAATTTTACTCTGCTCCGACATTCGGAAG 1080
QY      361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
      |||||
Db      1081 ATTGATCATGAGATATTCACAAAAGATMAAACCCAGACAGTGGAGGCTGCTTACCACTG 1140
QY      381 GlnLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
      |||||
Db      1141 GAATTAACCATGATATGAGATTGCTCTGCTCCAGAGAGATCTCTGATTAACATAATGGG 1200
QY      401 SerCysLeuAlaSerIleLysAlaSerPheMetThrValLeuCysLeuSerSerIleTyr 420
      |||||
Db      1201 AGTTGCTGGCTCCGCAAGAAACCTTTTATGACACCTGTGCTTACCAATATCTTA 1260
QY      421 GluAspLeuLysMetLysGlnMetGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
      |||||
Db      1261 GAGGATTTGAGATGTACCAAGTGGAGTTCAGAGCCATGATCAATCAAGCTGTTAATGAT 1320
QY      441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuGln 460
      |||||
Db      1321 CCTAAAGGACAGATCTTCTGATCAAAACATGCTGACAGCTATTGATGAGTGTATACAG 1380
QY      461 AlaLeuAsnPheAsnSerValThrValProGlnLysSerSerLeuLugluProAspPhe 480
      |||||
Db      1381 GCCCTAAATGTCAACAGTGTGACTGTGCCACAAACAACTCTCTTGGAGAACCGGATTTT 1440
QY      481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
      |||||
Db      1441 TATATAAACTATAATCAAGCTGTGCTATCTTCTTCAATGCTTTTCAGAAATTTGTGCGAGTGACC 1500

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QY      501 IleAsnArgMetMetSerTyrIleuAsnSer 511
      |||||
Db      1501 ATCAATAGAAATGATGATGATATCTGATGCTTCC 1533

RESULT 6
US-09-917-265-45/c
; Sequence 45, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Botroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus
; US-09-917-265-45

Alignment Scores:
Pred. No.: 2,93e-288 Length: 1533
Score: 2546.00 Matches: 482
Percent Similarity: 96.67% Conservative: 12
Best Local Similarity: 94.32% Mismatches: 17
Query Match: 94.54% Indels: 0
DB: 10 Gaps: 0

US-09-917-265-67 (1-511) x US-09-917-265-45 (1-1533)
QY      1 IleTrpGluLeuGlnLysAspValTyrValAlaGluLeuAspThrPheProAspAlaPro 20
      |||||
Db      1533 ATATGGGAACGTGAGAAAACGTTTATGTTGTAAGAGTGGAGCGCACCTGATGCCCCC 1474
QY      21 GlyGluMetValValLeuThrCysHisThrProGluGluAspAspIleThrTrpThrSer 40
      |||||
Db      1473 GCGAATAATGTGTCTCTCACTGCAATTAATCTCTGAAAGAAATGACTTCACCTGGACTCT 1414
QY      41 AlaGlnSerSerGluValLeuGlnLysGlyLysThrLeuThrIleGlnValLysGluPhe 60
      |||||
Db      1413 GACCAAGACGAGTAATCTTACGCTCTGTAAGTAACCTGACCATCAAGTCAAAAGATTT 1354
QY      61 GlyAspAlaGlyGlnTyrThrCysHisLysGlyGlyLysValLeuSerArgSerLeuLeu 80
      |||||
Db      1353 GCAGATGCTGGCCAGATACCTGTCAATAAAGGCGGAGTTCTGAGCCATTGCTTCCTC 1294
QY      81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGlu 100
      |||||
Db      1293 CTGATACACAAAAAGAAAGAAATGGAATTTGTTGTCACATGATATCTTAAGGACAGAAAGAA 1234
QY      101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
      |||||
Db      1233 TCCAAAAATTAAGATCTTCTTAATAATGTGAGCAAAAGAAATTAATCTGAGCTTACACTGC 1174
QY      121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
      |||||
Db      1173 TGGTGGCTGACGGCAATCACTACCGATTGGAATTCAGTGTCAAAAGCAGAGAGGCTCC 1114
QY      141 SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgVal 160
      |||||
Db      1113 TCTGACCCCAAGAGGTGACTTGTGAGCAGCAGACCTTCTCAGCAGAGAGGTGCAGAGTG 1054
QY      161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProSer 180
      |||||
Db      1053 GACAACAGGAGATTATTAAGAAGTACACAGTGGAGTGCAGAGGCGAGTCCGCGCGGCT 994
QY      181 AlaGluGluSerLeuProIleGluValValAlaValAlaIleHisLysLeuLysTyrGlu 200

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Db 993 GCCCAGAGACCCATGACCATGAGTGGCTGGACGCTATTACCAACCTCAGAGACAA 934
QY 201 AsnTyrThrSerSerPhePheIleArgAspIleIleLeuProAspProPheThrAsnLeu 220
Db 933 AACTACACACACACTCTTTCATCAGGACATCATCAAAACCGGACCCACCAAGACACTG 874
QY 221 GlnLeuLysProLeuLysAsnSerFargHisValGluValSerTProGluTyrProAspThr 240
Db 873 CAATGAAACCATTAATAAAATTCCTCGCATGTGGACAGTGGAGCTGGAAATACCTGACACC 814
QY 241 TrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnIleLysAsn 260
Db 813 TCGAGCACCCACCATCTCTACTCTCTTACATTTGGCGTACAGGTCCAGGCGCAAGAAC 754
QY 261 AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValValCysHis 280
Db 753 AACGAGAAAAAGAAAGACAGACTCGGTGGACAAGACCTCAGCCAAAGTGTGTGCCAC 694
QY 281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTTrpSerAsp 300
Db 693 AAGCATGCCAAGATCCCGCTGCCAAGCAGACCCGCTACTATAGCTCATCTCGAGACAC 634
QY 301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
Db 633 TGGCATCCGCTGCTCTCAGTGTGGCGGTGGCGGATCTAGAAACTTCCCAACCCCT 574
QY 321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaVal 340
Db 573 ACTTCATCCCGGGGAGTGTCCAGTGGCTCAACACACCCCAACCCCTCCGAGCCACT 514
QY 341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluTyrTyrSerCysThrSerGlnGlu 360
Db 513 AGCAGACGCTTCGAAAGGCCAGACAACTCTACAATTTTACTCTCTCCGACCTCCGACAG 454
QY 361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
Db 453 ATTGCATCATGAGATATACAAAAGATAAAACCGACAGTGGAGCGCTGCTTACCACTG 394
QY 381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
Db 393 GAATTAACCATGATGAGAGTGGCTGGCTTCAGAGAGATCTCTGATTAACTAATGGC 334
QY 401 SerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeuCysLeuSerSerIleTyr 420
Db 333 AGTTGCTGGCTCCAGAAAGACCTCTTTTATGACGACCCGTGCTTACGAGATATCAT 274
QY 421 GluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
Db 273 GAGCACTTGAAAGATGACCAAGGTGAGTTCAAGGCCATGAATGCAAAAGCTGTAATGAT 214
QY 441 ProLysArgGlnIlePheLeuAspGluAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
Db 213 CCTTAAAGCAGATCTTCTCGATCAAAACATGCTGACAGCTATTGATGACCTCTTACG 154
QY 461 AlaLeuAsnPheAsnSerValThrValProGlnLysSerSerLeuGlnGluProAspPhe 480
Db 153 GCCCTGAATGTCAACACTGTGACTGTGCCACAGAACTCTCTTGGAAAGACCGGATTTT 94
QY 481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
Db 93 TATTAACCTAAATCAAGACTCTGATCTCTTCTCATGCTTTCAGAAATTCGTCAGTAGCC 34
QY 501 IleAsnArgMetMetSerTyrLeuAsnSerSer 511
Db 33 ATCAATAGATGATGAGCTATCTGAAATGCTTCC 1

RESULT 7

US-09-917-265-38

: Sequence 38, Application US/09917265

: Patent No. US20020052030A1

: GENERAL INFORMATION:

: APPLICANT: Wonderling, Ramani S.

: APPLICANT: Boroughs, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
: FILE REFERENCE: IM-5
: CURRENT APPLICATION NUMBER: US/09/917, 265
: CURRENT FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: PRIOR FILING DATE: 2000-08-04
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO: 38
: LENGTH: 1599
: TYPE: DNA
: ORGANISM: Felis catus
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(1599)
: OTHER INFORMATION:
US-09-917-265-38

Alignment Scores:

| | | | |
|------------------------|-----------|---------------|------|
| Pred. No.: | 3,13e-288 | Length: | 1599 |
| Score: | 2546.00 | Matches: | 482 |
| Percent Similarity: | 96.67% | Conservative: | 12 |
| Best Local Similarity: | 94.32% | Mismatches: | 17 |
| Query Match: | 94.54% | Indels: | 0 |
| DB: | 10 | Gaps: | 0 |

US-09-917-265-67 (1-511) x US-09-917-265-38 (1-1599)

QY 1 IleTrpGluLeuGluLysAspValTyrValValGluLeuAspTrpHisProAspAlaPro 20
Db 67 ATATGGAGACCGGAGAAACGTTATGTGTAGAGTTGGAGCTGGACCCGATGCCCC 126
QY 21 GlyIuMetValValLeuThrCysHisThrProGluGluAspAspIleThrTrpThrSer 40
Db 127 GGAGAAATGGCGTCCCTCACCTGCATACTCTGAGAAAGATGACATCCTGGACCTCT 186
QY 41 AlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
Db 187 GACCAGACACTGAAGTCTTAGGCTCTGGTAAACTCTGACCAATCCAAAGTAAGAAATTT 246
QY 61 GlyAspAlaGlnTyrThrCysHisLysGlyLysValLeuSerArgSerLeuLeu 80
Db 247 GCAGATGCTGGCCAGTATACCTGTCATTAAGGAGCGAGTTCGAGGCATTCGTCCTC 306
QY 81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGlu 100
Db 307 CTGATACACAAAAGAAAGATGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
QY 101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
Db 367 TCCAAAATTAAGATCTTTCTTAATATGTGAGGCAAAAGATTTATTCGACGTTTACCTGC 426
QY 121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
Db 427 TGGTGGCTGAGCGCAATCAGTACCGATTGGAATTTCACTGCAAAAGAGCAGAGGCTCC 486
QY 141 SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgVal 160
Db 487 TCTGACCCCAAGAGGTGACTTGTGAGACACGACACTCTCAGCAGAGAAAGCTCAGAGTG 546
QY 161 AspAsnArgAspPyrLysLysTyrThrValGluCysGlnGluLysSerAlaCysProSer 180
Db 547 GACAACAGGATTTTAAGAACTACACAGTGGAGTGTACAGAGGACACTGCTGCCGGCT 606
QY 181 AlaGlnLysLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
Db 607 GCCCAGAGACCCATGACCATGAGTGGTGGACCGTATTTCACAGCTCAAGCTCAGTACGAA 666
QY 201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPheThrAsnLeu 220
Db 667 AACTACACACACACTCTTCTCATCAGGACATCATCAAAACCGGACCCACCAAGAACCTG 726

QY 221 GlnLeuLeuProLeuLysAsnSerArgHisValGluValSerTrpGluTrpProAspThr 240
 |||||
 Db 727 CAACGTGAAGCCATTAAAAATTCCTCGCATGTGGAACTGGAGTGGAAATACCCCTGACACC 786
 QY 241 TrpSerThrProHisSerTrpPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 260
 |||||
 Db 787 TGGAGCACCCACATTCCTACTTCTCTTAACATTGGCGTACAGGTCCAGGGCAAAAC 846
 QY 261 AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValLysHis 280
 |||||
 Db 847 AACAGAGAAAAAGAAAGACACACTCCGTGACAAAGACCTCAGCAAGTCGTGTGCCAC 906
 QY 281 LysAspAlaLysIleArgValGlnAlaArgAspArgTrpTrpSerSerSerTrpSerAsp 300
 |||||
 Db 907 AAGATCCCAAGATCCCGGTGCAAGCCAGACCGCTACATTAAGCTCATCTCGAGCAAC 966
 QY 301 TrpAlaSerValSerCysSerGlyGlyGlyGlyLysSerArgAsnLeuProThrPro 320
 |||||
 Db 967 TGGGCAATCCGTCTCTCAGTGGTGGCGGTGGCGGGATCTAGAACTTGCACACCCT 1026
 QY 321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaVal 340
 |||||
 Db 1027 ACTCCATCCCGGGGATGTCAGTCCAGTCCACACACTCCCAACCCTGCTGCGAGCATC 1086
 QY 341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGlnLeuTrpSerCysThrSerGlu 360
 |||||
 Db 1087 AGCAACACGCTTCAGAAAGCCAGACAACTCTAGAAATTTACTCTCTCCACTTCCGAAGAG 1146
 QY 361 IleAspHisGlnAspIleThrLysAspLysThrSerThrValGlnAlaCysLeuProLeu 380
 |||||
 Db 1147 ATTGATCATGAAGATATCACAAAAAGATAAACCGACAGCTGGAGGCGCTCTTACCACTG 1206
 QY 381 GlnLeuThrMetAsnGlnSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
 |||||
 Db 1207 GAATTTAACCTGATGAGTGTGCTGCTCCAGAGAGATCTCTGATTAACATAAGGG 1266
 QY 401 SerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeuCysLeuSerSerIleTrp 420
 |||||
 Db 1267 AGTTGCTGSCCTCCAGAAAGACCTCTTTATGCGCCCTGTGCTTACAGATATCTAT 1326
 QY 421 GluAspLeuLysMetTrpGlnMetGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
 |||||
 Db 1327 GAGGACTTGAAGATGTACAGAGTGGAGTCAAGGCCATGATGCAAAAGCTGTAATGAT 1386
 QY 441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuGln 460
 |||||
 Db 1387 CCTAAAGCGAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTACAG 1446
 QY 461 AlaLeuAsnPheAsnSerValThrValProGlnLysSerSerLeuGluGluProAspPhe 480
 |||||
 Db 1447 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCTCTTGGAGAAACCGGATTTT 1506
 QY 481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
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 Db 1507 TATTAACACTTAATCAAGCTGTGCATATCTTCAATGCTTTCAGAAATTCGTGAGTACC 1566
 QY 501 IleAsnArgMetSerTrpLeuAsnSerSer 511
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 Db 1567 ATCAATAGAAATGATGACTATCTGAAATGCTTCC 1599

RESULT 8 US-09-917-265-40/c

; Sequence 40, Application US/09917265
 ; Patent No. US20020052030A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wonderling, Ramani S.
 ; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
 ; FILE REFERENCE: IM-5
 ; CURRENT APPLICATION NUMBER: US/09/917,265
 ; CURRENT FILING DATE: 2001-07-27
 ; PRIOR APPLICATION NUMBER: 60/223,016
 ; PRIOR FILING DATE: 2000-08-04

; NUMBER OF SEQ ID NOS: 109
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 40
 ; LENGTH: 1599
 ; TYPE: DNA
 ; ORGANISM: Felis catus
 US-09-917-265-40
 Alignment Scores:
 Pred. No.: 3,13e-288
 Score: 2546.00
 Percent Similarity: 96.67%
 Best Local Similarity: 94.32%
 Query Match: 94.54%
 Gaps: 0
 US-09-917-265-67 (1-511) x US-09-917-265-40 (1-1599)
 QY 1 IleTrpGluLeuGlnLysAspValTyrValValGluLeuAspTrpHisProAspAlaPro 20
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 Db 1533 ATATGGCACTGGAGAAAAAGTTTATGTGTAGAGTTGGATGGCACCCCTGATGCCCCC 1474
 QY 21 GlyGluMetValIleLeuThrCysHisThrProGluGlnAspAspIleThrTrpHiser 40
 |||||
 Db 1473 GGAAGAAATGGTGTCTCTCACTCTCAATACTCTGAAGAAATACATCACCTGGACCTCT 1414
 QY 41 AlaGlnSerSerGluValLeuGlnLysSerGlyLysThrLeuThrIleGlnValLysGluPhe 60
 |||||
 Db 1413 GACCAGAGCAGTGAAGCTCTAGAGCTCTGTGTAAAGCTGTGACCATCCAAAGCAAGATT 1354
 QY 61 GlyAspAlaGlyGlnTrpTrpCysHisLysGlyGlyLysValLeuSerArgSerLeuLeu 80
 |||||
 Db 1353 GCAGATGCTGGCCAGATACCTCTCATAAAGGAGGAGAGGTTTGAGCCATTGTTCTTC 1294
 QY 81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluGlnLysGlu 100
 |||||
 Db 1293 CTGATACACAAAAAGCAAGATGCAATTTGCTCCACTGATATCTTAAAGGACGAAAGAA 1234
 QY 101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTrpSerGlyArgPheThrCys 120
 |||||
 Db 1233 TCCAAAAATTAAGATCTTTCTTAAATGTGACGCAAAAGATTATCTGGAGCTTTCACCTCG 1174
 QY 121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
 |||||
 Db 1173 TGTGTGCTGACGGCAATCACTACGATTTGAAATTCACCTCAAAAGACAGAGCTCC 1114
 QY 141 SerAspProGlnIleValThrCysGlyAlaValThrLeuSerIleGluArgValAlaArgVal 160
 |||||
 Db 1113 TCTGACCCCAAGAGTGAAGTGTGACGACGACACTCTCAGCAGAAAGTCAAGTGTG 1054
 QY 161 AspAsnArgAspTrpLysLysTrpThrValGluCysGlnGluLysSerAlaCysProSer 180
 |||||
 Db 1053 GACAAACAGGATTAAGAAAGTACACAGTGCAGAGAGGCGAGTGTCCCGGCT 994
 QY 181 AlaGlnGluSerLeuProIleGluValValAlaAspAlaIleHisLysLeuLysTrpGlu 200
 |||||
 Db 993 GCCGAGAGAGCTTACCATTTGAAGTGGTGGAGCAATTCAACAAAGCTCAAGTTCGAA 934
 QY 201 AsnTrpThrSerSerPhePheIleArgAspIleIleLysProAspProThrThrAsnLeu 220
 |||||
 Db 933 AACCTACACAGCAGCTTCTTCACTCAGGAGCATCATATAACCGGACCCCAAGAACTGTG 874
 QY 221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTrpProAspThr 240
 |||||
 Db 873 CAACGTGAAGCCATTAAAAATTCCTCGCATGTGGAACTGGAGTGGAAATACCCCTGACACC 814
 QY 241 TrpSerThrProHisSerTrpPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 260
 |||||
 Db 813 TGGAGCACCCACATTCCTACTTCTCTTAACATTGGCGTACAGGTCCAGGGCAAGAAC 754
 QY 261 AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValLysHis 280
 |||||
 Db 753 AACAGAGAAAAAGAAAGACAGCTCTCCGTGACAAAGACTTCAAGCAAGGTGTGTGCCAC 694

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Oy 281 LysAspAlaIysIleArgValGlnAlaArgAspArgTyrTrpSerSerTrpSerasp 300
Db 693 AAGCATGCCAGATCCGGTCCAGACCCGAGACCTGACTATAGCTCATCTCGAGGCAC 634
Oy 301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
Db 633 TGGGCATCCGTCTGCTGAGTGGTGGCGCGGATCTAGAACTTGGCAACCCCT 574
Oy 321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaVal 340
Db 573 ACTCCATCCCGGGGATGTTCCAGTCCCTCAACCACTCCCAACCCCTCCGAGCCATC 514
Oy 341 SerAsnThrLeuGlnIleValIleArgGlnThrLeuGlnLeuTyrSerCysThrSerGlnGlu 360
Db 513 AGCAACACCGCTTTCAGAAAGCCAGACAACTCTAGATTCTTACTCTCTGCACCTTCCAAAG 454
Oy 361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGlnAlaCysLeuProLeu 380
Db 453 ATTGATCATGAAGATATCACAAGATATAAACCAACAGTGGAGCGCTTGCCTTACCACTG 394
Oy 381 GluLeuThrMetAsnGlnIleSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
Db 393 GAATTAACCATGAATGAGAGCTTGGCTTCCAGAGAGATCTCTGATTAATAATGGG 334
Oy 401 SerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeuCysLeuSerSerIleTyr 420
Db 333 AGTTGCTCGCCCTCCAGAAACACTCTTTATAGACACCCTGGTGGCTTAGAGATATCTAT 274
Oy 421 GluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
Db 273 GAGACATTGAAGATGTACAGGCTGAGCTTCAAGGCCATGATGCAACCTGTTAATGAT 214
Oy 441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuGln 460
Db 213 CCTAAAGCGCAGCTTCTTGATCAAAACATGCTGACAGCTATTGATGAGCTGTACAG 154
Oy 461 AlaLeuAsnPheAsnSerValThrValProGlnLysSerSerLeuGluGluProAspPhe 480
Db 153 GCCCTGAATCTCAACAGCTGCTACTGTGCGACAGAACTCTCTTGGAAACCGGATTTT 94
Oy 481 TyrIleThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
Db 93 TATAAACTAAATCAACCTCTGCATACTCTTCACTGTTTCAGAAATCGTGGAGTGACC 34
Oy 501 IleAsnArgMetMetSerTyrLeuAsnSerSer 511
Db 33 ATCAATAGAAATGATGAGCTATCTGATCTTCC 1

RESULT 9
US-09-828-825-7
: Sequence 7, Application US/09828825
: Patent No. US20020018767A1
: GENERAL INFORMATION:
: APPLICANT: Kim, Han-soo
: APPLICANT: Lee, Seewoo
: TITLE OF INVENTION: Anti-cancer Cellular Vaccine
: FILE REFERENCE: 84906-102
: CURRENT APPLICATION NUMBER: US/09/828, 825
: CURRENT FILING DATE: 2001-04-10
: PRIOR APPLICATION NUMBER: KR00-43498
: PRIOR FILING DATE: 2000-07-27
: NUMBER OF SEQ ID NOS: 16
: SOFTWARE: Patent In Ver. 2.1
: SEQ ID NO: 7
: LENGTH: 8608
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: plasmid
: NAME/KEY: misc_feature
: LOCATION: (1)..(750)
: OTHER INFORMATION: CMV enhancer and promoter

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: NAME/KEY: misc_feature
: LOCATION: (890)..(1002)
: OTHER INFORMATION: Intervening sequence
: NAME/KEY: Promoter
: LOCATION: (1067)..(1085)
: OTHER INFORMATION: T7 RNA polymerase promoter
: NAME/KEY: misc_feature
: LOCATION: (1090)..(1984)
: OTHER INFORMATION: human B7.1 (1090-1956 is coding sequence)
: NAME/KEY: RBS
: LOCATION: (2013)..(2593)
: OTHER INFORMATION: IRES sequence
: NAME/KEY: misc_feature
: LOCATION: (2627)..(4263)
: OTHER INFORMATION: human IL12.2 sequence (2460-4253 is coding
: OTHER INFORMATION: sequence, 13 amino acid flexible linker at
: OTHER INFORMATION: 3606-3676)
: NAME/KEY: CDS
: LOCATION: (2640)..(4253)
: OTHER INFORMATION: IL12.2 coding sequence (13 amino acid linker)
: NAME/KEY: Promoter
: LOCATION: (4362)..(4383)
: OTHER INFORMATION: T3 RNA Polymerase promoter
: NAME/KEY: polyA_signal
: LOCATION: (4393)..(4614)
: OTHER INFORMATION: SV40 fragment containing polyadenylation signal
: NAME/KEY: rep_origin
: LOCATION: (4709)..(5164)
: OTHER INFORMATION: fl origin of replication
: NAME/KEY: misc_feature
: LOCATION: (5228)..(6595)
: OTHER INFORMATION: Neo r expression cassette
: NAME/KEY: misc_feature
: LOCATION: (7006)..(7866)
: OTHER INFORMATION: Ampicillin resistance
US-09-828-825-7

Alignment Scores:
Preld. No.: 2,88e-259 Length: 8608
Score: 2309.00 Matches: 439
Percent Similarity: 90.31% Conservative: 27
Best Local Similarity: 85.08% Mismatches: 44
Query Match: 85.74% Indels: 6
DB: 10 Gaps: 3

US-09-917-265-67 (1-511) x US-09-828-825-7 (1-8608)
Oy 1 IleTrrGluLeuGluLysAspValTyrValGluLeuAspTrpHisProAspAlaPro 20
Db 2706 ATATGGAGACGAGAAAGATGTTATGTCGTAGAAATGGATTGGTATCCGAGTCCCT 2765
Oy 21 GlyIleMetValIleLeuThrCysHisThrProGluGluAspAspIleThrTrpThrSer 40
Db 2766 GGAGAAATAGGTGGTCTCACCCTGTGACCCCTGAGAAAGATGGATGATCACTCGACCTTG 2825
Oy 41 AlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValIleGluPhe 60
Db 2826 GACCAGACAGCTGAGGCTTGTAGGCTCTGCAAAACCCGACCATCAAGTAAGAGATT 2885
Oy 61 GlyAspAlaGlyGlnTyrThrCysHisLysGlyLysValIleLeuSerArgSerLeuLeu 80
Db 2886 GGACATGCTGGCCAGTACACCTGTCACAAAGAGCGAGTTCTTAAGCATTCCTCTG 2945
Oy 81 LeuIleHisLysLysGluAspGlyIleTrrSerThrAspIleLeuLysGluGlnLysGlu 100
Db 2946 CTGCTTCACAAAGGAAGATGAAATTGGTCCACTGATATTAAAGAGACCAGAAAGAA 3005
Oy 101 SerLysAsnLysIlePheLeuLysCysGlnAlaLysAsnTyrSerGlyArgPheThrCys 120
Db 3006 CCCAAATAAGACCTTTCTAAGATGCGAGGCCAAGATTATCTGGACGTTTCACCTGC 3065
Oy 121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
Db 121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140

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Db      3066 TGGTGGCTGACGCAATCACTGATTTGACATTGACATTCAGTGTCAAAGGACGACAGGCTCT 3125
Qy      141 SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgVal 160
Db      3126 TCTGACCCCAAGGGGGGAGCTGCGGAGCTGCTACACTCTCTCAGAGAGAGTCAAGGG 3185
Qy      161 AspAsnArgAspTyrIleLysTyrThrValGluCysGlnGluLysSerAlaCysProSer 180
Db      3186 GACACAGAGAGATAT--GAGTACTCAGTGTGAGTGCAGAGAGAGAGTGCCTCCAGCT 3242
Qy      181 AlaGluGluSerLeuProIleGluValAlaValAlaPalatIleHisLysLeuLysTyrGlu 200
Db      3243 GGTGAGAGAGAGTGTGCCATTCAGTGTGATGATGATGATGATGATGATGATGATGATGAT 3302
Qy      201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProthAsnLeu 220
Db      3303 AACTACACCGACGAGCTCTTCATCAGGAGCATCATCAAACTGACCCCAACCAACTTG 3362
Qy      221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTyrPgluTyrProAspThr 240
Db      3363 CAGCTAAGCCATTAAAGATTCCTCGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 3422
Qy      241 TrpSerThrProHisSerTyrPheSerLeuThrPheCysTyrIleGlnAlaGlnLysAsn 260
Db      3423 TGGAGTACTCCATTCCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3482
Qy      261 AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValAlaCysHis 280
Db      3483 AAGAGAGAAAGAAAGATAGACTTCTCACCAGCAAGAGCTCAGCCAGCCAGCTCAGCTGCGC 3542
Qy      281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTyrPserAsp 300
Db      3543 AAAAATGCCAGCTTGTAGCGTGGCCGCAAGAGCCGCTACATATAGCTCATCTTGTGAGAGAA 3602
Qy      301 TrpAlaSerValSerCysSerGlyGly-----GlyGlyGlyGlySer-----Arg 315
Db      3603 TGGGCACTGTGTGCTGCTGCACTGTGTGCGGCGTGAAGCGGTGGCGGTGAGAACCCCATGGA 3662
Qy      316 AsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThr 335
Db      3663 AACCTCCCGTGGCCATCCAGACCCAGAGAAATGTCCAGTCCCTTCCAGCCATCCCAAAAC 3722
Qy      336 LeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluTyrSer 355
Db      3723 CTGCTAGAGGCCCTCAGCAACATGCTCCAGAAAGCCAGAACACTAGAAATTTTACCT 3782
Qy      356 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 375
Db      3783 TGCACCTTCGACAGATGATCATGAAAGATATCACAAGATTAAGAACACGACAGTGGAG 3842
Qy      376 AlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSer 395
Db      3843 GCCTGTTTACCATTTGAATTAACCAAGAAATGAGATTGCTTAATTCAGAGACCTCT 3902
Qy      396 LeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeuGly 415
Db      3903 TTCATTAACCTAATGGAGTTGCTGCTGCCAGAAAGACCTTTTATGATGGCCGTGTGC 3962
Qy      416 LeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAla 435
Db      3963 CTTAGTAGTATTATGAACTTGAAGATTTACAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 4022
Qy      436 LysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIle 455
Db      4023 AACCTTCTGATGATCTTAAGAGGAGCATCTTCTAGATCAAAACATGCTGCGAGTTAT 4082
Qy      456 AspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSerLeu 475
Db      4083 GATGAGCTGATGAGGCGCTGGAATTCACACAGGAGAGCTGTGCCAAAAAATCTCCCTT 4142
Qy      476 GluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArg 495
Db      4143 GAAGAACCGGATTTTATAAACTAAATCAAGCTCTGCTACTTCTTCTTCTTCTTCTTCTTCT 4202

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Qy      496 IleArgAlaValThrIleAsnArgMetMetSerTyrIleAsnSerSer 511
Db      4203 ATTCGGGAGTGTGACTATGATAGAGTGTGAGTGTGATGATGATGATGATGATGATGAT 4250

RESULT 10
US-09-828-825-15
? Sequence 15, Application US/09828825
? Patent No. US20020018767A1
? GENERAL INFORMATION:
? APPLICANT: Lee, Seewoo
? APPLICANT: Kim, Han-soo
? TITLE OF INVENTION: Anti-cancer Cellular Vaccine
? FILE REFERENCE: 84906-102
? CURRENT APPLICATION NUMBER: US/09/828,825
? PRIORITY FILING DATE: 2001-04-10
? PRIOR APPLICATION NUMBER: KR00-43498
? PRIORITY FILING DATE: 2000-07-27
? NUMBER OF SEQ ID NOS: 16
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 15
? LENGTH: 8629
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: plasmid
? NAME/KEY: misc.feature
? LOCATION: (1)..(750)
? OTHER INFORMATION: CMV enhancer and promoter
? NAME/KEY: promoter
? LOCATION: (1067)..(1085)
? OTHER INFORMATION: T7 RNA polymerase promoter
? NAME/KEY: misc.feature
? LOCATION: (1090)..(1276)
? OTHER INFORMATION: Human IL12.2 (coding sequence is 1103-2716, 10
? OTHER INFORMATION: amino acid linker at 2087-2116)
? NAME/KEY: CDS
? LOCATION: (1103)..(2716)
? OTHER INFORMATION: Human IL12.2 (10 amino acid linker)
? NAME/KEY: RBS
? LOCATION: (2752)..(3332)
? OTHER INFORMATION: IRES sequence
? NAME/KEY: misc.feature
? LOCATION: (3369)..(4263)
? OTHER INFORMATION: Human B7.1 sequence
? NAME/KEY: promoter
? LOCATION: (4383)..(4404)
? OTHER INFORMATION: T3 RNA Polymerase promoter
? NAME/KEY: polyA_signal
? LOCATION: (4414)..(4635)
? OTHER INFORMATION: SV40 fragment containing polyadenylation signal
? NAME/KEY: rep_origin
? LOCATION: (4730)..(5185)
? OTHER INFORMATION: fl origin of replication
? NAME/KEY: misc.feature
? LOCATION: (5249)..(6616)
? OTHER INFORMATION: Neo r expression cassette
? NAME/KEY: misc.feature
? LOCATION: (7027)..(7887)
? OTHER INFORMATION: Ampicillin resistance gene
US-09-828-825-15

Alignment Scores:
Pred. No.: 2,9e-259 Length: 8629
Score: 2309.00 Matches: 439
Percent Similarity: 90.31% Conservative: 27
Best Local Similarity: 85.08% Mismatches: 44
Query Match: 85.74% Indels: 6
DB: 10 Gaps: 3

US-09-917-265-67 (1-511) x US-09-828-825-15 (1-8629)
Qy      1 IleTrrGluLeuGluLysAspValTyrValGluLeuAspTrrHisProAspAlaPro 20

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Db 1169 ATATGCGAAGTGAAGAAAGATGTTATGTCGAGAAATGGATTGGTATCCGATCCCT 1228
Oy 21 GlyGluMetValValLeuThrCysHisThrProGluGluAspAspIleThrTrpHisSer 40
Db 1229 GCGAGAAAGTGGTCTCTACCTGACCCCTGAAGAAGATGATATCACTGGACCTTG 1288
Oy 41 AlaInserSerGluValLeuGlySerGlySerThrLeuThrIleGlnValGlyIuphe 60
Db 1289 GACCAGACGACTGAGCTTGAAGCTTGGCAAAACCCCTGACCATTCAAGTCAAGAGCTTT 1348
Oy 61 GlyAspAlaGlyGlnTyThrCysHisLysGlyLysValLeuSerArgSerLeuLeu 80
Db 1349 GGAATGCTGCCCGACCTACACCTGTCACAAAGAGCGCGTTCTAAGCCATTGCTCTCG 1408
Oy 81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGlnLysGlu 100
Db 1409 CTGCTTCAACAAAGAAAGAAAGATGAAATTTGCTCCACTGATATTTAAAGACCAGAAAGAA 1468
Oy 101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrsSerGlyArgPheThrCys 120
Db 1469 CCCAAATATAGACCTTTCTTAAGATCGAGGCCAAAGATTTCTTGACGTTTCACTGCG 1528
Oy 121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
Db 1529 TGGTGGCTGACGACATCAGTACTGATTTGACATTCACTGTCAAAAGCAGCAGAGCTCT 1588
Oy 141 SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgVal 160
Db 1589 TCTGACCCCAAGGCGTACGCTGCGAGCTCTCTACACTCTCTGAGAGAGATGACAGAGG 1648
Oy 161 AspaAsnArgAspTyrlLysLysTyThrValGluCysGlnGluGlySerAlaCysProSer 180
Db 1649 GACAAACAAGAGAT---GACTACTCACTGGAGTGCAGAGAGACAGTCCCTGCCAGCT 1705
Oy 181 AlaGluGluSerLeuProIleGluValValAlaAspAlaIleHisLysLeuLysTyGlu 200
Db 1706 CGTGAGGAGACTGCCCATTCCTGAGCTGATGCTGATGCCGTTCAACAACCTCAAGATGAA 1765
Oy 201 AsnTrpTrpSerSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeu 220
Db 1766 AACTACACACACACTTCTTCATCAGAGACATCAACAACCTGACCCCAACACACTTG 1825
Oy 221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyProAspThr 240
Db 1826 CACCTGAAGCATTAAGAATTTCTGCGCAGGTGGAGTGCACCTGGAGTACCCTGACACC 1885
Oy 241 TrpSerThrProHisSerTyrlPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 260
Db 1886 TGGAGTACTCCACATTCCTACTCTCTCCCTGACATTCGCTTCAGGTCCAGGCGCAAGGC 1945
Oy 261 AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaIleValCysHis 280
Db 1946 AAGAGAGAAAGAAAGATAGAGTCTTCACCGCAAGACCTCAGCCAGCCGTCGCGCC 2005
Oy 281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrlTyrsSerSerSerTrpSerAsp 300
Db 2006 AAAAATGCCACCATTTACCGTCGGGCGCAGACCCGCTACTACTCTCTTTGGAGCCAA 2065
Oy 301 TrpAlaSerValSerCysSerGlyLys-----GlyGlyGlyGlySer-----Arg 315
Db 2066 TGGCCATCTGTCCTCCTCAGTGGTGGCGTGGAGACGGGTGGCGGTGAAGCCCATGGAGA 2125
Oy 316 AsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThr 335
Db 2126 AACCTCCCGCGGCCACTCCAGACCCAGAGATTTCCCATGCTTCACACACTCCCAAAAC 2185
Oy 336 LeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgIleThrLeuGlnLeuTyrsSer 355
Db 2186 CTGCTGAGGCCCGTCAGAACATGCTCCAGAAAGCCAGACAAACTCTAAGAAATTTTACCCT 2245
Oy 356 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 375
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Db 2246 TGCACCTCTGAAGACATTGATCATGAGATATCACAAAGAATAAAACAGCAGACTGAG 2305
Oy 376 AlaCysLeuProLeuGlnLeuThrMetLsnGlnSerCysLeuAlaIleSerArgIleSer 395
Db 2306 GCTGTGTTAACATTGGAATTTAAACAAGATAGAGATTGCCAAATTCACAGAGACCTCT 2365
Oy 396 LeuIleThrAsnGlySerCysLeuAlaSerGlyLysValSerPheMetThrValLeuCys 415
Db 2366 TTCAATACCTAATGGAGATGGCTGCTGCTGCCAGAAAGACCTTTTATATAGTCCCTGTC 2425
Oy 416 LeuSerSerIleTyrlGluAspLeuLysMetTyrlGlnMetGluPheLysAlaMetAsnAla 435
Db 2426 CTTACTAGTATTTATGAGACCTTGAAGATGTACACGAGTGAGTTCAACACCATGAATGCA 2485
Oy 436 LysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIle 455
Db 2486 AAGCTTCGATGATCACTCAAGAGCAGATCTTTCTAGATCAAAACATGCTGCGAGTTT 2545
Oy 456 AspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSerLeu 475
Db 2546 CATGACGCTGATGCAAGCCCTGAATTTCAACAGTGAAGCTGTGCCCAAAAATTCCTCCCT 2605
Oy 476 GluGluProAspPheTyrlLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArg 495
Db 2606 GAAGAACCGGATTTTATTAATAACTAAATCAAGCTCTGCATACTCTTCATGCTTTCAGA 2665
Oy 496 IleArgAlaValThrIleAsnArgMetLysTyrlLeuAsnSerSer 511
Db 2666 ATTCGGGCGAGTACTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2713

RESULT 11
US-09-828-825-5
: Sequence 5, Application US/09828825
: Patent No. US20020018767A1
:
: GENERAL INFORMATION:
: APPLICANT: Lee, Han-soo
: TITLE OF INVENTION: Anti-cancer Cellular Vaccine
: FILE REFERENCE: 84906-102
: CURRENT APPLICATION NUMBER: US/09/828,825
: PRIOR FILING DATE: 2001-04-10
: PRIOR APPLICATION NUMBER: KR00-43498
: NUMBER OF SEQ ID NOS: 16
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO: 5
: LENGTH: 8623
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)..(750)
: OTHER INFORMATION: CMV enhancer and promoter
: NAME/KEY: misc_feature
: LOCATION: (890)..(1002)
: OTHER INFORMATION: Intervening sequence
: NAME/KEY: promoter
: LOCATION: (1067)..(1085)
: OTHER INFORMATION: T7 RNA polymerase promoter
: NAME/KEY: misc_feature
: LOCATION: (1090)..(1984)
: OTHER INFORMATION: Human B7.1 (1090-1956 is coding sequence)
: NAME/KEY: RBS
: LOCATION: (2013)..(2593)
: OTHER INFORMATION: IRES sequence
: NAME/KEY: misc_feature
: LOCATION: (2627)..(4278)
: OTHER INFORMATION: Human IL12.3 - 2640-4268 is coding sequence,
: OTHER INFORMATION: flexible linker from 3606-3690
: NAME/KEY: CDS
: LOCATION: (2640)..(4268)
: OTHER INFORMATION: IL 12.3 coding sequence - has 28 amino acid linker
: OTHER INFORMATION: sequence
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NAME/KEY: promoter
LOCATION: (4398)..(4407)
OTHER INFORMATION: T3 RNA polymerase promoter
NAME/KEY: polyA_signal
LOCATION: (4408)..(4629)
OTHER INFORMATION: SV40 fragment containing polyadenylation signal
NAME/KEY: rep.origin
LOCATION: (4724)..(5179)
OTHER INFORMATION: fl origin of replication
NAME/KEY: misc.feature
LOCATION: (5243)..(6610)
OTHER INFORMATION: Neo r expression cassette
NAME/KEY: misc.feature
LOCATION: (7021)..(7881)
OTHER INFORMATION: Ampicillin resistance
OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-828-825-5

Alignment Scores:
Pred. No.: 5.68e-259 Length: 8623
Score: 2306.50 Matches: 439
Percent Similarity: 89.44% Conservative: 27
Best Local Similarity: 84.26% Mismatches: 44
Query Match: 85.65% Indels: 11
DB: 10 Gaps: 3

US-09-917-265-67 (1-511) x US-09-828-825-5 (1-8623)

QY 1 lletpGlulEuGlulysAspValTYrValGlulEuAspTrpHisProAspAlaPro 20
DB ATATGGAACTGAGAAAGATGTTATGTCGTAGAAATGGATGGATCCGATGCCCT 2765

QY 21 GlyGluMetValValLeuThrCysHisThrProGluGluAspAspIleThrTrpThrSer 40
DB GGAGAAATGGTGGTCTCCTCACCCTGACACCCCTGAGAAAGATGGATACCTGGACCTTG 2825

QY 41 AlaGluSerSerGluValLeuGluSerGlyLysThrLeuThrIleGluValLysGluPhe 60
DB GACCAAGACGAGTGGCTTACCTGCGCAAAACCTGACCATCCAAAGTCAAGTCAAGAGTTT 2885

QY 61 GlyAspAlaGlyLysIleThrCysHisLysGlyLysValLeuSerIleThrLeu 80
DB GGAGATGCTGGCCAGTACACCTGCAAAAGAGGGAGGAGTCTTAAGCCATTCGCTCCTG 2945

QY 81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysGluLysGlu 100
DB CTGCTTCACAAAAAGAGATGGAATTTGCTCCACTGATTTTAAAGGACCAAGAA 3005

QY 101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTrpSerGlyArgPheThrCys 120
DB CCCAAAAATRAAGACCTTTCTTAAGATCGAGGCCAAGAAATTTATCTGACCTTCACCTGC 3065

QY 121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerIleGlyPhe 140
DB TGTGTGCTGACGACATCACTGATGATTTGACATTCAGTGTCAAAAGACCAAGAGCTCT 3125

QY 141 SerAspProGluGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValAlaVal 160
DB TCTGACCCCAAGGGGTGACGTGCGAGCTGCTACTCTCTCAGAGAGACAGAGGG 3185

QY 161 AspAsnArgAspTrpLysLysTrpThrValGluGluGluGluGluSerAlaCysProSer 180
DB GACAAACAGGAGATAT---GAGTACTCAGTGGAGTGGCCAGAGAGAGAGCTCTCCAGCT 3242

QY 181 AlaGluGluSerLeuProIleGluValAlaValAspAlaIleHisLysLeuLysTrpGlu 200
DB GCTGAGAGAGTGTGCTGCCATTTGATGATGCTGATGCGCTTCAACAAGCTCAAGTATGAA 3302

QY 201 AsnTrpThrSerSerPhePheIleArgAspIleIleLysProAspProPheTrpAsnLeu 220
DB AACTTACACGAGAGCTTCTTCAACAGGACATCATCAACCTGACCCCAACAACCTTG 3362

QY 221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTrpProAspThr 240

DB CAGCTGAAGCCATTAAAGATTTCTGCGAGGTGAGGTGAGCTGGAGTACCTGAGACCC 3422

QY 241 TrpSerThrProHisSerTrpPheSerLeuThrPheCysIleGluGlnGlyLysAsn 260
DB TCGAGTACTGACATTTCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3482

QY 261 AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValLysHis 280
DB AGAGAGAAAAAGAAAGATAGAGTCTTCCAGCAAGACATCCAGCCAGCTCATCTCGCGC 3542

QY 281 LysAspAlaLysIleArgValGlnAlaArgAspArgTrpTrpSerSerTrpSerAsp 300
DB AAAAATGCCAGATTTACCGTCCGCGCCAGAGCCGCTACTATAGCTCATCTTGGAGGAA 3502

QY 301 TrpAlaSerValSerCysSerGlyGly-----GlyGlyGly 312
DB TGGGCACTCTGCGCTCCTGAGTGGTGGGCGGTGCAAGCCGCTGCAAGCGGTGGCGGT 3662

QY 313 GlySer-----ArgAsnLeuProThrProThrProSerProGluMetPheGlnCysLeu 330
DB GGAAGCCCATGAGAAACCTCCCGTGGCCACTGCAGACCCAGAGAAATGTTCCCATGCTT 3722

QY 331 AsnHisSerGlnThrLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThr 350
DB CACCCTCCCAAAACCTGCTGAGGCGCTGAGCAACATGCTCCAGAAAGGCCAGACAAACT 3782

QY 351 LeuGluLeuTrpSerCysThrSerGluLysIleAspHisGluAspIleThrLysAspLys 370
DB CTAGAAATTTTACCTTCTGCACTTCTGAGAGATTCATCATCAATATCAAAAAAGTAA 3842

QY 371 ThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAla 390
DB ACCAGCAACATGAGAGCCTGTTTACCATTTGAATTAACCAAGATAGAGATGCTTAAT 3902

QY 391 SerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPhe 410
DB TCCAGAGAGACCTCTTTCATTAAGTAAAGAGTGGCTGCTGCTCCAGAAAGACCTCTTT 3962

QY 411 MetThrValLeuCysLeuSerSerIleTrpGluAspLeuLysMetTrpGluMetGluPhe 430
DB ATGATGGCCCTGTGCTTACTAGTATTTATGAAGACTGAAGATGAACAGGTGGAGTTT 4022

QY 431 LysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsn 450
DB AAGACCATGATCAAAAGCTTCTGATGATGATCTTAAGAGCAGATCTTTCTAGATCAAAAC 4082

QY 451 MetLeuThrAlaIleAspGluLeuGlnAlaLeuAsnPheAsnSerValThrValPro 470
DB ATCTGACAGTATTGATGAGCTGATGACAGGCCCTGAATTTCAACAGTGAAGCTGTGCCA 4142

QY 471 GlnLysSerSerLeuGluProAspPheTrpLysThrLysIleLysLeuCysIleLeu 490
DB CAATAATCCCTCCCTGAGAGACCGGATTTTATTAATAAATCAAGCTCTGCACTACT 4202

QY 491 LeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetCysTrpLeuAsnSer 510
DB CTTCATGCTTTCAGAAATGGGCGAGTATGATGATGATGATGATGATGATGATGATGAT 4262

QY 511 Ser 511
DB 4263 TCC 4265

RESULT 12
US-09-828-825-13
Sequence 13, Application us/0982825
Patent No. US20020018767A1
GENERAL INFORMATION:
APPLICANT: Lee, Seewoo
APPLICANT: Kim, Han-soo
TITLE OF INVENTION: Anti-cancer Cellular Vaccine
FILE REFERENCE: 84906-102
CURRENT APPLICATION NUMBER: US/09/828, 825

CURRENT FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: KR00-43498
PRIOR FILING DATE: 2000-07-27
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 8644
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: plasmid
NAME/KEY: misc_feature
LOCATION: (1)..(750)
OTHER INFORMATION: CMV enhancer and promoter
NAME/KEY: promoter
LOCATION: (1067)..(1085)
OTHER INFORMATION: T7 RNA polymerase promoter
NAME/KEY: misc_feature
LOCATION: (1090)..(2731)
OTHER INFORMATION: Human IL12.3 (1103-2731 is coding sequence, 15
NAME/KEY: CDS
LOCATION: (1103)..(2731)
OTHER INFORMATION: IL12.3 (15 amino acid linker)
NAME/KEY: RBS
LOCATION: (2767)..(3347)
OTHER INFORMATION: IRES sequence
NAME/KEY: misc_feature
LOCATION: (3384)..(4278)
OTHER INFORMATION: Human B7.1 sequence
NAME/KEY: promoter
LOCATION: (4398)..(4419)
OTHER INFORMATION: T3 RNA polymerase promoter
NAME/KEY: poly_signal
LOCATION: (4429)..(4650)
OTHER INFORMATION: SV40 fragment containing polyadenylation signal
NAME/KEY: rep_origin
LOCATION: (4745)..(5200)
OTHER INFORMATION: fl origin of replication
NAME/KEY: misc_feature
LOCATION: (5264)..(5681)
OTHER INFORMATION: Neo r expression cassette
NAME/KEY: misc_feature
LOCATION: (7042)..(7902)
OTHER INFORMATION: Ampicillin resistance gene
US-09-828-825-13

Alignment Scores:
Pred. No.: 5.7e-259 Length: 8644
Score: 2306.50 Matches: 439
Percent Similarity: 89.44% Conservative: 27
Best Local Similarity: 84.26% Mismatches: 44
Query Match: 85.65% Indels: 11
DB: 10 Gaps: 3

US-09-917-265-67 (1-511) x US-09-828-825-13 (1-8644)

QY 1 lterpGluLeuGluLysAspValTyrValGluLeuAspTrpHisProAspAlaPro 20
DB 1169 ATATGGGAAGTGAAGAAAGATGTTATGTCGTAGAAATGGATTGCTATCCGATGCCCT 1228

QY 21 GlyGluMetValIleuThrCysHisThrProGluGluAspAspIleThrTrpHisSer 40
DB 1229 GCAGAAAGTGGTGGTCTCACTGTCACACCCCTGCAAGAGATGGATATCACTGGACCTTG 1288

QY 41 AlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
DB 1289 GACCAAGACAGTGAAGCTTAAAGCTCTGCAAAACCCGACCATCACAAGTCAAGAGTTT 1348

QY 61 GlyAspAlaGlyGlnTyrThrCysHisLysGlyGlyLysValLeuSerArgSerLeuLeu 80
DB 1349 GCAGATGCTGGCAGCATACCTGTCACAAAGAGCGAGTTTAAAGCCATTCCGCTCTG 1408

QY 81 LeuIleHisLysLysGluAspGlyLterpSerThrAspIleLeuLysGluGlnLysGlu 100
DB 1409 CTGCTTCACAAAGAAAGATGCAATTTGGTCCACTGATATTTTAAAGACCAAGAAAGA 1468

QY 101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
DB 1469 CCCAAAAATTAAGACCTTCTTAAGATGCCAGGCCAAGAAATTAATTGACAGTTTCACCTGC 1528

QY 121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
DB 1529 TGGTGCTGGACACATAGTACTGATTGACATTGACGTGCAAAAGACGAGAGCTCT 1588

QY 141 SerAspProGlnGlyValThrCysGlyAlaValThrLysSerAlaArgValArgVal 160
DB 1589 TCTGACCCCCCAAGGGGTACGCGGAGCTGCTACACTCTCTGCCAAGAGACTCAGACGG 1648

QY 161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProSer 180
DB 1649 GACACAAAGAGAGTAT---GAGTACTCAGTGGAGTCCAGAGAGACAGTCCGCCCCAGCT 1705

QY 181 AlaGluGluSerLeuProIleGluValValAlaLysAlaIleHisLysLeuLysTyrGlu 200
DB 1706 CCTGAGAGAGTCTGCCATGAGGTCAATGCTGATGCCGTTACACAACTCAAGTATGAA 1765

QY 201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeu 220
DB 1766 AACTACACCAGACGCTTCTTCACTCAGGACATCATCAAACTGACCCACCACTTG 1825

QY 221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
DB 1826 CAGCTGAAGCATTAAAGAAATTCGCGCAGGTGGAGTCACTGCGAGTACCTGCACACC 1885

QY 241 TrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 260
DB 1886 TGGAGTACTCCACATTCCTACTTCCTCCGTGATTCGCTCAGTCCAGTCCAGGCAAGACC 1945

QY 261 AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValValLysHis 280
DB 1946 AAGAGAGAAAGAAACATAGAGTCTTCCACCCGCAAGACCTCAGCCAGCTATCTGCCGCC 2005

QY 281 LysAspAlaLysIleArgValGlnAlaIleAspAspArgTyrTyrSerSerSerTrpSerAsp 300
DB 2006 AAAAATGCCAGCATTAAGCGTGGGGCCGACGAGCCGCTACTATAGCTCATCTGGAGCGAA 2065

QY 301 TrpAlaSerValSerCysSerGlyGly-----GlyGlyGly 312
DB 2066 TGGGCATCTGGCCCTGAGTGGTGGCGGTGGAACGGTGGCGGTGCAAGCGGTGGCGGT 2125

QY 313 GlySer-----ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeu 330
DB 2126 GGAAGCCATGAGAGAAACCTCCCGCTGGCCACTCCAGACCCAGAGATGTTCCCATGCTT 2185

QY 331 AsnHisSerGlnThrLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThr 350
DB 2186 CACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAACGCCAGACAAACT 2245

QY 351 LeuGluLeuTyrSerCysThrSerGluGluLysPheHisGluAspIleThrLysAspLys 370
DB 2246 CTAGAATTTTACCCCTTGACCTTGTGAAGATGATCATGAAGATATACCAAAATATAA 2305

QY 371 ThrSerThrValGlnAlaCysLeuProLeuGluLeuThrMetAsnGlnSerCysLeuAla 390
DB 2306 ACCAGCACAGTGGAGGCTGTTTACCATTTGCAATTAACCAAGAAATGAGATGGCTTAAT 2365

QY 391 SerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPhe 410
DB 2366 TCCAGAGAGACCTTCTTCAATAAATGAGGATGGCTGCGCTCCAGAAAGACCTCTTT 2425

QY 411 MetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPhe 430
DB 2426 ATGATGGCCCTGCTGCTTAGTAATTAATGAAGCTTGAAGATGTACAGGTGAGAGTTC 2485

QY 431 LysAlaMetAsnAlaLysLeuLeuMetLysProLysArgGlnIlePheLeuAspGlnAsn 450

Db 2486 AAGACCATGATGCAAGCTTCGATCGATCTAAGAGGAGATCTTCTAGATCAAAAC 2545
Qy 451 MetLeuThrAlaIleAspGluLeuGlnAlaLeuSnpheSnsrValThValPro 470
Db 2546 ATGCTGACGCTTATTGATGAGCTGATCGAGCCCTGAATTCAACAGTGAAGCTGCCA 2605
Qy 471 GlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuGlnLeu 490
Db 2606 CAAAAATCTCCCTTGAAGAACCGGATTTTATTAATCAATCAACGCTCTGATCTT 2665
Qy 491 LeuHisAlaPheArgIleAlaGlnAlaValThrIleAsnArgMetMetSerTyrLeuAsnSer 510
Db 2666 CTTCATCTGCTTCAAGAAATTCGGCGAGTACTATGATGAGAGTACTATCTGAATGCT 2725
Qy 511 Ser 511
Db 2726 TCC 2728
RESULT 13
US-09-828-825-9
; Sequence 9, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Seewoo
; APPLICANT: Kim, Han-soo
; TITLE OF INVENTION: Anti-cancer Cellular Vaccine
; FILE REFERENCE: 84906-102
; CURRENT APPLICATION NUMBER: US/09/828, 825
; CURRENT FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: KR00-43498
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 8638
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
; NAME/KEY: misc_feature
; LOCATION: (1) ..(750)
; OTHER INFORMATION: CMV enhancer and promoter
; NAME/KEY: misc_feature
; LOCATION: (890) ..(1002)
; OTHER INFORMATION: Intervening sequence
; NAME/KEY: promoter
; LOCATION: (1067) ..(1085)
; OTHER INFORMATION: T7 RNA polymerase promoter
; NAME/KEY: misc_feature
; LOCATION: (1090) ..(1984)
; OTHER INFORMATION: Human B7.1 (1090-1954 is coding sequence)
; NAME/KEY: RBS
; LOCATION: (2013) ..(2593)
; OTHER INFORMATION: IRES sequence
; NAME/KEY: misc_feature
; LOCATION: (2657) ..(4293)
; OTHER INFORMATION: Human IL12.4 (coding sequence is 2640-4283, 33
; OTHER INFORMATION: amino acid linker at 3606-3706)
; NAME/KEY: CDS
; LOCATION: (2640) ..(4283)
; OTHER INFORMATION: IL12.4 coding sequence (33 amino acid linker)
; NAME/KEY: promoter
; LOCATION: (4392) ..(4413)
; OTHER INFORMATION: T3 RNA polymerase promoter
; NAME/KEY: polyA_signal
; LOCATION: (4423) ..(4644)
; OTHER INFORMATION: SV40 fragment containing polyadenylation signal
; NAME/KEY: rep_origin
; LOCATION: (4739) ..(5194)
; OTHER INFORMATION: fl origin of replication
; NAME/KEY: misc_feature
; LOCATION: (5258) ..(5625)

; OTHER INFORMATION: Neo r expression cassette
; NAME/KEY: misc_feature
; LOCATION: (7036) ..(7896)
; OTHER INFORMATION: Ampicillin resistance
US-09-828-825-9
Alignment Scores:
Pred. No.: 1,12e-258 Length: 8638
Score: 2304.00 Matches: 439
Percent Similarity: 88.59% Conservative: 27
Best Local Similarity: 83.46% Indels: 44
Query Match: 85.56% Gaps: 16
DB: 10 Gaps: 3
US-09-917-265-67 (1-511) x US-09-828-825-9 (1-8638)
Qy 1 IleTprGluLeuGlnLysAspValTyrValGlnLeuAspTrrPheSnsrValPro 20
Db 2706 ATATGGAACTGAAGAAAGATGTTTATGTCGTGAATGGATTGGATTCGGATGCCCT 2765
Qy 21 GlyLysMetValIleuThrCysHisThrProGluGluAspPheThrTrrPheSer 40
Db 2766 GGAAGAAATGCTGCTCTCCTCCTGACCTGACACCCCTGAAGAAAGATGATCACTGACCTTG 2825
Qy 41 AlaGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
Db 2826 GACCAGAGCAGTGAAGCTTGAAGCTCTGCGCAAAACCTGCACATCCAAAGTCAAGAGATT 2885
Qy 61 GlyAspAlaGlyLysLysThrCysHisLysGlyGlyLysValLeuSerArgSerLeuLeu 80
Db 2886 GGAGATGCTGGCCAGTACACCTGTCACAAAGAGGCGAGGTTCTTAAGCATTCGCTCTG 2945
Qy 81 LeuIleHisLysLysGluAspGlyIleTrrPheThrAspIleLeuLysGluGlnLysGlu 100
Db 2946 CTCGCTTCACAAAGCAAGATGGAATTTGCTCAGATGATTTTAAAGACCAAGAAAGAA 3005
Qy 101 SerLysAsnLysIlePheLeuLysCysGlnAlaLysAsnTrrSerGlyArgPheThrCys 120
Db 3006 CCCAAATTAAGACCTTTCTTAAGATGCGAGCCCAAAATTAATTCGACCTTCACCTGC 3065
Qy 121 TrrTrrPheThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
Db 3066 TGGTGGCTGACGCAATCACTACTGATTGACATTCAAGTCCAAAGACCAAGAGCTCT 3125
Qy 141 SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgVal 160
Db 3126 TCTGACCCCAAGAGGAGTGGAGCTGCGAGCTGTACACTCTCTCAGAGAGAGTCAAGAGG 3185
Qy 161 AspAsnArgAspTrrLysLysTyrThrValGlnCysGlnGluLysSerAlaCysProSer 180
Db 3186 GACAAACAAAGAGATAT--GAGTACTCAGTGAAGTCCAGGAGGACAGTGGCTCCAGCT 3242
Qy 181 AlaGluGlnSerLeuProIleGlnValAlaValAspAlaIleHisLysLeuLysTyrGlu 200
Db 3243 GCTGAGAGAGTGTGCCCATTTGAGTCACTGATGATGATGATGATGATGATGATGATGAT 3302
Qy 201 AsnTrrThrSerSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeu 220
Db 3303 AACTACACGACGAGCTTCTTCATCAGGACATCATCAAAACCTGACCAACCAACCAACTTG 3362
Qy 221 GlnLeuLysProLeuLysAsnSerArgHisValGlnValSerTrrPheGluTrrProAspThr 240
Db 3363 CACTGAAAGCAATTAAGAAATTCCTCGCAGCTGAGAGTGAAGTGGAGTGAAGTGAAGTGA 3422
Qy 241 TrrSerThrProHisSerTrrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 260
Db 3423 TGGAGTACTCCACATTCCTACTCTCCCTGACATTCCTGCTTGAAGTCCAGGCAAGAGAGC 3482
Qy 261 AsnArgGluLysLysAspArgLysValAspLysThrSerAlaLysValLysHis 280
Db 3483 AAGAGCAAAAGAAAGATGAGTCTTCACCGCAAGACCTCACACGAGGATGATCTGCCGC 3542
Qy 281 LysAspAlaLysIleArgValGlnAlaArgAspArgTrrTrrSerSerSerTrrSerAsp 300


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Db      3543 AAAAATGCCACCATTAGCGTGGCGGCCAGGACCGCTACTATAGCTCATCTTGAGCGAA 3602
OY      301 TTPAlaSerValSerCysSerGlyGly----- 309
Db      3603 TGGGATCTCTGCTCCCTGCAGTGTGTGGCGGTGGAACGGCGGCGGGAACCGTGGCGGT 3662
OY      310 -----GlyGlyGlyGlySer-----ArgAsnLeuProThrProThrProSerProGly 325
Db      3663 GCAACGGGTGGCGGTGGAAGCCCATGGAAGAACCTCCCGTGGCAGCTCCACACCGAGGA 3722
OY      326 MetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaValSerAsnThrLeuGln 345
Db      3723 ATGTTCCCATCTGCTTACACCACTCCCAAAACCTGCTGAGGCGCGCTCAGCAACATGCTCCAG 3782
OY      346 LysAlaArgGlnThrLeuGlnLeuLeuThrSerCysThrSerGlnGlnLysAspHisGlnLysP 365
Db      3783 AAGGCCAGACAACTCTAGAAATTTTACCTTGCACCTTCTGAGAGATTCATCATGAAGAT 3842
OY      366 11ethrLysAspLysThrSerThrValGlnAlaCysLeuProLeuGlnLeuThrMetAsn 385
Db      3843 ATCACAAAAGATAAACACGACACACTGGAGGCTGTTTACCACTTGGAAATTAACCAAGAT 3902
OY      386 GluSerCysLeuAlaSerArgGlnLysLeuLysThrAsnGlySerCysLeuAlaSer 405
Db      3903 GAGACTGCTGCTAAATTCACAGAGACACTTTCATCACTAAATGGAGATTCGCTGCTCC 3962
OY      406 GlyLysAlaSerPheMetThrValLeuLeuLeuSerSer11ethrGlnAspLeuLysMet 425
Db      3963 AGAAAGACCTCTTTATATATGACCCCTGTCCTTACTACTATTTATGAAGACTTGAAGATG 4022
OY      426 TyrGlnMetGlnPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnLys 445
Db      4023 TACACGGTGGAGTTCAAGACCATGATGCACAAAGCTTTCATGATGATCCCTTAAGAGCGCATC 4082
OY      446 PheLeuAspGlnAsnMetLeuThrAlaLeuAspGlnLeuGlnAlaLeuAsnPheAsn 465
Db      4083 TTTCTAGATCAAAACATCTGCGACGTATTGATGAGTCAGTCAGCGCCCTGAATTTCAAC 4142
OY      466 SerValThrValProGlnLysSerSerLeuGlnGlnProAspPheThrLysThrLysIle 485
Db      4143 AGTGAGACTGTGCCCAAAATCCCTCTGAAGAACCGGATTTTATAAACCTVAAAATTC 4202
OY      486 LysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMet 505
Db      4203 AAGCTCTGCATACCTTCTCATGCTTTCAGAAATTCGGGACAGTCACATTGATAGATGATG 4262
OY      506 SerTyrLeuAsnSerSer 511
Db      4263 AGCTATCTGAATTCCTTCC 4280
RESULT 14
US-09-828-825-11
: Sequence 11, Application US/09628825
: Patent No. US20020018767A1
: GENERAL INFORMATION:
: APPLICANT: Kim, Han-soo
: TITLE OF INVENTION: Anti-cancer Cellular Vaccine
: FILE REFERENCE: 84906-102
: CURRENT APPLICATION NUMBER: US/09/828, 825
: PRIOR FILING DATE: 2001-04-10
: PRIOR APPLICATION NUMBER: KR00-43498
: NUMBER OF SEQ ID NOS: 16
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 11
: LENGTH: 8659
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)..(750)

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: OTHER INFORMATION: CMV enhancer and promoter
: NAME/KEY: promoter
: LOCATION: (1067)..(1085)
: OTHER INFORMATION: T7 RNA polymerase promoter
: NAME/KEY: misc_feature
: LOCATION: (1090)..(2756)
: OTHER INFORMATION: Human IL12.4 (coding sequence 1103-2746, 19 amino
: NAME/KEY: CDS
: LOCATION: (1103)..(2746)
: OTHER INFORMATION: Human IL12.4 (19 amino acid linker)
: NAME/KEY: RBS
: LOCATION: (2782)..(3362)
: OTHER INFORMATION: IRES sequence
: NAME/KEY: misc_feature
: LOCATION: (3399)..(4293)
: OTHER INFORMATION: Human B7.1 sequence
: NAME/KEY: promoter
: LOCATION: (4413)..(4434)
: OTHER INFORMATION: T3 RNA polymerase promoter
: NAME/KEY: polyA_signal
: LOCATION: (4444)..(4665)
: OTHER INFORMATION: SV40 fragment containing polyadenylation signal)
: NAME/KEY: rep_origin
: LOCATION: (4760)..(5215)
: OTHER INFORMATION: fl origin of replication
: NAME/KEY: misc_feature
: LOCATION: (5279)..(6646)
: OTHER INFORMATION: Neo r expression cassette
: NAME/KEY: misc_feature
: LOCATION: (7057)..(7917)
: OTHER INFORMATION: Ampicillin resistance gene
: OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-828-825-11

Alignment Scores:
Pred. No.: 1,12e-258 Length: 8659
Score: 2304.00 Matches: 439
Percent Similarity: 88.59% Conservative: 27
Best Local Similarity: 83.46% Mismatches: 44
Query Match: 85.56% Indels: 16
Gaps: 3

US-09-917-265-67 (1-511) x US-09-828-825-11 (1-8659)
OY      1 11ethrGlnLeuGlnLysAspValThrValGlnLeuAspTTPRHisProAspAlaPro 20
Db      1169 ATATGGAACTGAAAGAAAGATGTTATGTCGTAGAAATGGATTCGATCCGATGCCCT 1228
OY      21 GlyGlnMetValLeuThrCysHisThrProGlnGlnAspPheThrTTPRHisSer 40
Db      1229 GCAGAAATGGTGCTCTCACTGACACCCCTGAAGAGATGATATACCTGGACCTTG 1288
OY      41 AlaGlnSerSerGlnValLeuGlnLysSerGlyThrLeuThrIleGlnValLysGlnPhe 60
Db      1289 GACCAAGACAGTGAAGAGTCTTAGGCTCTGCAAAACCCAGACCATCAAGTCAAGAGTTT 1348
OY      61 GlyAspAlaGlyGlnThrThrCysHisLysGlyGlyLysValLeuSerArgSerLeuLeu 80
Db      1349 GCAGATGCTGGCACTACACCTGACCAAAAGAGCGAGGTTCATGAAGCATTCGCTCCG 1408
OY      81 LeuIleHisLysLysGlnAspGlyThrPheSerThrAspIleLeuLysGlnLysGln 100
Db      1409 CTGCTTCAAAAAGGAAGATGAGATTGGTCCACTGATATTTTAAAGACCAAGAAATA 1468
OY      101 SerLysAsnLysIlePheLeuLysCysGlnAlaLysAsnTyrSerGlyArgPheThrCys 120
Db      1469 CCCAAAATAATAGACCTTTCTTAAGATGCCAGGCCAAGATTAATTCGAGCGTTTACCTGCC 1528
OY      121 TTPRTPLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
Db      1529 TGGTGGCTGACGACGACATCAGTACGATTTGACATTCAGTGCACAAAGCAGCAGGCGCT 1588

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QY 141 SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgVal 160
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 Db 1589 TCTGACCCCAAGGGGTGACGTGGGAGCTGCTACCTCTCTGAGAGAGAGTACAGAGG 1648
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 QY 161 AspAsnArgAspTyrLeuSerTyrThrValGluCysGlnGluSerAlaCysProSer 180
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 Db 1649 GACACACAGAGGATAT--GAGTACTCAGTGGAGTGGACGAGGACAGTGCCTGCCAGCT 1705
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 QY 181 AlaGluSerLeuProLeuGluValAlaValAspAlaLeuHisLeuLysLeuTyrGlu 200
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 Db 1706 GCTGAGAGAGTGTGCCCATGTAGCATGTGATGCCGTCCGTCACAGGCTCAAGTATGAA 1765
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 QY 201 AsnTyrThrSerSerPhePheIleArgAspIleLeuSerProAspProPheThrAsnLeu 220
 |||||||
 Db 1766 AACACACACAGCAGCTCTCTCATCAGGACATCATCAAACTGACCCACCCCAACACTTG 1825
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 QY 221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerPheGluTyrProAspThr 240
 |||||||
 Db 1826 CAGCTGAGCCATTAAAGAAATCTCGGACAGTGGAGTCAAGTGGAGTACCTGACACCC 1885
 |||||||
 QY 241 TrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 260
 |||||||
 Db 1886 TGGAGTACTCCACATTCCTACTCTCCCTGACATTCGCTGACGTCAGGCCAGGCAAGAC 1945
 |||||||
 QY 261 AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValLysHis 280
 |||||||
 Db 1946 AAGGAGAGAAAGAAAGATAGAGTCTCACCGACAGACCTCAGCCAGGTCATCTGCCGC 2005
 |||||||
 QY 281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsp 300
 |||||||
 Db 2006 AAAAATGCCAGCATTTACGCTGGGGGCCAGAGCCGCTACTACTACTCTTGGAGCGAA 2065
 |||||||
 QY 301 TrpAlaSerValSerCysSerGlyGly----- 309
 |||||||
 Db 2066 TGGGCATCTGTGCCCTCAGTGTGGGTGAGAGCCGTGAGGAGCGGTGAGAGCGGTGGCGGT 2125
 |||||||
 QY 310 -----GlyGlyGlyGlySer-----ArgAsnLeuProThrProThrProSerProGly 325
 |||||||
 Db 2126 GGAAGCGGTGGCGGTGGAGGCCCATGAGAAACCTCCCGTGGCCACTCCAGACCCAGGA 2185
 |||||||
 QY 326 MetPheGlnLysLeuAsnHisSerGlnThrLeuLeuArgAlaValSerAsnThrLeuGln 345
 |||||||
 Db 2186 ATGTTCCTCATGCTTACACCATCCCAAAACCTGCTGAGGGCCGTCACCAACATGCTCCAG 2245
 |||||||
 QY 346 LysAlaArgGlnThrLeuGluLeuLeuTyrSerCysThrSerGluGluIleAspHisGluAsp 365
 |||||||
 Db 2246 AAGGCCAGACAACTAGAAATTTTACCCTTGACCTTCGAAAGAGATTGATCATGAGAT 2305
 |||||||
 QY 366 IleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsn 385
 |||||||
 Db 2306 ATCACAATAAGATAAACACGACACAGTGGAGCCGTTTACCATTTGAATTAACCAAGAAAT 2365
 |||||||
 QY 386 GluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSer 405
 |||||||
 Db 2366 GAGAGTTGCCTAAATTTCCAGAGACCTCTTTCACTAATGGAATTTGCTTGGCTTCC 2425
 |||||||
 QY 406 GlyLysAlaSerPheMetThrValLeuCysLeuSerIleTyrGluAspLeuLysMet 425
 |||||||
 Db 2426 AGAAAGACCTCTTTATGATGGCCCTGCTAGTAGTATTTATGAAGACTTGAACATG 2485
 |||||||
 QY 426 TyrGlnMetGluThrLeuLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIle 445
 |||||||
 Db 2486 TACCAAGTGGAGTTCAAGACCATGAATGAAAGCTTCTGATGATCTTAAGAGGACATC 2545
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 QY 446 PheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsn 465
 |||||||
 Db 2546 TTTCTAATCAAAACATGCTGGCAGATTATGATGAGCTGATGCCAGGCCCTGAATTTTCAAC 2605
 |||||||
 QY 466 SerValThrValProGlnLysSerSerLeuGluGluProAspPheTyrLysIle 485
 |||||||
 Db 2606 AGTGAGACTGTCGCACAAATAATCCTCCCTTGAAGAACCGGATTTTATAAACAATAATC 2665
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 QY 486 LysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMet 505

Db 2666 AAGCTCGCATCTTCTTCATGCTTTCAGAAATTCGGGACGACTGACTATTGATGATGATG 2725
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 QY 506 SerTyrLeuAsnSerSer 511
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 Db 2726 AGCTATCTGAATGCTTCC 2743
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 RESULT 15
 US-09-828-825-1
 : Sequence 1, Application US/09828825
 : Patent No. US20020018767A1
 : GENERAL INFORMATION:
 : APPLICANT: Lee, Seewoo
 : APPLICANT: Kim, Han-soo
 : TITLE OF INVENTION: Anti-cancer Cellular Vaccine
 : FILE REFERENCE: 84906-102
 : CURRENT APPLICATION NUMBER: US/09/828,825
 : CURRENT FILING DATE: 2001-04-10
 : PRIOR APPLICATION NUMBER: KR00-43498
 : PRIOR FILING DATE: 2000-07-27
 : NUMBER OF SEQ ID NOS: 16
 : SOFTWARE: PatentIn Ver. 2.1
 : SEQ ID NO 1
 : LENGTH: 8578
 : TYPE: DNA
 : ORGANISM: Artificial Sequence
 : FEATURE:
 : NAME/KEY: enhancer
 : LOCATION: (1)..(659)
 : OTHER INFORMATION: CMV IE
 : NAME/KEY: promoter
 : LOCATION: (669)..(750)
 : OTHER INFORMATION: CMV IE
 : NAME/KEY: promoter
 : LOCATION: (1067)..(1085)
 : OTHER INFORMATION: T7 RNA Promoter
 : NAME/KEY: mRNA
 : LOCATION: (1090)..(1984)
 : OTHER INFORMATION: Human B7.1 (1090-1956 is coding sequence)
 : NAME/KEY: RBS
 : LOCATION: (2013)..(2593)
 : OTHER INFORMATION: IRES sequence
 : NAME/KEY: mRNA
 : LOCATION: (2627)..(4263)
 : OTHER INFORMATION: Human IL12.0 (2640-4223 coding sequence, flexible
 : OTHER INFORMATION: linker at 3624-3629)
 : NAME/KEY: rep.origin
 : LOCATION: (4352)..(4431)
 : OTHER INFORMATION: T3 RNA polymerase promoter
 : NAME/KEY: polyA_signal
 : LOCATION: (4362)..(4583)
 : OTHER INFORMATION: SV40 fragment containing polyadenylation signal
 : NAME/KEY: misc.feature
 : LOCATION: (5197)..(6564)
 : OTHER INFORMATION: Neo r expression cassette
 : NAME/KEY: misc.feature
 : LOCATION: (6975)..(7835)
 : OTHER INFORMATION: Ampicillin resistance
 : OTHER INFORMATION: Description of Artificial Sequence: Plasmid
 : NAME/KEY: CDS
 : LOCATION: (2640)..(4223)
 : OTHER INFORMATION: IL 12.0 coding sequence - 2 amino acid linker at
 : OTHER INFORMATION: 3624
 : US-09-828-825-1
 Alignment Scores:
 Pred. No.: 2,79e-255 Length: 8578
 Score: 2275.00 Matches: 432
 Percent Similarity: 89.82% Conservative: 27
 Best Local Similarity: 84.54% Mismatches: 46

Query Match: 84.48% Indels: 6
DB: 10 Gaps: 2

US-09-917-265-67 (1-511) x US-09-828-825-1 (1-8578)

QY 1 ILeuPGLuLeuGluLysAspValTyrValValGluLeuAspTrpHisProAspAlaPro 20
DB 2706 ATATGGCACTGAAAGAAAGATGTTATGCTGAGAAATGATGATGATCGGATGCCCT 2765
QY 21 GlycIuMeValValLeuThrCysHisThrProGluGluAspSerIleThrTrpThrSer 40
DB 2766 GGAGAAATGCTGCTCCACCTGACCTGACACCCCTGAAGAAGATGATACCTGACCTTG 2825
QY 41 AlaGlnSerSerGluValLeuGluSerGlyLysThrLeuThrIleGluValLysGluPhe 60
DB 2826 GACCAGACGACTGACCTTATAGCTCTGCAAAACCTGACCATCCAAAGTCAAGAGTTT 2885
QY 61 GlyAspAlaGluGlnTyrThrCysHisLysGlyGlyLysValLeuSerArgSerLeuLeu 80
DB 2886 GGAGATGCTGGCCAGTACACCTGTACAAAGAGGAGGAGTTCTTAAGCCATTCGCTCTG 2945
QY 81 LeuIleHisLysLysGluAspGlyIleThrSerThrAspIleLeuLysGluGlnLysGlu 100
DB 2946 CTGCTTCAACAAAGAGATGGAATTTGCTCCACTGATATTAAAGACACAGAAAGAA 3005
QY 101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
DB 3006 CCCAAATTAAGACCTTCTTAAGATGCGAGCCCAAGAAATTATCTGACGTTTACCTGC 3065
QY 121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheSerValLysSerSerArgGlyPhe 140
DB 3066 TGGTGGCTGACACATGACTGATGATTTGACATGCTGTCMAAGCAGCAGAGGCTCT 3125
QY 141 SerAspProGlnGlyValThrCysGlyAlaValThrLeuSerAlaGluArgValArgVal 160
DB 3126 TCTGACCCCAAGGGGTGACGTGCGAGCTGCTACACTCTCTGCAGAGAGATCGAGAGG 3185
QY 161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProSer 180
DB 3186 GACAAACAAAGAGTAT--GAGTACCTGAGTGGAGTCCAGAGAGACAGTGCCTGCCACT 3242
QY 181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
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QY 201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProThrAsnLeu 220
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QY 221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
DB 3363 CAGCTGAAGCCATTAAAGATTCTCGGCAGGTGAGGTGAGGTGAGGTGAGGTGAGGTG 3422
QY 241 TrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnAlaGlnGlyLysAsn 260
DB 3423 TGGAGTACTCCACATTCCTACTCTCCCTGACATTCCTGGCTCAGGTCAGGCGCAGAG 3482
QY 261 AsnArgGluLysLysAspArgLeuCysValAspLysThrSerAlaLysValValCysHis 280
DB 3483 AAGAGAGAAAGAAAGTAGAGTCTTCACCGACACAGACCTCAGCCAGGTCACTGCCGC 3542
QY 281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsp 300
DB 3543 AAAAATGCGACATTTACCTGCGGCGCCAGAGCCGCTACTATAGCTCATCTTGAGCGAA 3602
QY 301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyLysSerArgAsnLeuProThrPro 320
DB 3603 TGGCATCTGCTGCTCCAGTCCATGC-----AGAAACCTCCCGTGGCC 3647
QY 321 ThrProSerProGlnMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaVal 340
DB 3648 ACTCCAGACCCAGAGATCTTCATGCTTACACACTCCCAAAACCTGCTGAGGCGCGCTC 3707

QY 341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyrSerCysThrSerGluGlu 360
DB 3708 AGCAACATGCTCCAGAAAGGCCAGACAAACTGTACAAATTTTAACTCTGCACCTTGAGAG 3767
QY 361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
DB 3768 ATTGATCATGAAAGATATCAAAAGATAAACACGACACAGTGGAGGCGCTGTTACCATG 3827
QY 381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
DB 3828 GAATTAACCAAGAAAGAGATTGCTTAATTCACAGAGACTCTTTATATACATAGAGCG 3887
QY 401 SerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeuCysLeuSerSerIleTyr 420
DB 3888 AGTTGCTGCTGCCCAAGAAAGACCTTTTATGATGAGCCCTGCTTATGATATTAT 3947
QY 421 GluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
DB 3948 GAAGACTTGAAGATGTACACAGGTGAGGTTCAGACCATGAATGCAAAAGCTTCTGATGAT 4007
QY 441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuGln 460
DB 4008 CCTTAAGAGCAGATCTTTCTAGATCAAAACATGCTGCGAGTTATGATGACCTGATCGAG 4067
QY 461 AlaLeuAsnPheAsnSerValThrValProGlnLysSerSerLeuGluGluProAspPhe 480
DB 4068 GCCCTGATTTTCAACAGTGAAGACTGTGCCCAAAATCTCTCCCTGAAGACCGGATTTT 4127
QY 481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
DB 4128 TATTAACCTAAATCAAGCTCTGCATACCTTCTTCATGCTTTCAGATTCGGCAGAGACT 4187
QY 501 IleAsnArgMetSerTyrLeuAsnSerSer 511
DB 4188 ATTGATGAGTGAATGAGCTATCTGAATGCTTCC 4220

Search completed: July 17, 2003, 09:57:24
Job time : 379.106 secs

